

Forest Modeling Exercise

Process-based and empirical modeling exercises

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1 Overview

This document contains the instructions and solutions of the modeling group assignments. First, you will find the section for the process model approach (Section 2) and after that the section for the empirical modelling (Section 3). This document is very long because it describes all the exercises and solutions step by step.

You will work per groups in the four groups established at the beginning of the week. Each of the four groups will be divided internally in four subgroups (A-D). Each subgroup (A-D) inside each group (1-4) will address one question that will have to be answered using one approach. In the table below you can find a link to the section to each question e.g. group 1 subgroup A will answer the questions “**How are biodiversity indices changing in time and across the simulated scenario(s) on Plot 1?**” using the approach based on the model iLand and will have the full instructions and solution in Section 2.2.7.

Please, always ask your coach if you do not know what is the section where you should be working in.

| Group | Subgroup Question | Question | Approach | Go to |
|-------|----------------------|---|----------|---------------|
| 1 | A | How are biodiversity indices changing in time and across the simulated scenario(s) on Plot 1? | iLand | Section 2.2.7 |
| 1 | B | How the species distribution and total living biomass C content changing in time on Plot 1? | iLand | Section 2.2.8 |
| 1 | C | Does a more diverse forest in structure and composition have more Bryophyte species? | GLM | Section 3.4.4 |

1 Overview

| Group | Subgroup Question | Question | Approach | Go to |
|-------|----------------------|--|----------|----------------|
| 1 | D | Is the number of Bryophyte species affected by forest management type and the forest structural diversity? | GLM | Section 3.4.5 |
| 2 | A | How are biodiversity indices changing in time and across the simulated scenario(s) on Plot 2? | iLand | Section 2.2.9 |
| 2 | B | How the species distribution and total living biomass C content changing in time on Plot 2? | iLand | Section 2.2.10 |
| 2 | C | Does a more diverse forest in structure and composition have more bird species? | GLM | Section 3.4.6 |
| 2 | D | Is the number of bird species affected by forest management type and the forest structural diversity? | GLM | Section 3.4.7 |
| 3 | A | How are biodiversity indices changing in time and across the simulated scenario(s) on Plot 3? | iLand | Section 2.2.11 |
| 3 | B | How the species distribution and total living biomass C content changing in time on Plot 3? | iLand | Section 2.2.12 |
| 3 | C | Is the presence of the Great spotted woodpecker affected by forest density? | BRT | Section 3.4.8 |

| Group | Subgroup Question | Question | Approach | Go to |
|-------|----------------------|---|----------|----------------|
| 3 | D | Is the presence of the Great spotted woodpecker affected by forest diversity? | BRT | Section 3.4.9 |
| 4 | A | How are biodiversity indices changing in time and across the simulated scenario(s) on Plot 4? | iLand | Section 2.2.13 |
| 4 | B | How the species distribution and total living biomass C content changing in time on Plot 4? | iLand | Section 2.2.14 |
| 4 | C | Is the presence of the Eurasian treecreeper affected by forest density? | BRT | Section 3.4.10 |
| 4 | D | Is the presence of the Eurasian treecreeper affected by forest management? | BRT | Section 3.4.11 |

1.1 Data and model

We provide all data, model and scripts for the exercises. However if you will use the model iLand for your research in the future please get in contact with the model developers at the Technical University Munich: Werner Rammer (werner.rammer@tum.de) and Rupert Seidl (rupert.seidl@tum.de). Regarding the biodiversity data used in the empirical modeling part please contact Jeřýk Hofmeister at the Czech University of Life Sciences Prague (jenyk.hofmeister@email.cz) if you are interested in using this data further.

1.1.1 The project folder

To do this exercise you first need to download the project folder. You can download the complete project folder from this link:

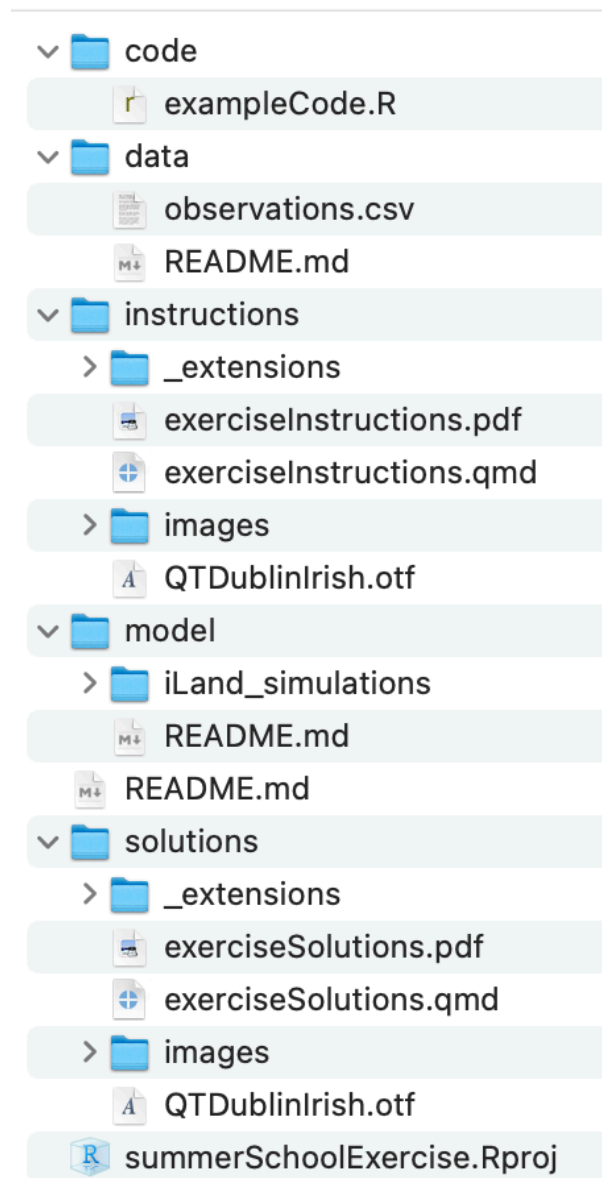
1 Overview

https://drive.google.com/drive/folders/1IXfJNIXw32lp1q4AmEZzt0nqgE3HDRIx?usp=drive_link.

In this project you will find the following folders and files:

- **summerSchoolExercise.Rproj**: this is the RStudio project file that you should open. This file contains various project options and is used as a shortcut for opening the project directly from the file system.
- **code**: this folder is where you should save the R scripts .
- **data**: this folder contains the data used in the empirical modeling.
- **instructions**: this folder is where you can find the pdf and qmd (source code document used to compile the pdf) with the step by step instructions for the exercises without the solutions; this folder also contains all the extensions and images needed to compile the document.
- **model**: this folder is where you will find the folder **iLand_simulations** with all the files needed to run the process based exercise.
- **solutions**: this folder is where you can find this document in pdf and in the qmd; this folder also contains all the extensions and images needed to compile the document

Our recommendation is that you follow this folder structure and that you use the **summerSchoolExercise.Rproj** to open RStudio. If you decide to organize things in a different way then you will have to change all the relative paths in the codes provided in the solutions documentation. The folder you have downloaded should look like this:



This project is also available in a github repository. You can clone via git the project in here:

<https://github.com/oldiya/summerSchoolExercise>

However in github the data file `data/observations.csv` and the folder `model/iLand_simulations` are missing and have to be downloaded separately (read the `README.md` files in these folders to learn how to download them).

2 Process-based modeling

2.1 iLand model

2.1.1 General

iLand is an ecosystem model that simulates forest landscape dynamics, including growth, regeneration, disturbance dynamics, and management in a spatially explicit manner. The main entity in the model is a tree, for which the demographic processes are simulated. Processes at the stand and landscape scale constrain the dynamics of individual trees and thus allow for the scaling of tree-scale processes to large areas. The model explicitly simulates tree competition for resources such as light, water, and nutrients. A light use efficiency approach is used to simulate the production physiology. Carbon starvation is used as a process oriented indicator of tree stress, which can result from competition for resources as well as suboptimal environmental conditions for tree growth (e.g., drought).

iLand's mechanistic representation of forest disturbances and vegetation dynamics, as well as the climatic sensitivity of these processes, makes it well suited for the research of disturbance dynamics under climate change. Additionally, flexible implementation of management operations, which include planting after harvests or natural disturbances, thinning, harvesting, and post-disturbance salvaging, allows for testing the effects of various disturbance management strategies.

A detailed model documentation is available on iLand WIKI page:

<https://iland-model.org/iLand+Hub>

2.1.2 Inputs and outputs of iLand

iLand needs information in specific formats about environment (mainly climate and soil) and trees. Daily climate data is needed (<https://iland-model.org/ClimateData>) for minimum, maximum temperature, precipitation, vapor pressure deficit and radiation. Soil depth and soil texture (sand, silt, clay %) information are needed. The soil is represented as a one-layer bucket, no depth-dependent information is needed. The model needs species-specific parameters (<https://iland-model.org/species+parameter>) that are describing the behavior of each tree species (growth, mortality, competition etc.). Currently there are 31 species parametrized for iLand, and the species specific parameters

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are stored in a database that is an input for the model. The parameters were previously calibrated for European conditions (species_param_europe.sqlite). iLand uses short codes for species derived from the latin names (e.g. Picea Abies - piab, Fagus Sylvatica - fasy, ..) Information on the initial forest is also required to start a simulation.

As iLand is a landscape scale model, both climate, soil and tree information need to be set spatially. For larger areas environmental maps can be set using a 100x100m resolution grid, a so called resource grid with resource units, and tree information can be set by maximum 10x10m resolution grid on a stand grid using stand IDs. There are more options how to initialize a landscape in iLand depending on our spatial scales and available data (<https://iland-model.org/initialization>).

In our case now we will use iLand in a stand-scale mode (called torus), where we simulate only one 100x100m pixel, 1 ha forest area. We will use single-tree initialization method, where we set the x-y coordinates of the trees inside the 100x100m area, tree species, dbh and height of each tree. From inventory we have data for the a circle with 13.82m radius. We generated trees for the 1ha area based on the plot-data. See details in the Appendix Section 5 on this document.

The output of the model is an sqlite database file. The output produced by the model is highly versatile and needs to be set in advance of the simulation which output tables we would like to get.

2.1.3 How to work with the model

Simulations are driven by one xml file, the project file. After starting iland.exe, we should call the project file, load the initial forest and then run the simulation for the required length of period. iLand comes with a graphical interface where you can visualize single trees and many other things: <https://iland-model.org/iLand+viewer>

2.2 Exercises

Your group will work with the plot which you measured and worked with in the previous days (Plot1-Plot4). The 2 process based subgroups will do the same modeling experiment, just addressing different questions based on the results (see the 2 questions below).

You will simulate the growth and development using the process-based model, iLand. The task is to simulate your study plot for 100 years under reference conditions and one/two simplified scenarios that you could define upon your ideas. You can define scenarios assuming different temperature, precipitation and CO2 concentration levels (see more details how to do it later below). The questions that you should address forming 2 sub-groups are the following:

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- A) How are biodiversity indices changing in time and across the simulated scenario(s)?
- B) How are the species distribution and total living biomass C content changing in time? Compare 0 year and 100 year status in the reference case and in the case of your scenario(s)

2.2.1 Getting started

Navigate to this folder and download the materials for the process-based modeling exercise: https://drive.google.com/drive/folders/1o2_K3ZN-SnPR44UzZoHj9lFZQu-vU3wg?usp=drive_link

Go to the *iLand_simulations* folder. Here you will find several folders that are the part of the model, others are containing input data for the model and one folder is dedicated for the outputs. Additionally, you will find *iland.exe* and *.xml* files. The *.xml* file is called *project file*. This file is driving the settings of simulations, such as input/output file names, output variables and many other settings. This file is what you need to run in the model.

The xml file structure follows a tree structure, e.g:

```
<root>
  <child>
    <subchild>
      ...
    </subchild>
  </child>
</root>
```

The iLand project file consists of five main sections:

- system: settings like file path, database locations, or logging
- model: main settings of the models: extent (world), site specific setting, used climate, model initialization and management
- modules: settings related to the disturbance modules of iLand
- output: definition of which outputs should be created by the model
- user: this section can be used for user-defined settings

More details about the project file structure and meaning of each record can be found here: <https://iland-model.org/project+file>

We prepared one project file for each group (for each simulation plot). You can right away run it, and then copy-paste and modify it to specify your own scenarios for alternative simulations. You can open a project file in any text editor, but we recommend to use Notepad++ for this (<https://notepad-plus-plus.org/downloads/>).

2.2.2 Explore input files

The following input files are needed and prepared for you to run the model: This is all prepared, YOU DO NOT HAVE TO CHANGE ANYTHING:

- Species parameter file: database/species_param_europe.sqlite Containing the parameters for each species that are driving growth, mortality, establishment and other processes. <https://iland-model.org/species+parameter>

Set in project file:

```
<path>
<home></home>
<database>database</database> < ----- HERE
  <lip>lip</lip>
  <temp>temp</temp>
  <script>scripts</script>
  <init>init</init>
  <output>output</output>
</path>
...
<database>
  <in>species_param_europe.sqlite</in> < ----- HERE
  <out>Output_plot1_4deg_30percdrier.sqlite</out>
  <climate>E-OBSv27_Roznik_46.05_14.45_1961-1990.sqlite</climate>
</database>
```

- Climate file: database/E-OBSv27_Roznik_46.05_14.45_1961-1990.sqlite
Daily climate data for the area based on the E-OBS dataset. <https://iland-model.org/ClimateData> https://surfobs.climate.copernicus.eu/dataaccess/access_eobs.php#datafiles We are using the same climate input for all plots. The E-OBS data is representative for a 0.1x0.1 degree resolution gridbox

Set in project file:

```
<database>
  <in>species_param_europe.sqlite</in>
  <out>Output_plot1_4deg_30percdrier.sqlite</out>
  <climate>E-OBSv27_Roznik_46.05_14.45_1961-1990.sqlite</climate> < ---- HERE
</database>
```

- Environmental file: gis/Environment.txt
The structure of this file is very flexible, more or less columns can be set. If we would have a landscape with larger area with different environments, we could set

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more lines into this file. For now we have only one simulation pixel with 1ha area. Here we set which climate table to use from the climate file (there could be more tables, but now we have only one), what is the soil texture, soil depth. The column names are referring to specific lines in the project file.

For example: if we set here “model.site.pctSand”, the model will use this sand % value instead of the value that we have in the project file under:

```
<model>
...
  <site>
    <availableNitrogen>84</availableNitrogen> < -- kg/ha/yr -->
    <soilDepth>38</soilDepth> < -- in cm -->
    <pctSand>9</pctSand>
    <pctSilt>53</pctSilt>
    <pctClay>38</pctClay>
  ...
</site>
...
</model>
```

Set in project file:

```
<environmentGrid>gis/environment_grid.asc</environmentGrid>
<environmentFile>gis/Environment.txt</environmentFile> < ---- HERE
```

- Environment grid: gis/environment_grid.asc This would specify the map of different environments. Now we have only 1 pixel, with the id of 1. In the previous file we had also id column, this specifies we want to use that environment for our pixel.

Set in project file:

```
<environmentGrid>gis/environment_grid.asc</environmentGrid> < ---- HERE
<environmentFile>gis/Environment.txt</environmentFile>
```

- Tree initialization file: init/Tree_init_plot_1.txt This is the list of the tree with x,y coordinates, species, dbh, height and optionally with age. (age=0 means, there is no data on age, model will generate) There are other options to set initial trees/landscape (e.g. using distributions, number of trees in a given dbh range, or using outputs of another simulation) More details: <https://iland-model.org/initialize+trees>

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```
<initialization>
  <type>single</type>
  <mode>unit</mode>
  ...
  <file>Tree_init_plot_1.txt</file> < ---- HERE
    <saplingFile></saplingFile>
  ...
</initialization>
```

Here we initialize trees taller than 4 meters. Trees smaller than 4m are handled as sapling cohorts in separated input file. Now we do not put there saplings and we do not have a sapling file.

For the sake of simplicity we assume now no-management scenario for all simulations.

NOTE: in the graphical interface you also will not see trees smaller than 4m, because they are not simulated as individuals rather in cohorts. But as regeneration will work, after a while as they grow above 4m, they become individual trees and we can see them also visually and they have own properties (dbh, height, age,...<https://iland-model.org/tree+variables>). More details on saplings: <https://iland-model.org/sapling+growth+and+competition>

Setting the output tables: In the output section you can set which tables you want to enable. Here you can find more info on the structure and variables of each table: <https://iland-model.org/Outputs>

To answer the questions the most straight forward way is to look the *landscape* output and use the *total_carbon_kg* column (total carbon in living biomass (aboveground compartments and roots) of all living trees (including regeneration layer) (kg/ha)). This output table aggregates on the level of landscape x species. Values are always aggregated per hectare. The output is created after the growth of the year. We pre-set the project file to have this output. Additionally we will work with the *tree* output, where individual trees are recorded with position.

```
<output>

  <tree>
    <enabled>true</enabled>
  </tree>

  ...

  <landscape>
    <enabled>true</enabled>
  </landscape>
```

```
</output>
```

2.2.3 Run the model

- Double click on `iland.exe` and wait until the graphical interface opens.
- Load the required project file on the left-hand-side under *iLand project file* by browsing on your computer after clicking on the folder icon next to the box.
- After you selected a project file, click on the “Create Model” on the top-left part of the window with an icon of a Globe.
- Wait until the simulation area is shown in the middle.
- Try out some visualizations on the right hand-side “Visualization options”. e.g individual trees + color by species. Here you can explore the initial stage of the 1 ha simulation area.
- To run the model click on Run Model icon on the top and give 100 years to simulate.
- On the bottom of the window you can follow how fast the model is running and see if it is finished.
- Stage of the last year remains in the simulation area, and you can go to the folder *output* to check your output file.
- When you want to run another simulation, first click on “Destroy”, then start the process again by “Creating Model” for the same project file or loading new project file.

2.2.4 Working with the output

The output database has a *.sqlite* extension. You can explore outputs:

- Open and browse it in the *DB Browser* software that was on the software list. (<https://sqlitebrowser.org/>)
- Load the file into R, where you can make additional data analyses needed to answer the questions in the exercise.

```
# you should change the name of the file according to your group, e.g.
# Group 1 is Output_plot1.sqlite
# Group 2 is Output_plot2.sqlite
# Group 3 is Output_plot3.sqlite
# Group 4 is Output_plot4.sqlite
file <-
  here::here("model/iLand_simulations/output/Output_plot1.sqlite")

sqlite.driver <- RSQLite::dbDriver("SQLite")
```

```
db1 <-  
  RSQLite::dbConnect(sqlite.driver, dbname = file) # connect to the file  
tabs <- RSQLite::dbListTables(db1) # explore the tables in the file  
print(tabs)  
  
landscape <- RSQLite::dbReadTable(db1, "landscape")  
  
RSQLite::dbDisconnect(db1)  
  
summary(landscape)  
head(landscape)
```

There are different output tables in iLand and all have specific structure, column and spatial representation of the records. The landscape output gives information on the whole landscape, but here we will work with one 1 ha pixel that is our “whole” landscape for now. Here species specific information is also available for each year. More about the meaning of the columns in the landscape output you can find here: https://iland-model.org/Outputs#Landscape_aggregates_per_species Not always all outputs are produced, in the project file we can set which output tables we want to enable, and those will be created.

2.2.5 Run alternative scenarios

The prepared simulation is using the 30years climate of 1961-1990, and repeating during the simulation. (The model copy-paste the 30year time series after each other to fill up the simulation period). For CO2 concentration 400ppm is given. Your task is to run 1-2 extra alternative scenarios to modify the output data. For example assuming a CO2 concentration in the air of 800ppm, and 4degree warming, or keep CO2 on 400ppm and decrease precipitation by 20%.

All of these modifications can be done in the project file directly, you do not need to modify input data files

For this, go to the climate section and modify the values there, and save the project file with your alternative scenario.

```
<climate>  
<co2concentration>400</co2concentration> < ----- HERE  
  <tableName>Roznik</tableName>  
<batchYears>30</batchYears>  
  <temperatureShift>4</temperatureShift> < ----- HERE  
  <precipitationShift>0.8</precipitationShift> < ----- HERE  
  <randomSamplingEnabled>>false</randomSamplingEnabled>
```



```
<randomSamplingList></randomSamplingList>
</climate>
```

Note that the same CO₂ concentration will be used during the whole simulation period (there is a possibility to give annually changing CO₂ concentration using an external file, but for now we won't use it for simplicity). The temperature shift is applied by the model on each day's temperature values. The precipitation shift is a scaler that the model applies on each day's precipitation amount. (0.8 gives 20% decrease)

DO NOT FORGET TO CHANGE THE OUTPUT FILE NAME AS WELL for your alternative scenario, otherwise it will overwrite the previous output. You can do it in this section in the beginning of the project file:

```
<database>
<in>species_param_europe.sqlite</in>
<out>Output_plot1_4deg_20percdrier.sqlite</out> < ----- HERE
<climate>E-OBSv27_Roznik_46.05_14.45_1961-1990.sqlite</climate>
</database>
```

Running the alternative scenario follows the same steps as before.

2.2.6 Settings to consider for the assessment of model results

2.2.6.1 No management

We simulate stand development without management activities, which most likely generates accumulation of carbon and volume on the stands in this 100 years period. Generally iLand has a very sophisticated so called "agent based management engine" functionality for large landscapes, but also simple management activities are possible for stand-scale simulations. However, for the sake of simplicity in these examples we do not simulate any management activities.

2.2.6.2 Initialization of trees

iLand considers trees higher than 4m as individuals. All trees smaller than this size are simulated as cohorts. We initialize individual trees in year=0, but no regeneration layer, however the process of regeneration is turned on, consequently trees are producing seeds and after the establishment they start to grow. It takes some 15-20-25 years to be able to see this regeneration effect on the outputs which we will study (that are based on individual trees). You can find more information here: <https://iland-model.org/regeneration?highlight=regeneration>

2.2.6.3 Closed system

We assume no external seed input to our stand. This is highly unrealistic, as seeds can enter to our 1 ha area from the surrounding forests and bring species which are not there as individual trees in the beginning. Additionally, we are using the so-called torus mode so everything that escapes on one side of the pixel, enters on the other side. In iLand there is an option to set background seed availability to different species assuming probabilities for establishment in the project file, which we turned off for now. In this way new species cannot appear on the stand during the simulation time.

Practically the probabilities can be set based on the knowledge about the potential natural vegetation in the region, or based on the knowledge of the surrounding area. You can try to set external seeds if you wish in the project file turning the *externalSeedEnabled* from false to true. And set some probabilities (really small numbers) at *externalSeedBackgroundInput* a bit below down:

```
<externalSeedEnabled>true</externalSeedEnabled>
...

<externalSeedBackgroundInput>fasy 0.0004 abal 0.0004 qupe 0.0002 tico 0.00002
cabe 0.00001 potr 0.00001 frex 0.00001 pisy 0.00001 bepe 0.00001 soau 0.00001
piab 0.00001 acps 0.00001</externalSeedBackgroundInput>
```

More information on external seeds are here: <https://iland-model.org/external+seeds?highlight=seed>

2.2.7 Group 1 - Question A

- How are biodiversity indices changing in time and across the simulated scenario(s) on Plot 1?

Run the model as it is described in the previous chapters Section 2.2.3, Section 2.2.5 and Section 2.2.4 to have at least 2 simulations completed: one with reference conditions and one scenario with some changes in the environment. Check if you have the output files in the output folder: *iLand_simulations/output/*. We show all of the solutions on the example of one reference and one alternative scenario output file. Open the *summerSchoolExercise.Rproj* project in R studio and start working there.

2.2.7.1 Read the tree output table

Read in the *tree* output table from two outputs you have for your plot:

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```
path1 <- "model/iLand_simulations/output/Output_plot1.sqlite"
path2 <-
  "model/iLand_simulations/output/Output_plot1_4deg_20percdrier.sqlite"

file1 <- here::here(path1)
file2 <- here::here(path2)

# Give some name for the three simulations.
name1 <- "reference"
name2 <- "4deg_20percdrier"

# Read in data using the RSQLite package
sqlite.driver <- RSQLite::dbDriver("SQLite")
db1 <-
  RSQLite::dbConnect(sqlite.driver, dbname = file1) # connect to the file1

tables.in.the.file <-
  RSQLite::dbListTables(db1) # explore the tables in the file1
print(tables.in.the.file)
```

```
[1] "carbon"           "carbonflow"       "dynamicstand"
[4] "landscape"        "landscape_removed" "runinfo"
[7] "stand"            "tree"
```

```
# We will work with "tree" table and tree-scale data:
tree1 <- RSQLite::dbReadTable(db1, "tree")
RSQLite::dbDisconnect(db1) # disconnect to the file1

# READ IN DATA FROM THE SECOND FILE: -----
db2 <-
  RSQLite::dbConnect(sqlite.driver, dbname = file2) # connect to the file2
tree2 <- RSQLite::dbReadTable(db2, "tree")
RSQLite::dbDisconnect(db2)
```

Merge the data from the two files together and make a column caller run which tells which comes from which simulation, and study the table. The column “run” will support the plotting where we can use facets in ggplot.

```
tree <- rbind(tree1 |> dplyr::mutate(run = name1) ,
              tree2 |> dplyr::mutate(run = name2))

head(tree)
```

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| | year | ru | rid | species | id | x | y | dbh | height | basalArea | volume_m3 | age |
|---|-------------|---------------|-------------|------------|--------------|----------------|----|----------|----------|-----------|-----------|-----|
| 1 | 0 | 0 | 1 | fasy | 1 | 79 | 51 | 69.45111 | 39.46735 | 0.3788334 | 6.474022 | 493 |
| 2 | 0 | 0 | 1 | fasy | 2 | 69 | 91 | 68.95086 | 39.18307 | 0.3733956 | 6.335131 | 489 |
| 3 | 0 | 0 | 1 | fasy | 3 | 59 | 83 | 68.42681 | 38.88527 | 0.3677414 | 6.191780 | 486 |
| 4 | 0 | 0 | 1 | piab | 4 | 99 | 19 | 68.36907 | 45.96828 | 0.3671210 | 7.138516 | 492 |
| 5 | 0 | 0 | 1 | fasy | 5 | 63 | 61 | 66.87022 | 38.00070 | 0.3512007 | 5.778762 | 475 |
| 6 | 0 | 0 | 1 | fasy | 6 | 55 | 61 | 65.80000 | 37.39252 | 0.3400492 | 5.505722 | 467 |
| | leafArea_m2 | foliageMass | stemMass | branchMass | fineRootMass | coarseRootMass | | | | | | |
| 1 | 322.7507 | 29.34097 | 3099.621 | 378.6909 | 22.00573 | 337.2626 | | | | | | |
| 2 | 318.8086 | 28.98260 | 3049.604 | 372.4465 | 21.73695 | 331.6535 | | | | | | |
| 3 | 314.7003 | 28.60912 | 2997.693 | 365.9680 | 21.45684 | 325.8348 | | | | | | |
| 4 | 295.8482 | 69.61134 | 2192.064 | 365.2582 | 52.20850 | 526.4032 | | | | | | |
| 5 | 302.6273 | 27.51158 | 2846.413 | 347.1027 | 20.63368 | 308.8961 | | | | | | |
| 6 | 294.4398 | 26.76726 | 2744.921 | 334.4585 | 20.07544 | 297.5477 | | | | | | |
| | lri | lightResponse | stressIndex | reserve_kg | treeFlags | run | | | | | | |
| 1 | 0.2646746 | | 0 | 51.34669 | 0 | reference | | | | | | |
| 2 | 0.5870413 | | 0 | 50.71954 | 0 | reference | | | | | | |
| 3 | 0.3931382 | | 0 | 50.06596 | 0 | reference | | | | | | |
| 4 | 1.0000000 | | 0 | 121.81984 | 0 | reference | | | | | | |
| 5 | 0.3406834 | | 0 | 48.14526 | 0 | reference | | | | | | |
| 6 | 0.4422086 | | 0 | 46.84270 | 0 | reference | | | | | | |

2.2.7.2 Visualize trees in year 0 and year 100

To explore a bit the simulation, plot the tree locations at the beginning and the end of the simulation. For plotting we use the colors for the species, and the size of a circles to show dbh differences. Here we divided dbh with the value 20 just for visualization, not to have too huge circles shading each others completely, but still see the trees.

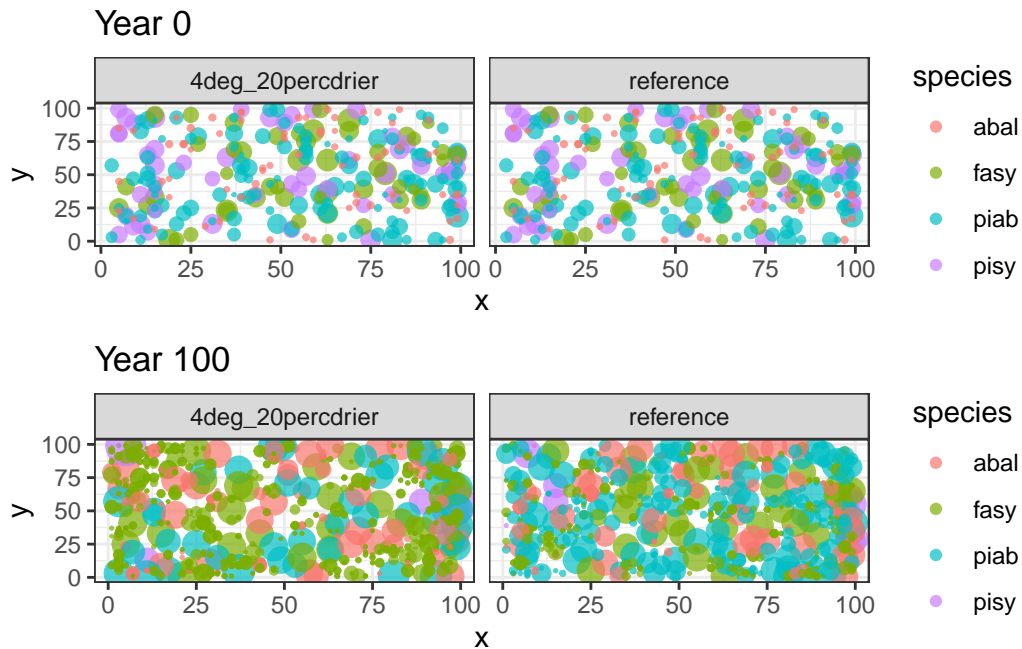
```
tree0 <- tree |> dplyr::filter(year == 0)
g1 <-
  ggplot2::ggplot(tree0, ggplot2::aes(x = x, y = y, color = species)) +
  ggplot2::geom_point(size = tree0$dbh / 20, alpha = 0.7) +
  ggplot2::ggtitle("Year 0") +
  ggplot2::facet_wrap( ~run) + ggplot2::theme_bw()

tree100 <- tree |> dplyr::filter(year == 100)
g2 <-
  ggplot2::ggplot(tree100, ggplot2::aes(x = x, y = y, color = species)) +
  ggplot2::geom_point(size = tree100$dbh / 20, alpha = 0.7) +
  ggplot2::ggtitle("Year 100") +
```

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```
ggplot2::facet_wrap(~ run) + ggplot2::theme_bw()

gridExtra::grid.arrange(g1, g2, ncol = 1)
```



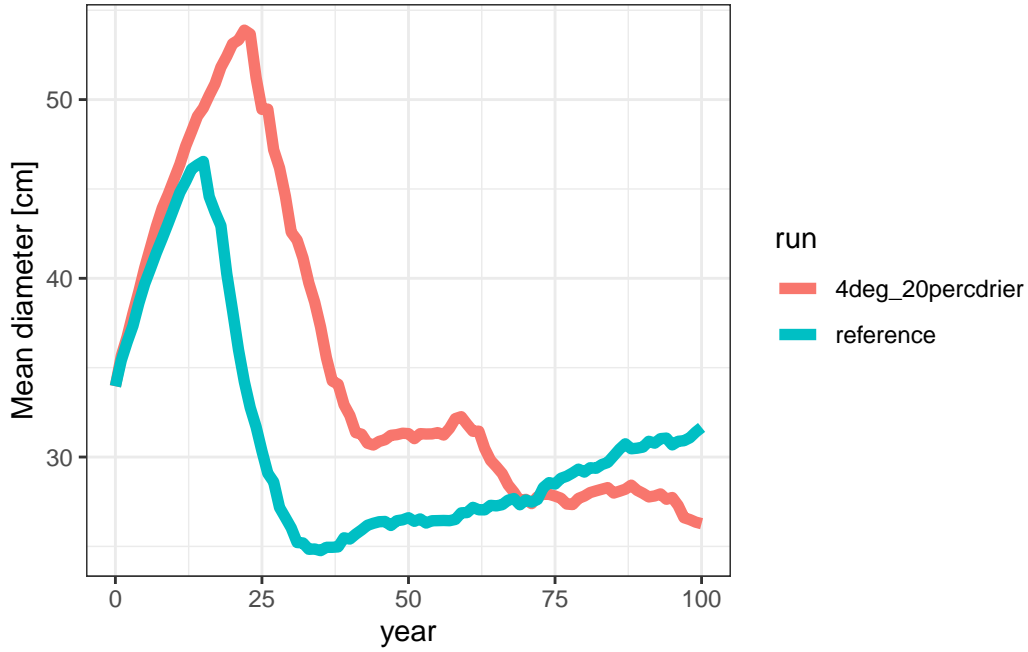
We can see that the species composition has changed and the forest become more dense. We can even identify the same trees at the same location.

2.2.7.3 Visualize some changes in time

```
sum.table <- tree |> dplyr::group_by(year, run) |>
  dplyr::summarise(
    N = dplyr::n(),
    MD = mean(dbh, na.rm = TRUE),
    #mean diameter
    BA = sum(basalArea)
  ) #basal area

ggplot2::ggplot(sum.table, ggplot2::aes(x = year,
                                          y = MD, color = run)) +
  ggplot2::geom_line(lwd = 2) +
  ggplot2::ylab("Mean diameter [cm]") + ggplot2::theme_bw()
```

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We can see that there is an initial increase in mean dbh, then a drop after 20/25 years. This is due to the growing regeneration layer that is produced the seeds of the existing trees. In the initial year we do not have regeneration layer in the simulations (it is possible to put there, but we do not have it now). And until the small trees grow up to higher than 4 m they are not appearing in the individual *tree* output as they are handled in cohorts.

2.2.7.4 Species diversity

To study biodiversity aspects, we can calculate biodiversity indicators. Let's use the *adiv* package for species diversity. First we need to change the database structure to have the number of trees for each species in different columns (`pivot_wider`) without any additional columns for the *adiv* package *speciesdiv* function. We work first only with tree data from one simulation (*tree1*). You can find the documentation of the *adiv* package here: "[documents/adiv.pdf](#)"

Shannon index is calculated as follows:

$$S = - \sum (p_i * \log(p_i))$$

Where p_i is the relative abundance of the species i , calculated as the ratio of the abundance of the species i and the abundance of all species. Shannon-index is 0 when

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we have only one species at the stand. Here we calculate the abundance based on the number of trees, but can be calculate based on the volume to give more weight to larger trees. We add N as the number of records in the summarizing process below, but we can sum up the volume_m3 column and prepare the table for the speciesdiv function based on the volume (or any other variable, e.g. basal area).

```
# First we need to change the
tlong1 <- tree1 |>
  dplyr::group_by(year, species) |> dplyr::summarise(N = dplyr::n()) |>
  tidyr::pivot_wider(
    id_cols = 'year',
    names_from = 'species',
    values_from = 'N',
    values_fill = 0
  ) |>
  dplyr::ungroup() |>
  dplyr::select(-year)

head(tlong1)
```

```
# A tibble: 6 x 4
  abal fasy piab pisy
<int> <int> <int> <int>
1     68    50   120    49
2     68    49   115    49
3     68    48   111    48
4     68    48   110    47
5     66    48   107    46
6     65    48   105    45
```

Then we apply the “speciesdiv” function and we add back the year and run columns to have the information.

```
div1 <- data.frame(activ::speciesdiv(tlong1)) |>
  dplyr::mutate(year = unique(tree1$year), run = name1)
head(div1)
```

| | richness | GiniSimpson | Simpson | Shannon | Margalef | Menhinick | McIntosh | year |
|---|----------|-------------|----------|----------|-----------|-----------|-----------|------|
| 1 | 4 | 0.7095388 | 3.442800 | 1.312005 | 0.5300838 | 0.2361125 | 0.4899779 | 0 |
| 2 | 4 | 0.7131369 | 3.485983 | 1.318098 | 0.5320701 | 0.2386200 | 0.4938655 | 1 |
| 3 | 4 | 0.7150017 | 3.508792 | 1.321063 | 0.5341147 | 0.2412091 | 0.4960613 | 2 |
| 4 | 4 | 0.7150505 | 3.509394 | 1.320996 | 0.5348097 | 0.2420910 | 0.4962264 | 3 |

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```
5      4    0.7162956 3.524796 1.323410 0.5369369 0.2447960 0.4978275    4
6      4    0.7169397 3.532816 1.324555 0.5383914 0.2466506 0.4987181    5
      run
1 reference
2 reference
3 reference
4 reference
5 reference
6 reference
```

We make the same steps for the other simulation results (tree2).

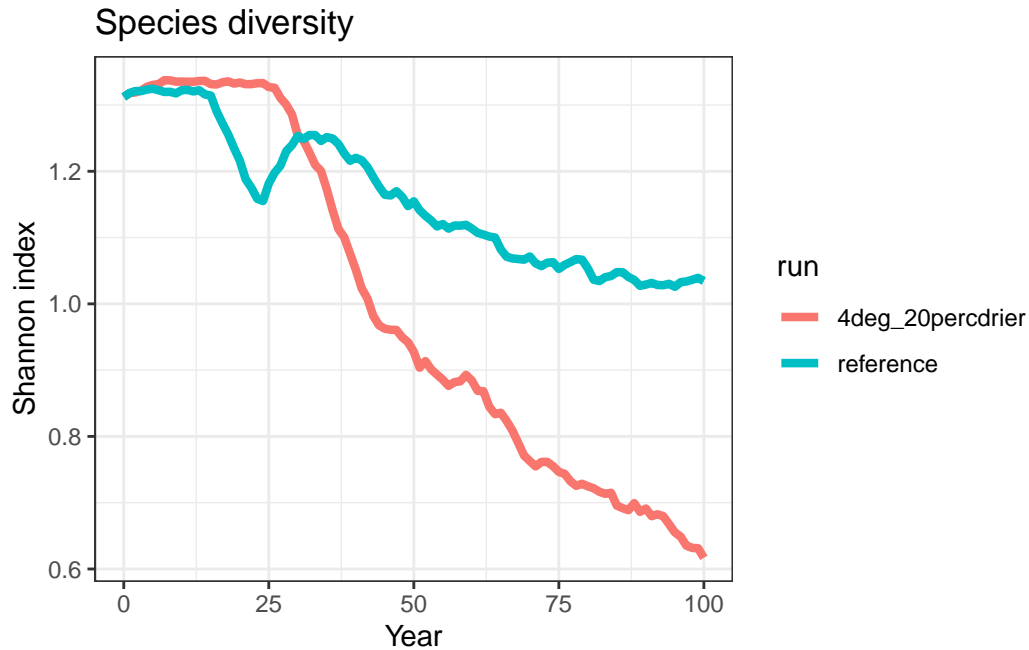
```
tlong2 <- tree2 |>
  dplyr::group_by(year, species) |> dplyr::summarise(N = dplyr::n()) |>
  tidyr::pivot_wider(
    id_cols = 'year',
    names_from = 'species',
    values_from = 'N',
    values_fill = 0
  ) |>
  dplyr::ungroup() |>
  dplyr::select(-year)

div2 <- data.frame(adiv::speciesdiv(tlong2)) |>
  dplyr::mutate(year = unique(tree2$year), run = name2)
```

We merge them all together and make a plot based on Shannon index.

```
div <- rbind(div1, div2)

ggplot2::ggplot(div, ggplot2::aes(year, Shannon , color = run)) +
  ggplot2::geom_line(lwd = 1.5) +
  ggplot2::ggtitle("Species diversity") +
  ggplot2::labs(x = "Year", y = "Shannon index") +
  ggplot2::theme_bw()
```

We see that the values of Shannon index are first stable and then tend to decrease, while the reduction under the 4deg_20percdrier is more substantial than under the reference scenario.

2.2.7.5 Spatial diversity

We can calculate some additional biodiversity indices targeting spatial diversity using the *treespac* package developed by Francesco Chianucci (fchianucci@gmail.com). You can find more information about this R package following this [link](<https://www.biorxiv.org/content/10.1101/2>

You can install the package using devtools:

```
devtools::install_gitlab('fchianucci/treespac')
```

Then, we are ready to use it. Let's calculate these two indices:

- Diameter differentiation (Gadow, 1993): Spatial size inequality defined as the mean of the ratio of smaller and larger plant sizes in the nearest neighbors of a tree. The value of the index increases with increasing average size difference between neighboring trees. 0 is implying that neighboring trees have equal size.

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- Mingling (Aguirre et al., 2003): One very intuitive extension of taxonomic species diversity (either richness or abundance) is considering spatial mingling, namely how plants of the same (con-specific neighbors) or different (hetero-specific neighbors) species are arranged in space. The mingling index calculates the proportion of the k nearest neighbors that do not belong to the same species as the reference tree. For example, with four neighbors, the mingling attribute can assume five values, ranging from 0 (all trees are of the same species) to 1 (all trees belong to different species).

Calculate the indices based on the reference run, then based on the scenario. For each index we add extra columns with the index name, and run name for further analyses. The `max.k` parameter is telling how many neighboring trees we want to account for.

```
# diameter differentiation:
# mingling
diff <-
  data.frame(
    treespat::DIFF(
      tree1,
      .x = x,
      .y = y,
      .mark = dbh,
      xmax = 100,
      ymax = 100,
      max.k = 4,
      shape = 'square',
      .groups = c('year')
    ) |>
    dplyr::mutate(index = "DIFF", name = "Diameter differentiation", run =
                  name1)
  )
head(diff)
```

| | year | DIFF index | | name | run |
|---|------|------------|------|--------------------------|-----------|
| 1 | 0 | 0.4317331 | DIFF | Diameter differentiation | reference |
| 2 | 1 | 0.4104274 | DIFF | Diameter differentiation | reference |
| 3 | 2 | 0.3988705 | DIFF | Diameter differentiation | reference |
| 4 | 3 | 0.3903934 | DIFF | Diameter differentiation | reference |
| 5 | 4 | 0.3775628 | DIFF | Diameter differentiation | reference |
| 6 | 5 | 0.3595558 | DIFF | Diameter differentiation | reference |

```

ming <-
  data.frame(
    treespat::MING(
      tree1,
      .x = x,
      .y = y,
      .species = species,
      xmax = 100,
      ymax = 100,
      max.k = 4,
      shape = 'square',
      .groups = c('year')
    ) |>
    dplyr::mutate(index = "MING", name = "Mingling", run = name1)
  )

indices1 <- rbind(diff |> dplyr::rename(value = DIFF),
  ming |> dplyr::rename(value = MINGLING))

```

We calculated each index as a separate variable and then merged them into indices1. Here I renamed the column names to have it all “value”, for easier plotting later on. (each line has the information on which run and which index is the value) We do the same for the scenario simulation, we merge them together and make the plotting.

```

diff <- data.frame(treespat::DIFF(tree2, .x = x, .y = y, .mark = dbh,
  xmax = 100, ymax = 100, max.k = 4, shape = 'square',
  .groups = c('year')) |>
  dplyr::mutate(index = "DIFF", name = "Diameter differentiation",
    run = name2))

ming <- data.frame(treespat::MING(tree2, .x = x, .y = y, .species = species,
  xmax = 100, ymax = 100, max.k = 4, shape = 'square', .groups = c('year')) |>
  dplyr::mutate(index = "MING", name = "Mingling", run = name2))

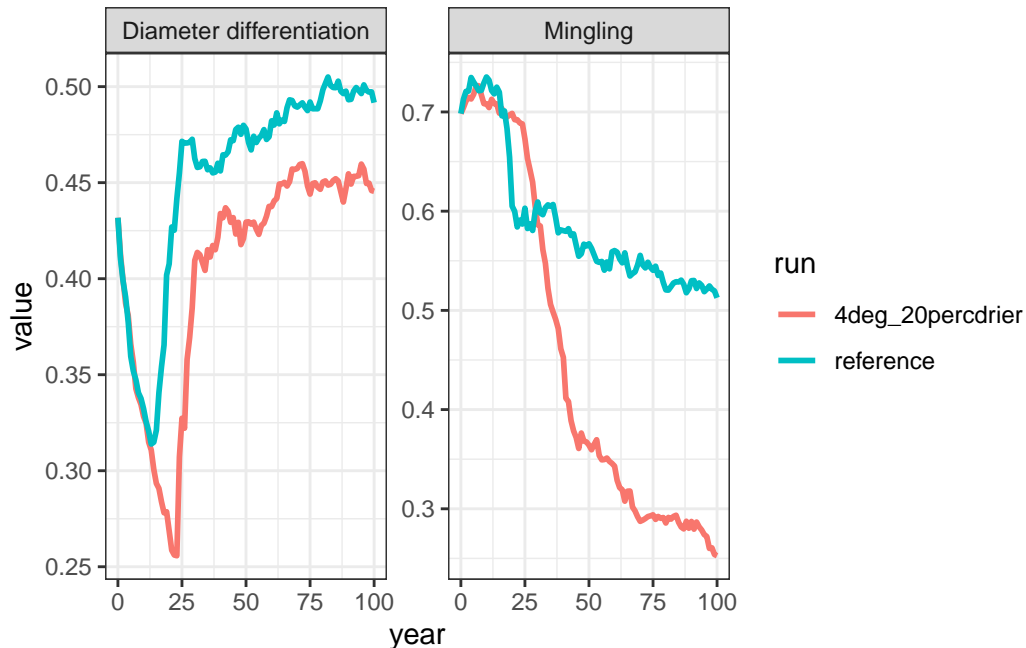
indices2 <- rbind(diff |> dplyr::rename(value = DIFF),
  ming |> dplyr::rename(value = MINGLING))

indices <- rbind(indices1, indices2)

ggplot2::ggplot(indices, ggplot2::aes(x = year, y = value, color = run)) +
  ggplot2::geom_line(lwd = 1) +
  ggplot2::facet_wrap(~ name, ncol = 2, scales = "free") +
  ggplot2::theme_bw()

```

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The diameter differentiation increases with the increasing average difference in diameter between neighboring trees. The value 0 indicates that neighboring trees have equal diameters. The development shows that the index values decrease during the first 20/25 years, after which it steeply increases due to the occurrence of ingrowth and then the values are stabilized. The values for the reference climate scenario are slightly higher than for the climate change scenario indicating slower growth under drier and warmer conditions and/or the differences in tree species composition (proportion of tree species). The mingling index is studying the neighboring trees regarding their species. In both development there is a decrease in the index after the occurrence of regeneration. Using the climate change scenario the index shows steeper decrease.

2.2.8 Group 1 - Question B

- How are the species distribution and total living biomass C content changing in time on Plot 1? Compare 0 year and 100 year status in the reference case and in the case of your scenario(s)

Run the model as it is described in the previous chapters Section 2.2.3, Section 2.2.5 and Section 2.2.4 to have at least 2 simulations completed: one with reference conditions and one scenario with some changes in the environment. Check if you have the output files in the output folder: *iLand_simulations/output/*. We show all of the solutions on the example of one reference and one alternative scenario output file. Open the *summerSchoolExercise.Rproj* project in R studio and start working there.

2.2.8.1 Read the landscape output table

Read in the *landscape* output table from two outputs you have for your plot:

```
path1 <- "model/iLand_simulations/output/Output_plot1.sqlite"
path2 <-
  "model/iLand_simulations/output/Output_plot1_4deg_20percdrier.sqlite"

file1 <- here::here(path1)
file2 <- here::here(path2)

# Give some name for the three simulations.
name1 <- "reference"
name2 <- "4deg_20percdrier"

# Read in data using the RSQLite package
sqlite.driver <- RSQLite::dbDriver("SQLite")

# We will work with "landscape" table and tree-scale data:
db1 <-
  RSQLite::dbConnect(sqlite.driver, dbname = file1) # connect to the file1
landscape1 <- RSQLite::dbReadTable(db1, "landscape")
RSQLite::dbDisconnect(db1) # disconnect to the file1

db2 <-
  RSQLite::dbConnect(sqlite.driver, dbname = file2) # connect to the file2
landscape2 <- RSQLite::dbReadTable(db2, "landscape")
RSQLite::dbDisconnect(db2)
```

Merge the data from the two files together and make a column caller run which tells which comes from which simulation, and study the table. The column “run” will support the plotting where we can use facets in ggplot.

```
landscape <- rbind(landscape1 |> dplyr::mutate(run = name1),
  landscape2 |> dplyr::mutate(run = name2))

head(landscape)
```

| | year | area | area_100m | species | count_ha | dbh_avg_cm | height_avg_m | volume_m3 |
|---|------|------|-----------|---------|----------|------------|--------------|-----------|
| 1 | 0 | 1 | 1 | abal | 68 | 12.55456 | 10.04365 | 4.33641 |
| 2 | 0 | 1 | 1 | fasy | 50 | 49.86496 | 28.33702 | 136.89579 |

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| | | | | | | | | |
|---|-----------------|---|-----------|---------------|-----|----------|-------------|------------|
| 3 | 0 | 1 | 1 | piab | 120 | 32.73141 | 22.00713 | 150.34005 |
| 4 | 0 | 1 | 1 | pisy | 49 | 50.45049 | 28.66693 | 126.09230 |
| 5 | 1 | 1 | 1 | abal | 68 | 14.15550 | 11.39836 | 6.12901 |
| 6 | 1 | 1 | 1 | fasy | 49 | 50.95480 | 28.84830 | 141.11347 |
| | total_carbon_kg | | gwl_m3 | basal_area_m2 | | NPP_kg | NPPabove_kg | LAI |
| 1 | 2264.490 | | 4.33641 | 0.8659201 | | 0.000 | 0.000 | 0.09848037 |
| 2 | 49667.453 | | 136.89579 | 10.2322163 | | 0.000 | 0.000 | 0.94517453 |
| 3 | 45424.641 | | 150.34005 | 12.1157843 | | 0.000 | 0.000 | 1.22598624 |
| 4 | 42580.564 | | 126.09230 | 9.9010286 | | 0.000 | 0.000 | 1.13237721 |
| 5 | 2784.089 | | 6.12901 | 1.0937620 | | 1657.542 | 1128.888 | 0.11701639 |
| 6 | 52091.802 | | 143.51049 | 10.4297469 | | 9855.392 | 6472.199 | 0.96978453 |
| | cohort_count_ha | | run | | | | | |
| 1 | 0 | | reference | | | | | |
| 2 | 0 | | reference | | | | | |
| 3 | 0 | | reference | | | | | |
| 4 | 0 | | reference | | | | | |
| 5 | 31 | | reference | | | | | |
| 6 | 54 | | reference | | | | | |

2.2.8.2 Visualize changes in time

We can see that the output is given for each year and each species in our 1ha area. Plot the living carbon (total_carbon_kg) in time, coloring by species. We give a unified species coloring in the beginning. Plot number of trees and mean diameter. Carbon and number of trees can be plotted in an additive way, but for mean dbh we do line plot per species.

```
cols.all=c( "rops"="#e0e0e0","acpl"="#A9A9A9","alin"="#696969","alvi"="#2e2e2e",
  "bepe"="#fadfad","casa"="#7eeadf","coav"="#20c6b6","tipl"="#645394",
  "ulgl"="#311432","saca"="#D8BFD8","soar"="#DDA0DD","soau"="#BA55D3",
  "pice"="#D27D2D","pini"="#a81c07","algl"="#2ECBE9","tico"="#128FC8",
  "potr"="#00468B","poni"="#5BAEB7","frex"="#fe9cb5","cabe"="#fe6181",
  "acps"="#fe223e","lade"="#FFFE71","abal"="#FFD800", "pisy"="#A4DE02",
  "fasy"="#76BA1B","piab"="#006600","quro"="#FF7F00", "qupe"="#FF9900",
  "qupu"="#CC9900")

# We set here the order of the run categories for the table, to have the first
#run first and then the second. (left-right of the plots)
landscape$run <- factor(landscape$run, levels = c(name1, name2))

# Plot the living carbon content, to have tonnes/ha, we divide total_carbon_kg by 1000.
g1 <- ggplot2::ggplot(landscape, ggplot2::aes(year, total_carbon_kg / 1000 ,
```

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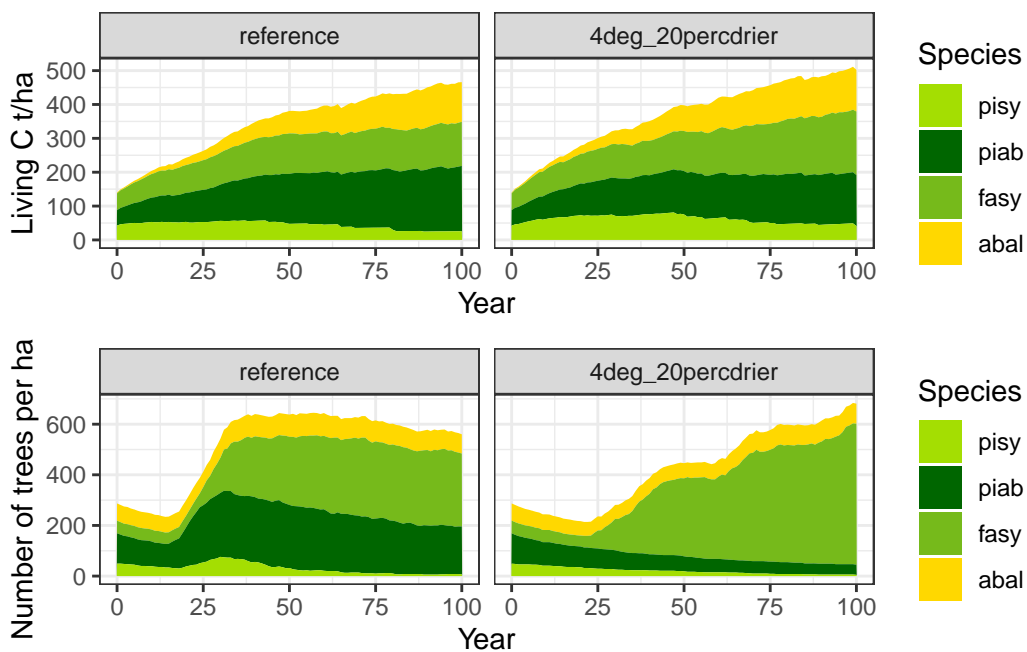
```

                                fill = factor(species))) +
ggplot2::geom_area() +
ggplot2::scale_fill_manual(values = cols.all,
                           guide = ggplot2::guide_legend(reverse = TRUE)) +
ggplot2::facet_wrap( ~ run, nrow = 1) +
ggplot2::labs(x = "Year", y = "Living C t/ha", fill = "Species") +
ggplot2::theme_bw()

g2 <-
ggplot2::ggplot(landscape, ggplot2::aes(year, count_ha , fill = factor(species))) +
ggplot2::geom_area() +
ggplot2::scale_fill_manual(values = cols.all,
                           guide = ggplot2::guide_legend(reverse = TRUE)) +
ggplot2::facet_wrap( ~ run, nrow = 1) +
ggplot2::labs(x = "Year", y = "Number of trees per ha", fill = "Species") +
ggplot2::theme_bw()

gridExtra::grid.arrange(g1, g2, ncol = 1)

```



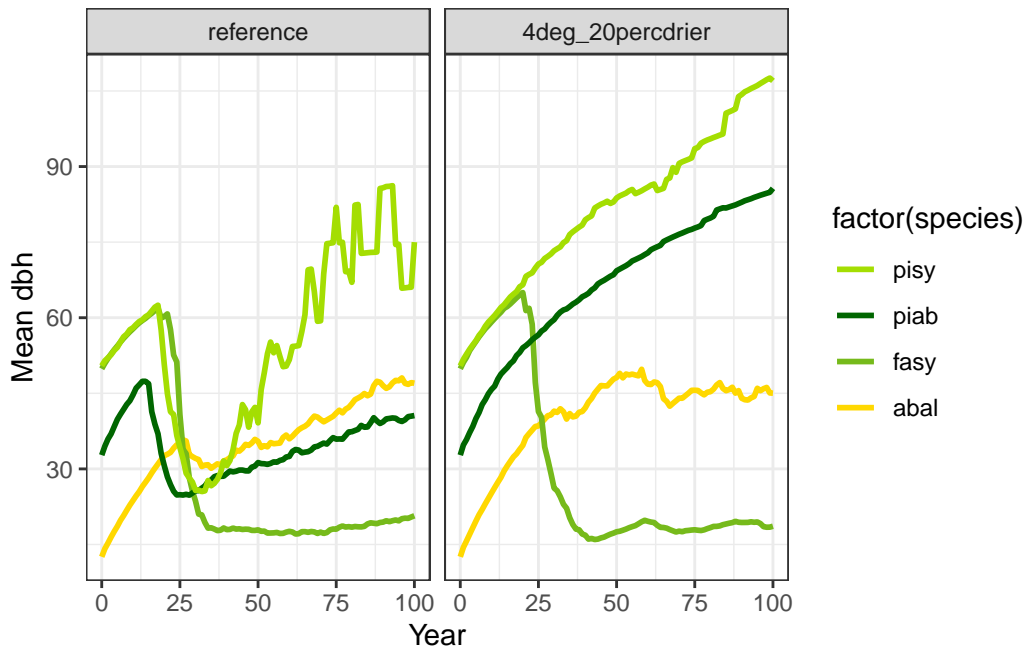
```

g3 <- ggplot2::ggplot(landscape,
                      ggplot2::aes(year, dbh_avg_cm , color = factor(species))) +
ggplot2::geom_line(lwd = 1) +

```

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```
ggplot2::scale_color_manual(values = cols.all,  
                             guide = ggplot2::guide_legend(reverse = TRUE)) +  
ggplot2::facet_wrap( ~ run, nrow = 1) +  
ggplot2::labs(x = "Year", y = "Mean dbh", fill = "Species") +  
ggplot2::theme_bw()  
  
print(g3)
```



Note that we do not have management intervention, and in the model trees shorter than 4m are not included in these outputs. However as they grow taller than 4m, model starts to handle them as individual trees and including in these outputs which we are looking now.

At the end of the simulated 100 years, the total simulated carbon stock in living biomass under climate change scenario was slightly higher than under the reference climate. The proportion of beech and pine increased under drier and warmer climate, while the proportion of spruce was lower, since spruce is in general more susceptible to dry conditions. The changes in the number of trees of individual tree species were more substantial than the changes in carbon stock. The number of spruce trees was substantially reduced under climate change, while under reference climate it was doubled after 30 years and then remain stable until the end of simulation. In contrast, the number of beech trees increased under both scenarios, but the increase was more pronounced under climate change scenario due to the reduction of spruce trees.

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Mean dbh of individual species reflected the development of the number of trees. The increase in the number of trees caused the reduction of mean dbh, e.g. of beech under both scenarios between 20 and 35 simulation years. The species-specific graphs for mean dbh indicates that some species do not have successful regeneration under the climate change scenario. Spruce and pine dbh decreased only under reference scenario, when we observed the increase of the number of trees, while under climate change scenario the mean dbh of spruce or pine was growing indicating the growth of remaining trees of the species at the plot. In the case of fir, we observed the continuous increase of dbh due to the more or less stable number of trees at the plots. While the mean dbh of fir was growing during the whole simulation period, under drier and warmer climate mean dbh of fir did not substantially change after 70 years.

2.2.8.3 Assess the stored carbon amount

Calculate the stored C amount in the initial year (year==0) and the last year (year==100)

```
livingC0 <-  
  data.frame(  
    landscape |> dplyr::filter(year == 0) |>  
    dplyr::group_by(run) |>  
    dplyr::summarize(sum.livingC = sum(total_carbon_kg / 1000))  
  )  
print(livingC0)
```

```
      run sum.livingC  
1      reference    139.9371  
2 4deg_20percdrier    139.9371
```

```
livingC100 <-  
  data.frame(  
    landscape |> dplyr::filter(year == 100) |>  
    dplyr::group_by(run) |>  
    dplyr::summarize(sum.livingC = sum(total_carbon_kg / 1000))  
  )  
print(livingC100)
```

```
      run sum.livingC  
1      reference    465.9313  
2 4deg_20percdrier    502.2416
```

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The initial conditions are same for the runs, but they are ending up at different C levels.

Calculate the stored C amount PER SPECIES in the initial year (year==0) and the last year (year==100)

```
species.livingC0 <-  
  data.frame(  
    landscape |> dplyr::filter(year == 0) |>  
    dplyr::group_by(run, species) |>  
    dplyr::summarize(livingC = sum(total_carbon_kg / 1000))  
  )  
print(species.livingC0)
```

| | run | species | livingC |
|---|------------------|---------|----------|
| 1 | reference | abal | 2.26449 |
| 2 | reference | fasy | 49.66745 |
| 3 | reference | piab | 45.42464 |
| 4 | reference | pisy | 42.58056 |
| 5 | 4deg_20percdrier | abal | 2.26449 |
| 6 | 4deg_20percdrier | fasy | 49.66745 |
| 7 | 4deg_20percdrier | piab | 45.42464 |
| 8 | 4deg_20percdrier | pisy | 42.58056 |

```
species.livingC100 <-  
  data.frame(  
    landscape |> dplyr::filter(year == 100) |>  
    dplyr::group_by(run, species) |>  
    dplyr::summarize(livingC = sum(total_carbon_kg / 1000))  
  )  
print(species.livingC100)
```

| | run | species | livingC |
|---|------------------|---------|-----------|
| 1 | reference | abal | 117.08641 |
| 2 | reference | fasy | 130.23479 |
| 3 | reference | piab | 192.96180 |
| 4 | reference | pisy | 25.64826 |
| 5 | 4deg_20percdrier | abal | 123.25491 |
| 6 | 4deg_20percdrier | fasy | 187.43320 |
| 7 | 4deg_20percdrier | piab | 150.38585 |
| 8 | 4deg_20percdrier | pisy | 41.16762 |

2.2.8.4 Assess the species proportions

Calculate the species proportions based on the stored C amount in the initial year (year==0) and the last year (year==100) For this we need the total C amount and the species-specific C amount.

```
LC0 <- dplyr::left_join(species.livingC0, livingC0, by = "run")
LC0 <-
  data.frame(LC0 |> dplyr::mutate(spec.prop = livingC / sum.livingC, year =
                                0))
print(LC0)
```

| | run | species | livingC | sum.livingC | spec.prop | year |
|---|------------------|---------|----------|-------------|------------|------|
| 1 | reference | abal | 2.26449 | 139.9371 | 0.01618219 | 0 |
| 2 | reference | fasy | 49.66745 | 139.9371 | 0.35492686 | 0 |
| 3 | reference | piab | 45.42464 | 139.9371 | 0.32460745 | 0 |
| 4 | reference | pisy | 42.58056 | 139.9371 | 0.30428349 | 0 |
| 5 | 4deg_20percdrier | abal | 2.26449 | 139.9371 | 0.01618219 | 0 |
| 6 | 4deg_20percdrier | fasy | 49.66745 | 139.9371 | 0.35492686 | 0 |
| 7 | 4deg_20percdrier | piab | 45.42464 | 139.9371 | 0.32460745 | 0 |
| 8 | 4deg_20percdrier | pisy | 42.58056 | 139.9371 | 0.30428349 | 0 |

```
LC100 <- dplyr::left_join(species.livingC100, livingC100, by = "run")
LC100 <-
  data.frame(LC100 |> dplyr::mutate(spec.prop = livingC / sum.livingC, year =
                                   100))
print(LC100)
```

| | run | species | livingC | sum.livingC | spec.prop | year |
|---|------------------|---------|-----------|-------------|------------|------|
| 1 | reference | abal | 117.08641 | 465.9313 | 0.25129545 | 100 |
| 2 | reference | fasy | 130.23479 | 465.9313 | 0.27951504 | 100 |
| 3 | reference | piab | 192.96180 | 465.9313 | 0.41414220 | 100 |
| 4 | reference | pisy | 25.64826 | 465.9313 | 0.05504730 | 100 |
| 5 | 4deg_20percdrier | abal | 123.25491 | 502.2416 | 0.24540961 | 100 |
| 6 | 4deg_20percdrier | fasy | 187.43320 | 502.2416 | 0.37319331 | 100 |
| 7 | 4deg_20percdrier | piab | 150.38585 | 502.2416 | 0.29942930 | 100 |
| 8 | 4deg_20percdrier | pisy | 41.16762 | 502.2416 | 0.08196777 | 100 |

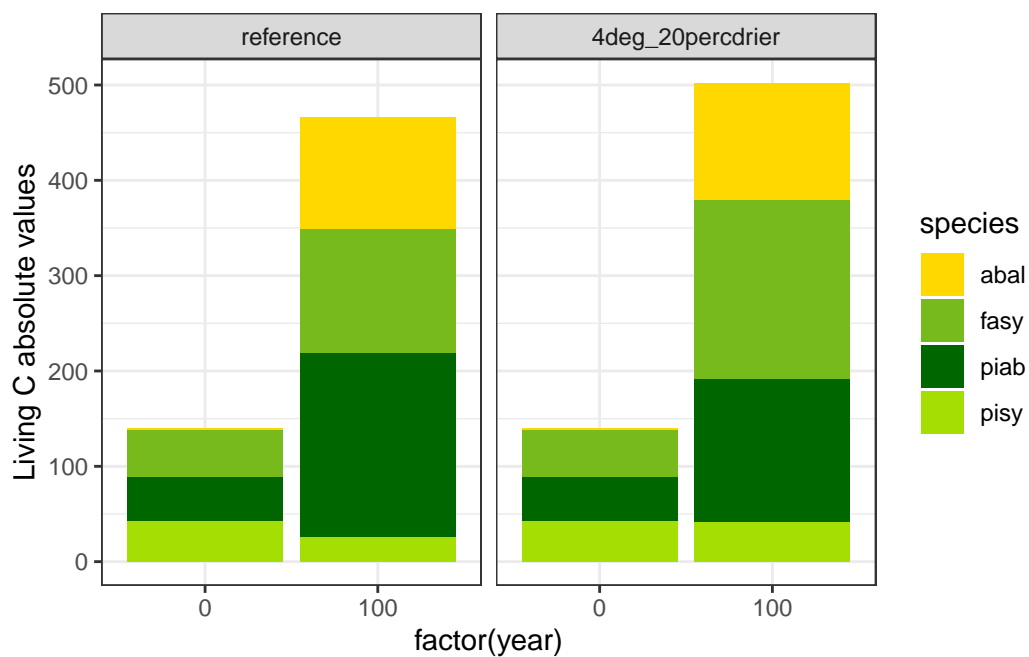
Put the two tables together and visualize the results

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```
LC <- rbind(LC0, LC100)

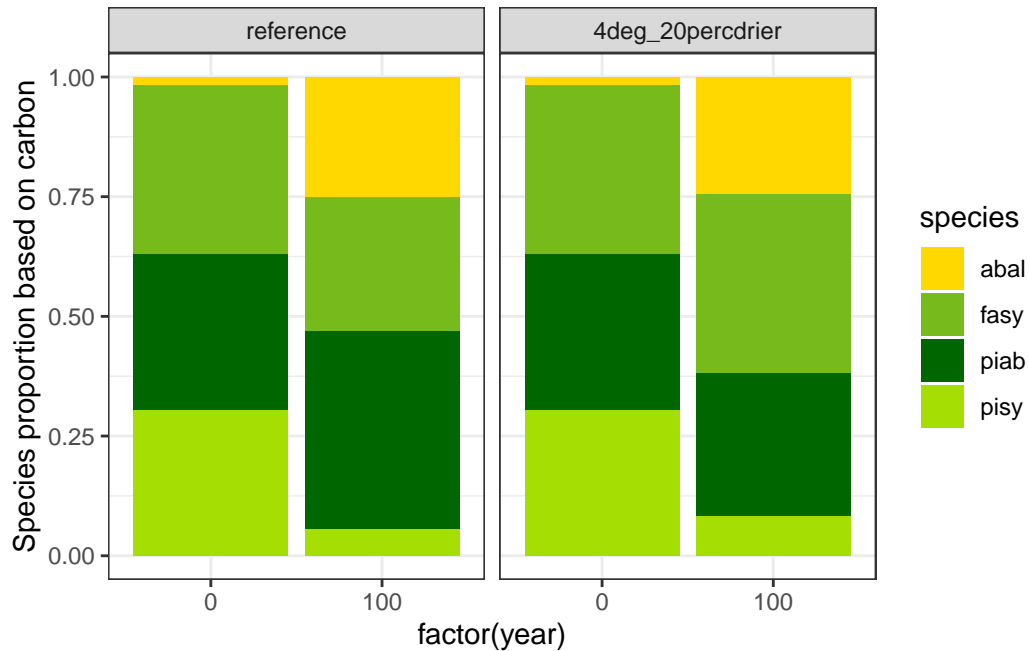
LC$run <- factor(LC$run, levels = c(name1, name2))

ggplot2::ggplot(LC, ggplot2::aes(fill = species, y = livingC , x = factor(year))) +
  ggplot2::geom_bar(position = "stack", stat = "identity") +
  ggplot2::scale_fill_manual(values = cols.all) +
  ggplot2::facet_wrap( ~ run) +
  ggplot2::ylab("Living C absolute values") +
  ggplot2::theme_bw()
```



```
ggplot2::ggplot(LC, ggplot2::aes(fill = species, y = spec.prop,
                                   x = factor(year))) +
  ggplot2::geom_bar(position = "stack", stat = "identity") +
  ggplot2::scale_fill_manual(values = cols.all) +
  ggplot2::facet_wrap( ~ run) +
  ggplot2::ylab("Species proportion based on carbon") +
  ggplot2::theme_bw()
```

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The living C stock tripled over 100 years due to the accumulation of biomass in trees and no management interventions. Moreover, the proportion of individual tree species changed with fir substantially increasing its share. The living C stock of pine was reduced under the reference climate or remained unchanged under the climate change scenario.

2.2.9 Group 2 - Question A

- How are biodiversity indices changing in time and across the simulated scenario(s) on Plot 2?

Run the model as it is described in the previous chapters Section 2.2.3, Section 2.2.5 and Section 2.2.4 to have at least 2 simulations completed: one with reference conditions and one scenario with some changes in the environment. Check if you have the output files in the output folder: *iLand_simulations/output/*. We show all of the solutions on the example of one reference and one alternative scenario output file. Open the *summerSchoolExercise.Rproj* project in R studio and start working there.

2.2.9.1 Read the tree output table

Read in the *tree* output table from two outputs you have for your plot:

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```
path1 <- "model/iLand_simulations/output/Output_plot2.sqlite"
path2 <-
  "model/iLand_simulations/output/Output_plot2_4deg_20percdrier.sqlite"

file1 <- here::here(path1)
file2 <- here::here(path2)

# Give some name for the three simulations.
name1 <- "reference"
name2 <- "4deg_20percdrier"

# Read in data using the RSQLite package
sqlite.driver <- RSQLite::dbDriver("SQLite")
db1 <-
  RSQLite::dbConnect(sqlite.driver, dbname = file1) # connect to the file1

tables.in.the.file <-
  RSQLite::dbListTables(db1) # explore the tables in the file1
print(tables.in.the.file)
```

```
[1] "carbon"           "carbonflow"       "dynamicstand"
[4] "landscape"        "landscape_removed" "runinfo"
[7] "stand"            "tree"
```

```
# We will work with "tree" table and tree-scale data:
tree1 <- RSQLite::dbReadTable(db1, "tree")
RSQLite::dbDisconnect(db1) # disconnect to the file1

# READ IN DATA FROM THE SECOND FILE: -----
db2 <-
  RSQLite::dbConnect(sqlite.driver, dbname = file2) # connect to the file2
tree2 <- RSQLite::dbReadTable(db2, "tree")
RSQLite::dbDisconnect(db2)
```

Merge the data from the two files together and make a column caller run which tells which comes from which simulation, and study the table. The column “run” will support the plotting where we can use facets in ggplot.

```
tree <- rbind(tree1 |> dplyr::mutate(run = name1) ,
              tree2 |> dplyr::mutate(run = name2))
```

```
head(tree)
```

| | year | ru | rid | species | id | x | y | dbh | height | basalArea | volume_m3 | age |
|---|-------------|---------------|-------------|------------|--------------|----------------|----|----------|----------|-----------|-----------|------|
| 1 | 0 | 0 | 1 | piab | 1 | 65 | 43 | 85.63804 | 57.57916 | 0.5760011 | 14.029073 | 616 |
| 2 | 0 | 0 | 1 | qupe | 2 | 9 | 47 | 78.57278 | 40.23281 | 0.4848798 | 8.856667 | 1072 |
| 3 | 0 | 0 | 1 | piab | 3 | 95 | 39 | 78.37173 | 52.69362 | 0.4824016 | 10.752442 | 564 |
| 4 | 0 | 0 | 1 | piab | 4 | 95 | 91 | 76.88074 | 51.69115 | 0.4642212 | 10.150361 | 553 |
| 5 | 0 | 0 | 1 | piab | 5 | 79 | 75 | 74.49680 | 50.08829 | 0.4358782 | 9.235103 | 536 |
| 6 | 0 | 0 | 1 | qupe | 6 | 89 | 49 | 71.96641 | 36.85005 | 0.4067706 | 6.805241 | 982 |
| | leafArea_m2 | foliageMass | stemMass | branchMass | fineRootMass | coarseRootMass | | | | | | |
| 1 | 420.3857 | 98.91427 | 3815.740 | 613.1350 | 74.18570 | 986.7341 | | | | | | |
| 2 | 394.8285 | 41.56089 | 3702.413 | 365.5260 | 31.17067 | 1160.0538 | | | | | | |
| 3 | 366.0804 | 86.13657 | 3067.633 | 500.0222 | 64.60242 | 770.4860 | | | | | | |
| 4 | 355.2738 | 83.59383 | 2925.986 | 478.4131 | 62.69537 | 730.2825 | | | | | | |
| 5 | 338.2381 | 79.58543 | 2707.714 | 444.9787 | 59.68908 | 668.8427 | | | | | | |
| 6 | 340.0686 | 35.79670 | 3147.565 | 311.7678 | 26.84752 | 936.2913 | | | | | | |
| | lri | lightResponse | stressIndex | reserve_kg | treeFlags | run | | | | | | |
| 1 | 0.4567858 | | 0 | 0 | 173.09998 | 0 reference | | | | | | |
| 2 | 0.2441241 | | 0 | 0 | 72.73156 | 0 reference | | | | | | |
| 3 | 1.0000000 | | 0 | 0 | 150.73898 | 0 reference | | | | | | |
| 4 | 1.0000000 | | 0 | 0 | 146.28922 | 0 reference | | | | | | |
| 5 | 0.4540371 | | 0 | 0 | 139.27451 | 0 reference | | | | | | |
| 6 | 0.2951740 | | 0 | 0 | 62.64423 | 0 reference | | | | | | |

2.2.9.2 Visualize trees in year 0 and year 100

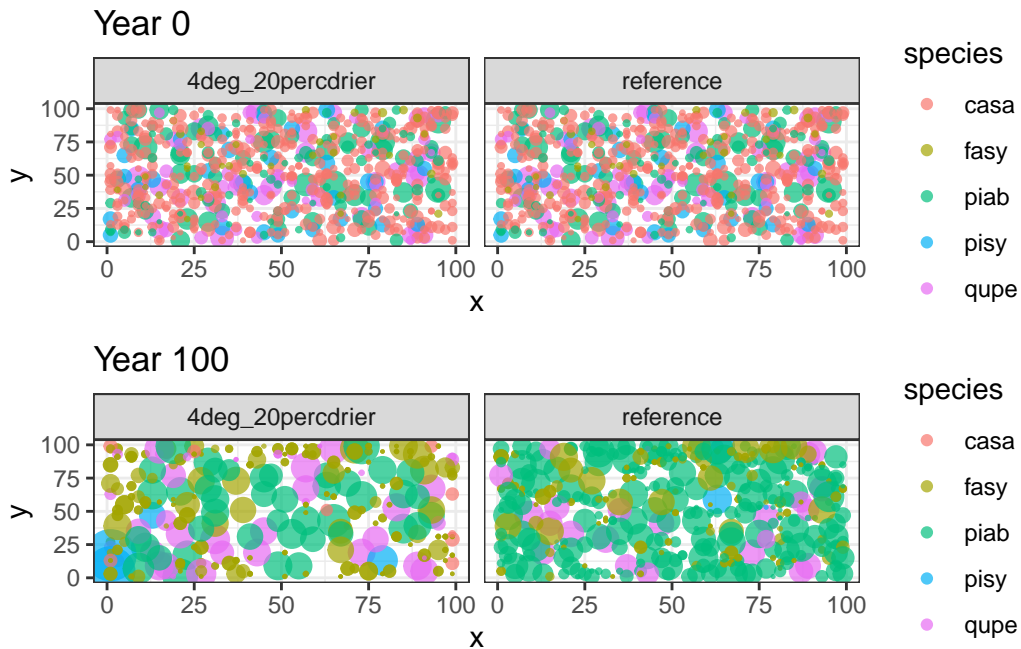
To explore a bit the simulation, plot the tree locations at the beginning and the end of the simulation. For plotting we use the colors for the species, and the size of a circles to show dbh differences. Here we divided dbh with the value 20 just for visualization, not to have too huge circles shading each others completely, but still see the trees.

```
tree0 <- tree |> dplyr::filter(year == 0)
g1 <-
  ggplot2::ggplot(tree0, ggplot2::aes(x = x, y = y, color = species)) +
  ggplot2::geom_point(size = tree0$dbh / 20, alpha = 0.7) +
  ggplot2::ggtitle("Year 0") +
  ggplot2::facet_wrap(~ run) + ggplot2::theme_bw()

tree100 <- tree |> dplyr::filter(year == 100)
g2 <-
```

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```
ggplot2::ggplot(tree100, ggplot2::aes(x = x, y = y, color = species)) +  
  ggplot2::geom_point(size = tree100$dbh / 20, alpha = 0.7) +  
  ggplot2::ggtitle("Year 100") +  
  ggplot2::facet_wrap(~ run) + ggplot2::theme_bw()  
  
gridExtra::grid.arrange(g1, g2, ncol = 1)
```



We can see that the species composition has changed and the dbh of the trees seems to be larger, than in the initial year. We can even identify the same trees at the same location.

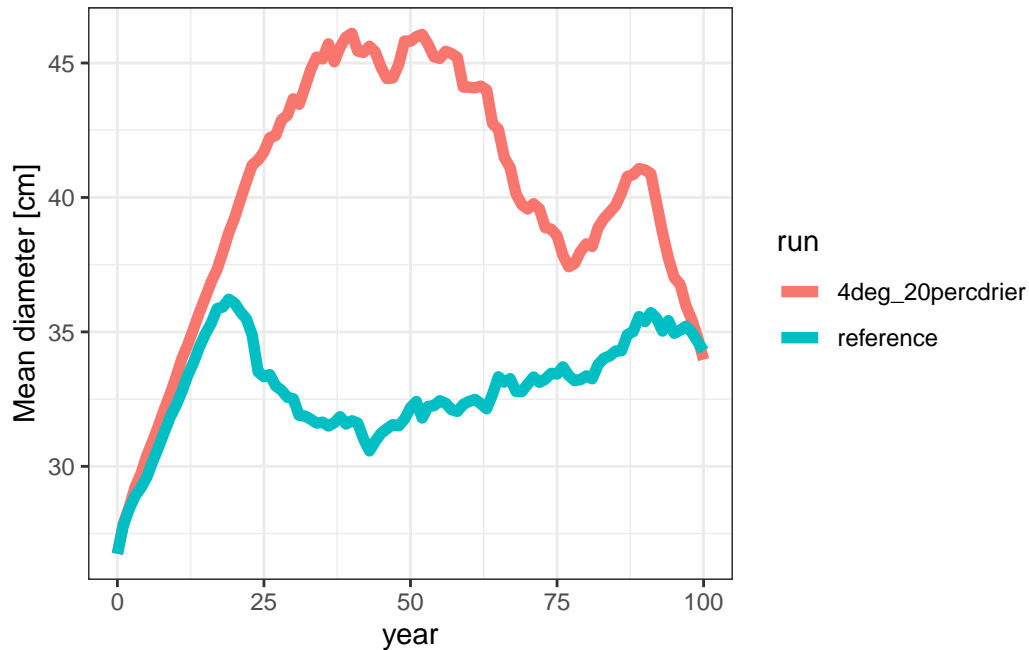
2.2.9.3 Visualize some changes in time

Visualize some changes in time, for example the mean diameter of the trees

```
sum.table <- tree |> dplyr::group_by(year, run) |>  
  dplyr::summarise(  
    N = dplyr::n(),  
    MD = mean(dbh, na.rm = TRUE),  
    #mean diameter  
    BA = sum(basalArea)
```


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```
) #basal area  
  
ggplot2::ggplot(sum.table, ggplot2::aes(x = year, y = MD, color = run)) +  
  ggplot2::geom_line(lwd = 2) +  
  ggplot2::ylab("Mean diameter [cm]") + ggplot2::theme_bw()
```



We can see that there is an initial increase in mean dbh, then a drop after 20/25 years under reference conditions. Under the climate change scenario, the mean dbh is growing for longer time and has the drop after 60 years. The dbh in the last year are very similar however the development of the simulations were different. The drop is due to the growing regeneration layer that is produced by the seeds of the existing trees. In the initial year we do not have regeneration layer in the simulations (it is possible to put there, but we do not have it now). And until the small trees grow up to higher than 4 m they are not appearing in the individual *tree* output as they are handled in cohorts.

2.2.9.4 Species diversity

To study biodiversity aspects, we can calculate biodiversity indicators. Let's use the *adiv* package for species diversity. First we need to change the database structure to have the number of trees for each species in different columns (pivot_wider) without any additional columns for the *adiv* package *speciesdiv* function. We work first only

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with tree data from one simulation (tree1). You can find the documentation of the adiv package here: *“documents/adiv.pdf”*

Shannon index is calculated as follows:

$$S = - \sum (p_i * \log(p_i))$$

Where p_i is the relative abundance of the species i , calculated as the ratio of the abundance of the species i and the abundance of all species. Shannon-index is 0 when we have only one species at the stand. Here we calculate the abundance based on the number of trees, but can be calculate based on the volume to give more weight to larger trees. We add N as the number of records in the summarizing process below, but we can sum up the volume_m3 column and prepare the table for the speciesdiv function based on the volume (or any other variable, e.g. basal area).

```
# First we need to change the
tlong1 <- tree1 |>
  dplyr::group_by(year, species) |> dplyr::summarise(N = dplyr::n()) |>
  tidyr::pivot_wider(
    id_cols = 'year',
    names_from = 'species',
    values_from = 'N',
    values_fill = 0
  ) |>
  dplyr::ungroup() |>
  dplyr::select(-year)

head(tlong1)
```

```
# A tibble: 6 x 5
  casa fasy piab pisy qupe
<int> <int> <int> <int> <int>
1   385    34   118    32    68
2   358    34   117    30    64
3   335    33   115    30    63
4   319    33   114    30    63
5   310    32   112    29    63
6   303    31   112    29    62
```

Then we apply the “speciesdiv” function and we add back the year and run columns to have the information.

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```
div1 <- data.frame(adiv::speciesdiv(tlong1)) |>
  dplyr::mutate(year = unique(tree1$year), run = name1)
head(div1)
```

| | richness | GiniSimpson | Simpson | Shannon | Margalef | Menhinick | McIntosh | year |
|---|----------|-------------|----------|----------|-----------|-----------|-----------|------|
| 1 | 5 | 0.5836227 | 2.401668 | 1.162161 | 0.6195048 | 0.1981072 | 0.3693616 | 0 |
| 2 | 5 | 0.5929556 | 2.456735 | 1.177198 | 0.6248128 | 0.2036157 | 0.3773673 | 1 |
| 3 | 5 | 0.6039255 | 2.524778 | 1.196665 | 0.6293160 | 0.2083333 | 0.3867710 | 2 |
| 4 | 5 | 0.6136885 | 2.588585 | 1.214413 | 0.6322962 | 0.2114775 | 0.3951745 | 3 |
| 5 | 5 | 0.6159951 | 2.604134 | 1.217670 | 0.6346568 | 0.2139802 | 0.3973226 | 4 |
| 6 | 5 | 0.6185478 | 2.621560 | 1.221342 | 0.6363349 | 0.2157659 | 0.3996270 | 5 |

run

1 reference
2 reference
3 reference
4 reference
5 reference
6 reference

We make the same steps for the other simulation results (tree2).

```
tlong2 <- tree2 |>
  dplyr::group_by(year, species) |> dplyr::summarise(N = dplyr::n()) |>
  tidyr::pivot_wider(
    id_cols = 'year',
    names_from = 'species',
    values_from = 'N',
    values_fill = 0
  ) |>
  dplyr::ungroup() |>
  dplyr::select(-year)

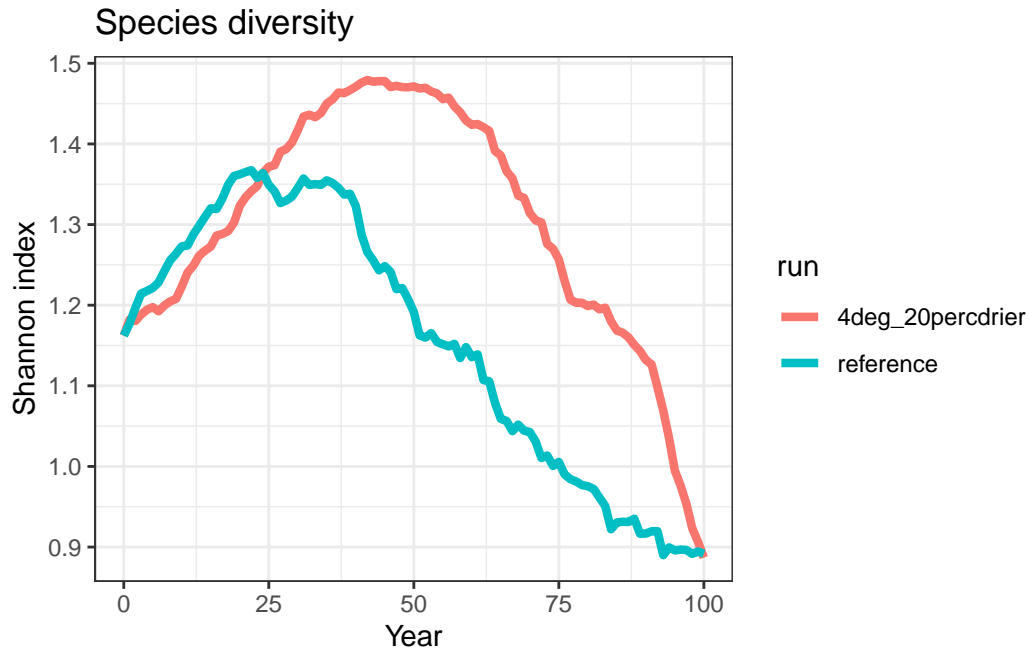
div2 <- data.frame(adiv::speciesdiv(tlong2)) |>
  dplyr::mutate(year = unique(tree2$year), run = name2)
```

We merge them all together and make a plot based on Shannon index.

```
div <- rbind(div1, div2)

ggplot2::ggplot(div, ggplot2::aes(year, Shannon, color = run)) +
  ggplot2::geom_line(lwd = 1.5) +
```

```
ggplot2::ggtitle("Species diversity") +
ggplot2::labs(x = "Year", y = "Shannon index") +
ggplot2::theme_bw()
```



We see that the values of Shannon index are first increasing and then tend to decrease, while the reduction under the 4deg_20percdrier is starting later than under the reference scenario.

2.2.9.5 Spatial diversity

We can calculate some additional biodiversity indices targeting spatial diversity using the *treesp* package developed by Francesco Chianucci (fchianucci@gmail.com). You can find a short description of the package here: [“documents/treepat_package.pdf”](#)

You can install the package using devtools:

```
devtools::install_gitlab('fchianucci/treepat')
```

Then, we are ready to use it Let's calculate these two indices:

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- Diameter differentiation (Gadow, 1993): Spatial size inequality defined as the mean of the ratio of smaller and larger plant sizes in the nearest neighbors of a tree. The value of the index increases with increasing average size difference between neighboring trees. 0 is implying that neighboring trees have equal size.
- Mingling (Aguirre et al., 2003): One very intuitive extension of taxonomic species diversity (either richness or abundance) is considering spatial mingling, namely how plants of the same (con-specific neighbors) or different (hetero-specific neighbors) species are arranged in space. The mingling index calculates the proportion of the k nearest neighbors that do not belong to the same species as the reference tree. For example, with four neighbors, the mingling attribute can assume five values, ranging from 0 (all trees are of the same species) to 1 (all trees belong to different species).

Calculate the indices based on the reference run, then based on the scenario. For each index we add extra columns with the index name, and run name for further analyses. The `max.k` parameter is telling how many neighboring trees we want to account for.

```
library(treespat)

# diameter differentiation:
# mingling

diff <- data.frame(treespat::DIFF(tree1, .x = x, .y = y, .mark = dbh, xmax = 100,
                                ymax = 100, max.k = 4, shape='square', .groups=c('year'))) |>
  dplyr::mutate(index="DIFF", name="Diameter differentiation", run=name1))
head(diff)
```

| | year | DIFF index | | name | run |
|---|------|------------|------|--------------------------|-----------|
| 1 | 0 | 0.4027813 | DIFF | Diameter differentiation | reference |
| 2 | 1 | 0.3793126 | DIFF | Diameter differentiation | reference |
| 3 | 2 | 0.3728755 | DIFF | Diameter differentiation | reference |
| 4 | 3 | 0.3672772 | DIFF | Diameter differentiation | reference |
| 5 | 4 | 0.3621167 | DIFF | Diameter differentiation | reference |
| 6 | 5 | 0.3617524 | DIFF | Diameter differentiation | reference |

```
ming <- data.frame(treespat::MING(tree1, .x = x, .y = y, .species = species,
                                xmax = 100, ymax = 100, max.k = 4, shape='square', .groups=c('year'))) |>
  dplyr::mutate(index="MING", name="Mingling", run=name1))

indices1<-rbind(diff |> dplyr::rename(value=DIFF),
  ming |> dplyr::rename(value=MINGLING ) )
```

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We calculated each index as a separate variable and then merged them into indices1. Here I renamed the column names to have it all “value”, for easier plotting later on. (each line has the information on which run and which index is the value) We do the same for the scenario simulation, we merge them together and make the plotting.

```
diff <- data.frame(treespat::DIFF(tree2, .x = x, .y = y, .mark = dbh,
                                xmax = 100, ymax = 100, max.k = 4,
                                shape = 'square', .groups = c('year')) |>
  dplyr::mutate(index = "DIFF",
               name = "Diameter differentiation", run = name2))

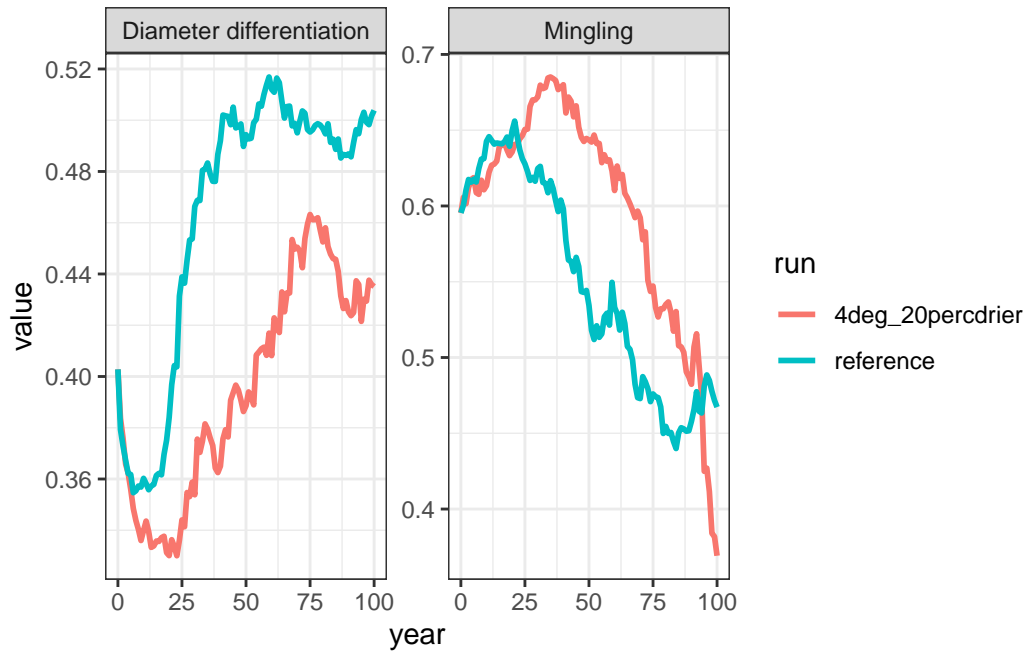
ming <- data.frame(treespat::MING(tree2, .x = x, .y = y, .species = species,
                                xmax = 100, ymax = 100, max.k = 4, shape = 'square', .groups = c('year')) |>
  dplyr::mutate(index = "MING", name = "Mingling", run = name2))

indices2 <- rbind(diff |> dplyr::rename(value = DIFF),
                 ming |> dplyr::rename(value = MINGLING ) )

indices <- rbind(indices1, indices2)

ggplot2::ggplot(indices, ggplot2::aes(x = year, y = value, color = run)) +
  ggplot2::geom_line(lwd = 1) +
  ggplot2::facet_wrap( ~ name, ncol = 2, scales = "free") +
  ggplot2::theme_bw()
```

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The diameter differentiation increases with the increasing average difference in diameter between neighboring trees. The value 0 indicates that neighboring trees have equal diameters. The development shows that the index values decrease during the first circa 10 years, after which it steeply increases due to the occurrence of ingrowth and then the values are stabilized. The increase is not that steep for the climate change scenario that is in accordance with the mean dbh graph. The values for the reference climate scenario are higher than for the climate change scenario indicating slower growth under drier and warmer conditions and/or the differences in tree species composition (proportion of tree species). The mingling index is studying the neighboring trees regarding their species. In both development there is a decrease in the index after the occurrence of regeneration. Using the climate change scenario the index shows steeper decrease and ending up at lower values after 100 years.

2.2.10 Group 2 - Question B

- How are the species distribution and total living biomass C content changing in time on Plot 2? Compare 0 year and 100 year status in the reference case and in the case of your scenario(s)

Run the model as it is described in the previous chapters Section 2.2.3, Section 2.2.5 and Section 2.2.4 to have at least 2 simulations completed: one with reference conditions and one scenario with some changes in the environment. Check if you have the output files in the output folder: *iLand_simulations/output/*. We show all of the solutions

on the example of one reference and one alternative scenario output file. Open the *summerSchoolExercise.Rproj* project in R studio and start working there.

2.2.10.1 Read the landscape output table

Read in the *landscape* output table from two outputs you have for your plot:

```
path1 <- "model/iLand_simulations/output/Output_plot2.sqlite"
path2 <-
  "model/iLand_simulations/output/Output_plot2_4deg_20percdrier.sqlite"

file1 <- here::here(path1)
file2 <- here::here(path2)

# Give some name for the three simulations.
name1 <- "reference"
name2 <- "4deg_20percdrier"

# Read in data using the RSQLite package
sqlite.driver <- RSQLite::dbDriver("SQLite")

# We will work with "landscape" table and tree-scale data:
db1 <-
  RSQLite::dbConnect(sqlite.driver, dbname = file1) # connect to the file1
landscape1 <- RSQLite::dbReadTable(db1, "landscape")
RSQLite::dbDisconnect(db1) # disconnect to the file1

db2 <-
  RSQLite::dbConnect(sqlite.driver, dbname = file2) # connect to the file2
landscape2 <- RSQLite::dbReadTable(db2, "landscape")
RSQLite::dbDisconnect(db2)
```

Merge the data from the two files together and make a column caller run which tells which comes from which simulation, and study the table. The column “run” will support the plotting where we can use facets in ggplot.

```
landscape <- rbind(landscape1 |> dplyr::mutate(run = name1) ,
  landscape2 |> dplyr::mutate(run = name2))

head(landscape)
```

```
year area area_100m species count_ha dbh_avg_cm height_avg_m volume_m3
```


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| | | | | | | | | |
|-----------------|-----------|--------|------------|---------------|----------|-------------|------------|------------|
| 1 | 0 | 1 | 1 | casa | 385 | 21.73276 | 18.052312 | 139.177831 |
| 2 | 0 | 1 | 1 | fasy | 34 | 12.91628 | 7.340003 | 1.600727 |
| 3 | 0 | 1 | 1 | piab | 118 | 34.75135 | 23.365242 | 215.003187 |
| 4 | 0 | 1 | 1 | pisy | 32 | 42.76543 | 24.300133 | 49.013727 |
| 5 | 0 | 1 | 1 | qupe | 68 | 40.62035 | 20.799453 | 118.797078 |
| 6 | 1 | 1 | 1 | casa | 358 | 22.49524 | 18.644885 | 138.166090 |
| total_carbon_kg | | gwl_m3 | | basal_area_m2 | NPP_kg | NPPabove_kg | LAI | |
| 1 | 73246.102 | | 139.177831 | 16.1066092 | 0.000 | 0.000 | 1.92032457 | |
| 2 | 1636.821 | | 1.600727 | 0.4644299 | 0.000 | 0.000 | 0.06445078 | |
| 3 | 58083.681 | | 215.003187 | 14.4589881 | 0.000 | 0.000 | 1.36948128 | |
| 4 | 18250.374 | | 49.013727 | 4.6099225 | 0.000 | 0.000 | 0.51041807 | |
| 5 | 56880.735 | | 118.797078 | 10.0244600 | 0.000 | 0.000 | 0.94624017 | |
| 6 | 73118.915 | | 141.336043 | 15.8220002 | 8338.849 | 5192.833 | 1.87298787 | |
| cohort_count_ha | | run | | | | | | |
| 1 | 0 | | reference | | | | | |
| 2 | 0 | | reference | | | | | |
| 3 | 0 | | reference | | | | | |
| 4 | 0 | | reference | | | | | |
| 5 | 0 | | reference | | | | | |
| 6 | 0 | | reference | | | | | |

2.2.10.2 Visualize changes in time

We can see that the output is given for each year and each species in our 1ha area. Plot the living carbon (total_carbon_kg) in time, coloring by species. We give a unified species coloring in the beginning. Plot number of trees and mean diameter. Carbon and number of trees can be plotted in an additive way, but for mean dbh we do line plot per species.

```
cols.all=c( "rops"="#e0e0e0","acpl"="#A9A9A9","alin"="#696969","alvi"="#2e2e2e",
  "bepe"="#fADFAD","casa"="#7EeAdF","coav"="#20c6b6","tipl"="#645394",
  "ulgl"="#311432","saca"="#D8BFD8","soar"="#DDA0DD","soau"="#BA55D3",
  "pice"="#D27D2D","pini"="#a81c07","algl"="#2ECBE9","tico"="#128FC8",
  "potr"="#00468B","poni"="#5BAEB7","frex"="#fe9cb5","cabe"="#fe6181",
  "acps"="#fe223e","lade"="#FFFE71","abal"="#FFD800","pisy"="#A4DE02",
  "fasy"="#76BA1B","piab"="#006600","quro"="#FF7F00","qupe"="#FF9900",
  "qupu"="#CC9900")

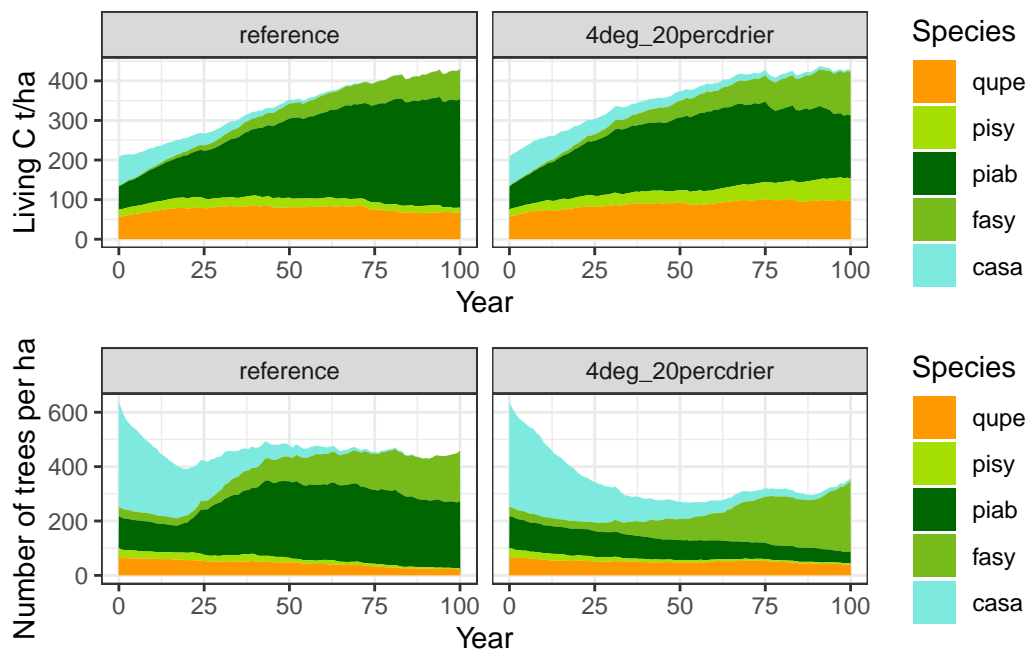
# We set here the order of the run categories for the table, to have the first
#run first and then the second. (left-right of the plots)
landscape$run <- factor(landscape$run, levels = c(name1, name2))
```

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```
# Plot the living carbon content, to have tonnes/ha, we divide total_carbon_kg by 1000.
g1 <-
  ggplot2::ggplot(landscape, ggplot2::aes(year, total_carbon_kg / 1000 , fill = factor(
  ggplot2::geom_area() +
  ggplot2::scale_fill_manual(values = cols.all,
                             guide = ggplot2::guide_legend(reverse = TRUE))) +
  ggplot2::facet_wrap( ~ run, nrow = 1) +
  ggplot2::labs(x = "Year", y = "Living C t/ha", fill = "Species") +
  ggplot2::theme_bw()

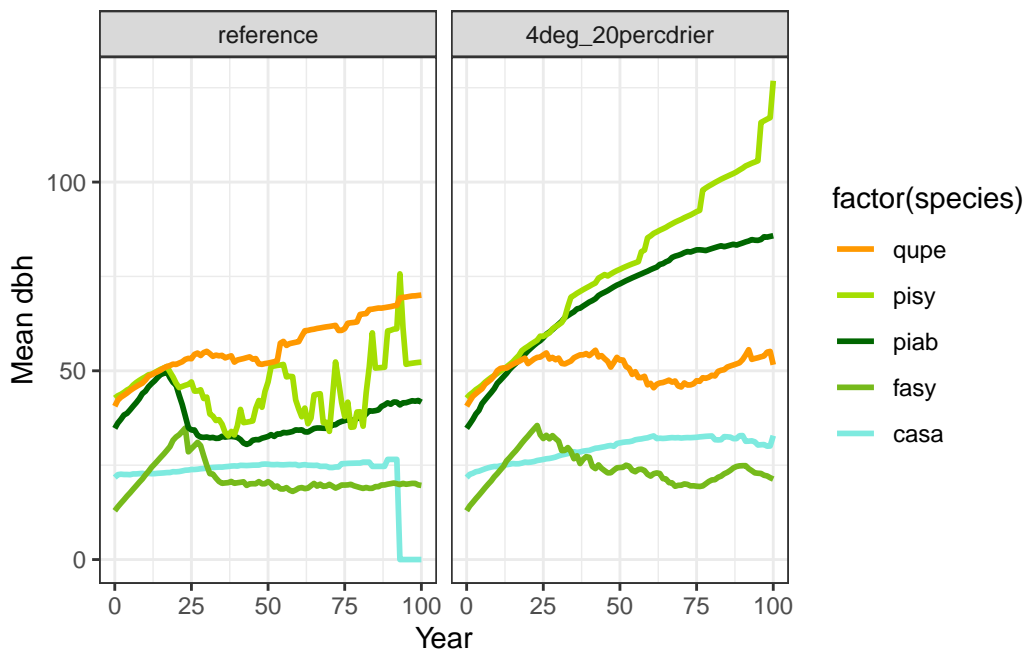
g2 <-
  ggplot2::ggplot(landscape, ggplot2::aes(year, count_ha , fill = factor(species))) +
  ggplot2::geom_area() +
  ggplot2::scale_fill_manual(values = cols.all,
                             guide = ggplot2::guide_legend(reverse = TRUE)) +
  ggplot2::facet_wrap( ~ run, nrow = 1) +
  ggplot2::labs(x = "Year", y = "Number of trees per ha", fill = "Species") +
  ggplot2::theme_bw()

gridExtra::grid.arrange(g1, g2, ncol = 1)
```



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```
g3 <-
  ggplot2::ggplot(landscape,
    ggplot2::aes(year, dbh_avg_cm , color = factor(species))) +
  ggplot2::geom_line(lwd = 1) +
  ggplot2::scale_color_manual(values = cols.all,
    guide = ggplot2::guide_legend(reverse = TRUE)) +
  ggplot2::facet_wrap( ~ run, nrow = 1) +
  ggplot2::labs(x = "Year", y = "Mean dbh", fill = "Species") +
  ggplot2::theme_bw()
print(g3)
```



Note that we do not have management intervention, and in the model trees shorter than 4m are not included in these outputs. However as they grow taller than 4m, model starts to handle them as individual trees and including in these outputs which we are looking now.

Castanea sativa gradually decreased during the simulation period under both scenarios. The reduction resulted from the mortality of chestnut trees, indicating their aging. By the end of the simulation period, chestnut almost completely disappeared from the stand due to the increased number of trees of other species at the plot, and hence higher inter-tree competition, especially under the reference climate, which hindered the chestnut regeneration and its survival. Mean dbh of chestnut is zero at the end of the simulation

period under the reference climate indicating that the species completely disappeared from the stand due to the high stand density, and inter-tree competition.

2.2.10.3 Assess the stored carbon amount

Calculate the stored C amount in the initial year (year==0) and the last year (year==100)

```
livingC0 <- data.frame(
  landscape |> dplyr::filter(year == 0) |>
    dplyr::group_by(run) |>
    dplyr::summarize(sum.livingC = sum(total_carbon_kg / 1000))
)
print(livingC0)
```

```
      run sum.livingC
1 reference      208.0977
2 4deg_20percdrier      208.0977
```

```
livingC100 <- data.frame(
  landscape |> dplyr::filter(year == 100) |>
    dplyr::group_by(run) |>
    dplyr::summarize(sum.livingC = sum(total_carbon_kg / 1000))
)
print(livingC100)
```

```
      run sum.livingC
1 reference      429.5477
2 4deg_20percdrier      428.2694
```

The initial conditions are same for the runs, but they are ending up at different C levels.

Calculate the stored C amount PER SPECIES in the initial year (year==0) and the last year (year==100)

```
species.livingC0 <-
  data.frame(
    landscape |> dplyr::filter(year == 0) |>
      dplyr::group_by(run, species) |>
      dplyr::summarize(livingC = sum(total_carbon_kg / 1000))
  )
print(species.livingC0)
```

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| | run | species | livingC |
|----|------------------|---------|-----------|
| 1 | reference | casa | 73.246102 |
| 2 | reference | fasy | 1.636821 |
| 3 | reference | piab | 58.083681 |
| 4 | reference | pisy | 18.250374 |
| 5 | reference | qupe | 56.880735 |
| 6 | 4deg_20percdrier | casa | 73.246102 |
| 7 | 4deg_20percdrier | fasy | 1.636821 |
| 8 | 4deg_20percdrier | piab | 58.083681 |
| 9 | 4deg_20percdrier | pisy | 18.250374 |
| 10 | 4deg_20percdrier | qupe | 56.880735 |

```
species.livingC100 <-  
  data.frame(  
    landscape |> dplyr::filter(year == 100) |>  
      dplyr::group_by(run, species) |>  
      dplyr::summarize(livingC = sum(total_carbon_kg / 1000))  
  )  
print(species.livingC100)
```

| | run | species | livingC |
|----|------------------|---------|------------|
| 1 | reference | casa | 0.000000 |
| 2 | reference | fasy | 75.469157 |
| 3 | reference | piab | 274.331862 |
| 4 | reference | pisy | 12.701789 |
| 5 | reference | qupe | 67.044909 |
| 6 | 4deg_20percdrier | casa | 4.546279 |
| 7 | 4deg_20percdrier | fasy | 110.708431 |
| 8 | 4deg_20percdrier | piab | 159.773037 |
| 9 | 4deg_20percdrier | pisy | 55.439370 |
| 10 | 4deg_20percdrier | qupe | 97.802295 |

2.2.10.4 Assess the species proportions

Calculate the species proportions based on the stored C amount in the initial year (year==0) and the last year (year==100) For this we need the total C amount and the species-specific C amount.

```
LC0 <- dplyr::left_join(species.livingC0, livingC0, by = "run")  
LC0 <-  
  data.frame(LC0 |> dplyr::mutate(spec.prop = livingC / sum.livingC, year =
```

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```
print(LC0)
```

| | run | species | livingC | sum.livingC | spec.prop | year |
|----|------------------|---------|-----------|-------------|-------------|------|
| 1 | reference | casa | 73.246102 | 208.0977 | 0.351979370 | 0 |
| 2 | reference | fasy | 1.636821 | 208.0977 | 0.007865637 | 0 |
| 3 | reference | piab | 58.083681 | 208.0977 | 0.279117344 | 0 |
| 4 | reference | pisy | 18.250374 | 208.0977 | 0.087700985 | 0 |
| 5 | reference | qupe | 56.880735 | 208.0977 | 0.273336665 | 0 |
| 6 | 4deg_20percdrier | casa | 73.246102 | 208.0977 | 0.351979370 | 0 |
| 7 | 4deg_20percdrier | fasy | 1.636821 | 208.0977 | 0.007865637 | 0 |
| 8 | 4deg_20percdrier | piab | 58.083681 | 208.0977 | 0.279117344 | 0 |
| 9 | 4deg_20percdrier | pisy | 18.250374 | 208.0977 | 0.087700985 | 0 |
| 10 | 4deg_20percdrier | qupe | 56.880735 | 208.0977 | 0.273336665 | 0 |

```
LC100 <- dplyr::left_join(species.livingC100, livingC100, by = "run")
LC100 <-
  data.frame(LC100 |> dplyr::mutate(spec.prop = livingC / sum.livingC, year =
    100))
print(LC100)
```

| | run | species | livingC | sum.livingC | spec.prop | year |
|----|------------------|---------|------------|-------------|------------|------|
| 1 | reference | casa | 0.000000 | 429.5477 | 0.00000000 | 100 |
| 2 | reference | fasy | 75.469157 | 429.5477 | 0.17569447 | 100 |
| 3 | reference | piab | 274.331862 | 429.5477 | 0.63865282 | 100 |
| 4 | reference | pisy | 12.701789 | 429.5477 | 0.02957015 | 100 |
| 5 | reference | qupe | 67.044909 | 429.5477 | 0.15608256 | 100 |
| 6 | 4deg_20percdrier | casa | 4.546279 | 428.2694 | 0.01061547 | 100 |
| 7 | 4deg_20percdrier | fasy | 110.708431 | 428.2694 | 0.25850184 | 100 |
| 8 | 4deg_20percdrier | piab | 159.773037 | 428.2694 | 0.37306666 | 100 |
| 9 | 4deg_20percdrier | pisy | 55.439370 | 428.2694 | 0.12944975 | 100 |
| 10 | 4deg_20percdrier | qupe | 97.802295 | 428.2694 | 0.22836629 | 100 |

Put the two tables together and visualize the results

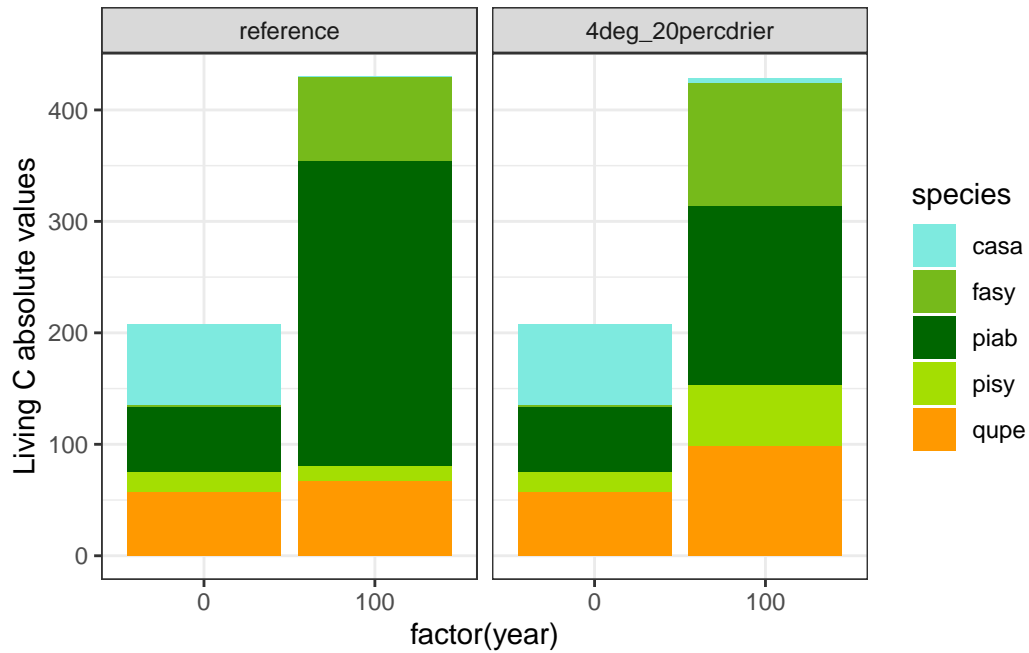
```
LC <- rbind(LC0, LC100)

LC$run <- factor(LC$run, levels = c(name1, name2))

ggplot2::ggplot(LC, ggplot2::aes(fill = species, y = livingC , x = factor(year))) +
  ggplot2::geom_bar(position = "stack", stat = "identity") +
```

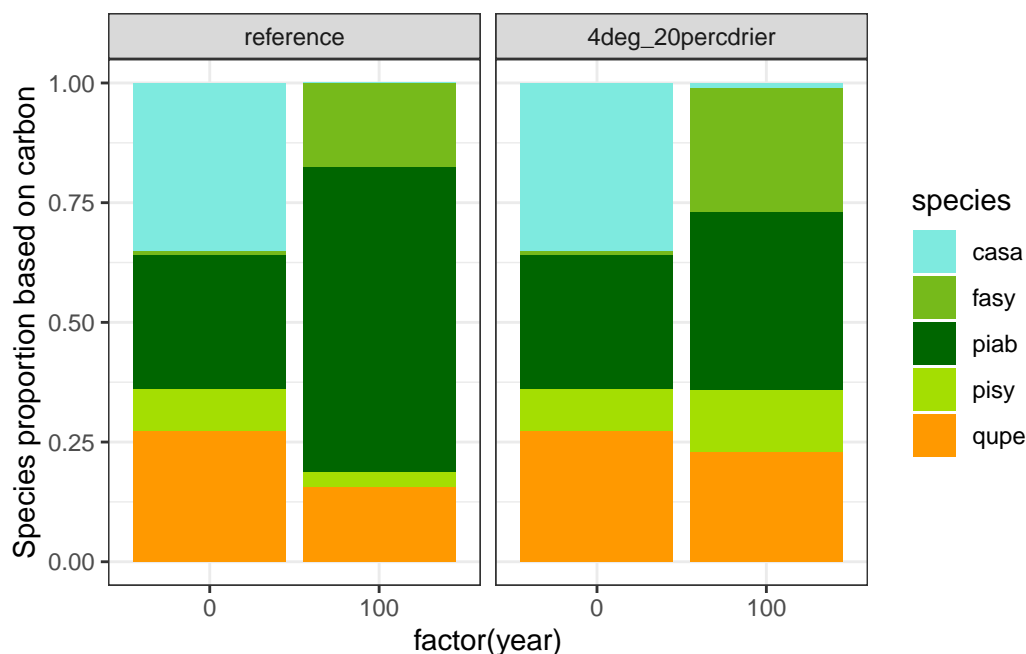
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```
ggplot2::scale_fill_manual(values = cols.all) +
ggplot2::facet_wrap( ~ run) +
ggplot2::ylab("Living C absolute values") +
ggplot2::theme_bw()
```



```
ggplot2::ggplot(LC, ggplot2::aes(fill = species, y = spec.prop,
                                   x = factor(year))) +
ggplot2::geom_bar(position = "stack", stat = "identity") +
ggplot2::scale_fill_manual(values = cols.all) +
ggplot2::facet_wrap( ~ run) +
ggplot2::ylab("Species proportion based on carbon") +
ggplot2::theme_bw()
```

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The living carbon stock doubled over 100 years due to the accumulation of biomass at the plot irrespective of the climate scenario. The comparison of the results between the two climate scenarios showed the difference in the tree species share. The living C stock of spruce was lower under the climate change reflecting its susceptibility to dry conditions, while the living C stock of *Quercus pubescens*, *Fagus sylvatica* and *Pinus sylvestris* were higher. Additionally, we see a significant increase in the share of the shade-tolerant beech at the expense of light-demanding chestnut.

2.2.11 Group 3 - Question A

- How are biodiversity indices changing in time and across the simulated scenario(s) on Plot 3?

Run the model as it is described in the previous chapters Section 2.2.3, Section 2.2.5 and Section 2.2.4 to have at least 2 simulations completed: one with reference conditions and one scenario with some changes in the environment. Check if you have the output files in the output folder: *iLand_simulations/output/*. We show all of the solutions on the example of one reference and one alternative scenario output file. Open the *summerSchoolExercise.Rproj* project in R studio and start working there.

2.2.11.1 Read the tree output table

Read in the *tree* output table from two outputs you have for your plot:

```
path1 <- "model/iLand_simulations/output/Output_plot3.sqlite"
path2 <-
  "model/iLand_simulations/output/Output_plot3_4deg_20percdrier.sqlite"

file1 <- here::here(path1)
file2 <- here::here(path2)

# Give some name for the three simulations.
name1 <- "reference"
name2 <- "4deg_20percdrier"

# Read in data using the RSQLite package
sqlite.driver <- RSQLite::dbDriver("SQLite")
db1 <-
  RSQLite::dbConnect(sqlite.driver, dbname = file1) # connect to the file1

tables.in.the.file <-
  RSQLite::dbListTables(db1) # explore the tables in the file1
print(tables.in.the.file)

[1] "carbon"           "carbonflow"       "dynamicstand"
[4] "landscape"        "landscape_removed" "runinfo"
[7] "stand"            "tree"

# We will work with "tree" table and tree-scale data:
tree1 <- RSQLite::dbReadTable(db1, "tree")
RSQLite::dbDisconnect(db1) # disconnect to the file1

# READ IN DATA FROM THE SECOND FILE: -----
db2 <-
  RSQLite::dbConnect(sqlite.driver, dbname = file2) # connect to the file2
tree2 <- RSQLite::dbReadTable(db2, "tree")
RSQLite::dbDisconnect(db2)
```

Merge the data from the two files together and make a column caller run which tells which comes from which simulation, and study the table. The column “run” will support the plotting where we can use facets in ggplot.

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```
tree <- rbind(tree1 |> dplyr::mutate(run = name1) ,
              tree2 |> dplyr::mutate(run = name2))

head(tree)
```

| | year | ru | rid | species | id | x | y | dbh | height | basalArea | volume_m3 | age |
|---|-------------|---------------|-------------|------------|--------------|----------------|----|----------|----------|-----------|-----------|-----|
| 1 | 0 | 0 | 1 | piab | 1 | 7 | 41 | 80.47096 | 54.10505 | 0.5085905 | 11.639825 | 579 |
| 2 | 0 | 0 | 1 | piab | 2 | 57 | 63 | 77.85299 | 52.34484 | 0.4760367 | 10.540342 | 560 |
| 3 | 0 | 0 | 1 | fasy | 3 | 33 | 45 | 77.32411 | 43.94139 | 0.4695910 | 8.934730 | 549 |
| 4 | 0 | 0 | 1 | fasy | 4 | 79 | 97 | 76.44166 | 43.43991 | 0.4589338 | 8.632307 | 542 |
| 5 | 0 | 0 | 1 | piab | 5 | 99 | 35 | 74.65018 | 50.19142 | 0.4376748 | 9.292261 | 537 |
| 6 | 0 | 0 | 1 | fasy | 6 | 11 | 77 | 74.61653 | 42.40273 | 0.4372804 | 8.028635 | 530 |
| | leafArea_m2 | foliageMass | stemMass | branchMass | fineRootMass | coarseRootMass | | | | | | |
| 1 | 381.4915 | 89.76272 | 3273.843 | 531.3649 | 67.32204 | 829.4560 | | | | | | |
| 2 | 362.3074 | 85.24881 | 3017.901 | 492.4429 | 63.93661 | 756.3417 | | | | | | |
| 3 | 387.3896 | 35.21723 | 3946.903 | 484.7826 | 26.41292 | 432.6764 | | | | | | |
| 4 | 379.9038 | 34.53671 | 3846.260 | 472.1521 | 25.90253 | 421.3067 | | | | | | |
| 5 | 339.3250 | 79.84119 | 2721.455 | 447.0886 | 59.88089 | 672.6917 | | | | | | |
| 6 | 364.6130 | 33.14663 | 3642.679 | 446.6253 | 24.85997 | 398.3362 | | | | | | |
| | lri | lightResponse | stressIndex | reserve_kg | treeFlags | run | | | | | | |
| 1 | 0.5557720 | | 0 | 0 | 157.08476 | 0 reference | | | | | | |
| 2 | 0.3826686 | | 0 | 0 | 149.18542 | 0 reference | | | | | | |
| 3 | 0.4321580 | | 0 | 0 | 61.63016 | 0 reference | | | | | | |
| 4 | 0.7127665 | | 0 | 0 | 60.43925 | 0 reference | | | | | | |
| 5 | 1.0000000 | | 0 | 0 | 139.72208 | 0 reference | | | | | | |
| 6 | 0.3028383 | | 0 | 0 | 58.00661 | 0 reference | | | | | | |

2.2.11.2 Visualize trees in year 0 and year 100

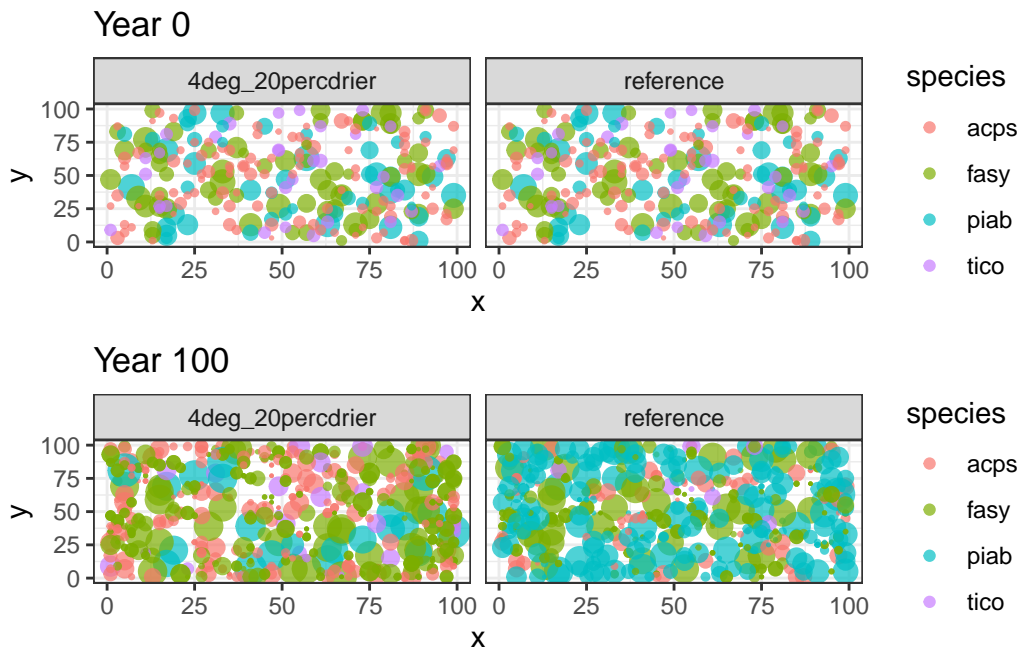
To explore a bit the simulation, plot the tree locations at the beginning and the end of the simulation. For plotting we use the colors for the species, and the size of a circles to show dbh differences. Here we divided dbh with the value 20 just for visualization, not to have too huge circles shading each others completely, but still see the trees.

```
tree0 <- tree |> dplyr::filter(year == 0)
g1 <-
  ggplot2::ggplot(tree0, ggplot2::aes(x = x, y = y, color = species)) +
  ggplot2::geom_point(size = tree0$dbh / 20, alpha = 0.7) +
  ggplot2::ggtitle("Year 0") +
  ggplot2::facet_wrap(~ run) + ggplot2::theme_bw()
```

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```
tree100 <- tree |> dplyr::filter(year == 100)
g2 <-
  ggplot2::ggplot(tree100, ggplot2::aes(x = x, y = y, color = species)) +
  ggplot2::geom_point(size = tree100$dbh / 20, alpha = 0.7) +
  ggplot2::ggtitle("Year 100") +
  ggplot2::facet_wrap(~ run) + ggplot2::theme_bw()

gridExtra::grid.arrange(g1, g2, ncol = 1)
```



We can see that the species composition is somewhat changed and the forest become more dense. We can even identify the same trees at the same location.

2.2.11.3 Visualize some changes in time

Visualize some changes in time, for example the mean diameter of the trees

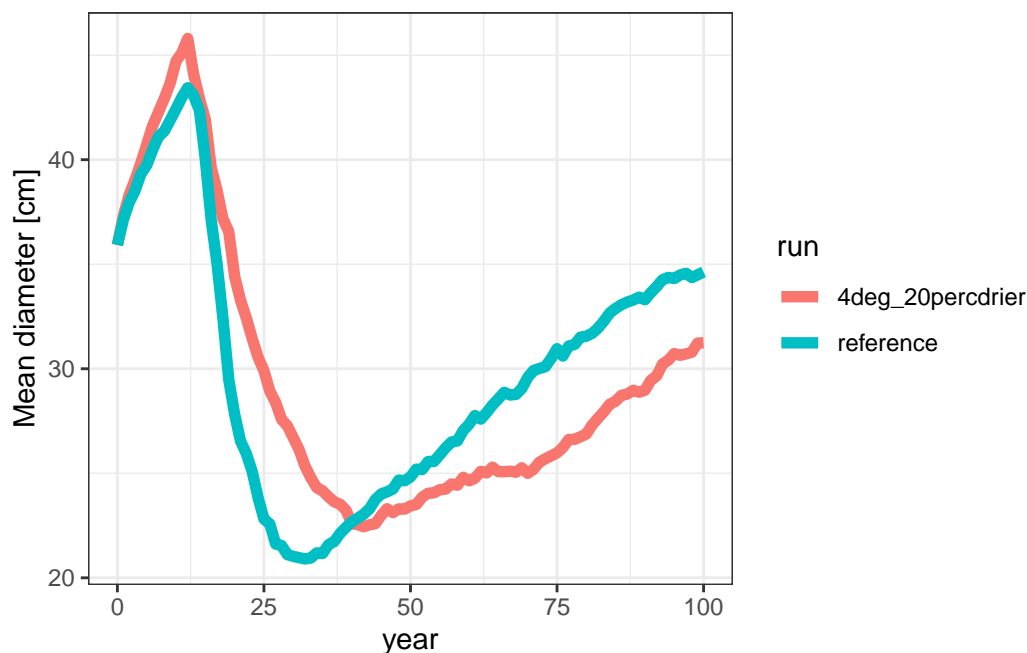
```
sum.table <- tree |> dplyr::group_by(year, run) |>
  dplyr::summarise(
    N = dplyr::n(),
    MD = mean(dbh, na.rm = TRUE),
    #mean diameter
```

```

    BA = sum(basalArea)
  ) #basal area

ggplot2::ggplot(sum.table, ggplot2::aes(x = year, y = MD, color = run)) +
  ggplot2::geom_line(lwd = 2) +
  ggplot2::ylab("Mean diameter [cm]") + ggplot2::theme_bw()

```



We can see that there is an initial increase in mean dbh, then a drop after 12/15 years. This is due to the growing regeneration layer that is produced by the seeds of the existing trees. In the initial year we do not have regeneration layer in the simulations (it is possible to put there, but we do not have it now). And until the small trees grow up to higher than 4 m they are not appearing in the individual *tree* output as they are handled in cohorts. After the stand canopy became closed, the mean DBH started to increase again until the end of the simulation period.

2.2.11.4 Species diversity

To study biodiversity aspects, we can calculate biodiversity indicators. Let's use the *adiv* package for species diversity. First we need to change the database structure to have the number of trees for each species in different columns (*pivot_wider*) without any additional columns for the *adiv* package *speciesdiv* function. We work first only

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with tree data from one simulation (tree1). You can find the documentation of the adiv package here: “[documents/adiv.pdf](#)”

Shannon index is calculated as follows:

$$S = - \sum (p_i * \log(p_i))$$

Where p_i is the relative abundance of the species i , calculated as the ratio of the abundance of the species i and the abundance of all species. Shannon-index is 0 when we have only one species at the stand. Here we calculate the abundance based on the number of trees, but can be calculate based on the volume to give more weight to larger trees. We add N as the number of records in the summarizing process below, but we can sum up the volume_m3 column and prepare the table for the speciesdiv function based on the volume (or any other variable, e.g. basal area).

```
# First we need to change the
tlong1 <- tree1 |>
  dplyr::group_by(year, species) |> dplyr::summarise(N = dplyr::n()) |>
  tidyr::pivot_wider(
    id_cols = 'year',
    names_from = 'species',
    values_from = 'N',
    values_fill = 0
  ) |>
  dplyr::ungroup() |>
  dplyr::select(-year)

head(tlong1)
```

```
# A tibble: 6 x 4
  acps fasy piab tico
<int> <int> <int> <int>
1   113    67   49   32
2   110    67   49   28
3   108    67   49   27
4   106    66   47   27
5   104    65   47   27
6   103    64   46   26
```

Then we apply the “speciesdiv” function and we add back the year and run columns to have the information.

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```
div1 <- data.frame(adiv::speciesdiv(tlong1)) |>
  dplyr::mutate(year = unique(tree1$year), run = name1)
head(div1)
```

| | richness | GiniSimpson | Simpson | Shannon | Margalef | Menhinick | McIntosh | year |
|---|----------|-------------|----------|----------|-----------|-----------|-----------|------|
| 1 | 4 | 0.6963785 | 3.293574 | 1.282865 | 0.5391300 | 0.2475938 | 0.4786064 | 0 |
| 2 | 4 | 0.6935024 | 3.262668 | 1.274467 | 0.5417769 | 0.2509823 | 0.4762610 | 1 |
| 3 | 4 | 0.6939255 | 3.267178 | 1.274173 | 0.5429419 | 0.2524778 | 0.4768591 | 2 |
| 4 | 4 | 0.6938000 | 3.265839 | 1.274493 | 0.5449263 | 0.2550307 | 0.4770630 | 3 |
| 5 | 4 | 0.6955241 | 3.284332 | 1.277850 | 0.5461435 | 0.2566001 | 0.4789300 | 4 |
| 6 | 4 | 0.6936853 | 3.264617 | 1.274063 | 0.5477988 | 0.2587385 | 0.4774250 | 5 |

run

1 reference
2 reference
3 reference
4 reference
5 reference
6 reference

We make the same steps for the other simulation results (tree2).

```
tlong2 <- tree2 |>
  dplyr::group_by(year, species) |> dplyr::summarise(N = dplyr::n()) |>
  tidyr::pivot_wider(
    id_cols = 'year',
    names_from = 'species',
    values_from = 'N',
    values_fill = 0
  ) |>
  dplyr::ungroup() |>
  dplyr::select(-year)

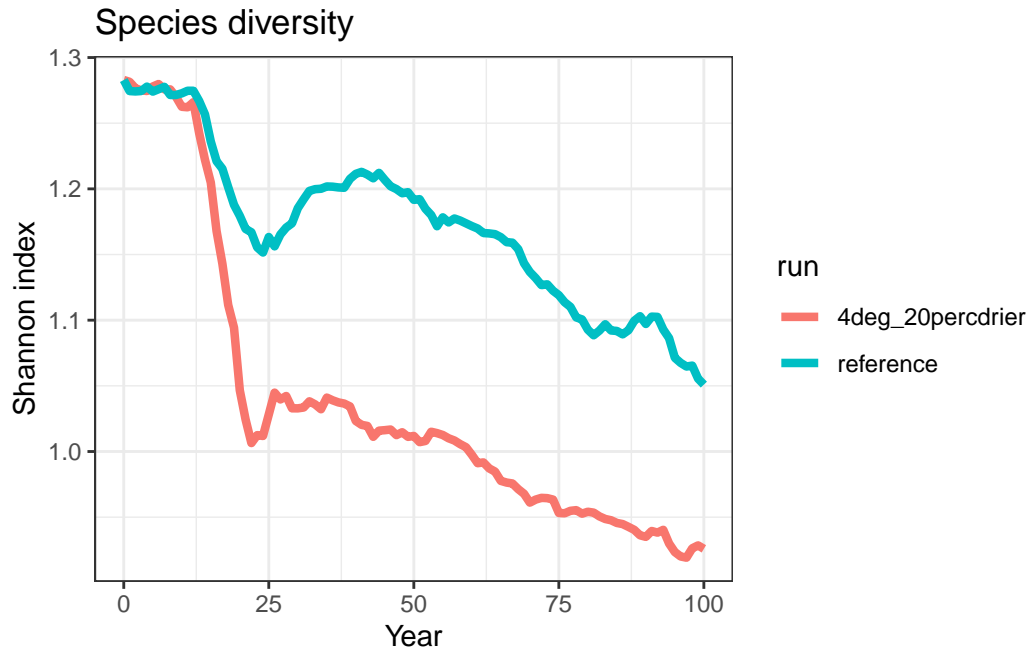
div2 <- data.frame(adiv::speciesdiv(tlong2)) |>
  dplyr::mutate(year = unique(tree2$year), run = name2)
```

We merge them all together and make a plot based on Shannon index.

```
div <- rbind(div1, div2)

ggplot2::ggplot(div, ggplot2::aes(year, Shannon, color = run)) +
  ggplot2::geom_line(lwd = 1.5) +
```

```
ggplot2::ggtitle("Species diversity") +
ggplot2::labs(x = "Year", y = "Shannon index") +
ggplot2::theme_bw()
```



We see that the values of Shannon index are first stable and then tend to decrease, while the reduction under the 4deg_20percdrier is more substantial than under the reference scenario.

2.2.11.5 Spatial diversity

We can calculate some additional biodiversity indices targeting spatial diversity using the *treesp* package developed by Francesco Chianucci (fchianucci@gmail.com). You can find a short description of the package here: [“documents/treepat_package.pdf”](#)

You can install the package using devtools:

```
devtools::install_gitlab('fchianucci/treepat')
```

Then, we are ready to use it Let's calculate these two indices:

2 Process-based modeling

- Diameter differentiation (Gadow, 1993): Spatial size inequality defined as the mean of the ratio of smaller and larger plant sizes in the nearest neighbors of a tree. The value of the index increases with increasing average size difference between neighboring trees. 0 is implying that neighboring trees have equal size.
- Mingling (Aguirre et al., 2003): One very intuitive extension of taxonomic species diversity (either richness or abundance) is considering spatial mingling, namely how plants of the same (con-specific neighbors) or different (hetero-specific neighbors) species are arranged in space. The mingling index calculates the proportion of the k nearest neighbors that do not belong to the same species as the reference tree. For example, with four neighbors, the mingling attribute can assume five values, ranging from 0 (all trees are of the same species) to 1 (all trees belong to different species).

Calculate the indices based on the reference run, then based on the scenario. For each index we add extra columns with the index name, and run name for further analyses. The `max.k` parameter is telling how many neighboring trees we want to account for.

```
# diameter differentiation:
# mingling

diff <- data.frame(treespat::DIFF(tree1, .x = x, .y = y, .mark = dbh, xmax = 100,
                                ymax = 100, max.k = 4, shape='square', .groups=c('year'))) |>
  dplyr::mutate(index="DIFF", name="Diameter differentiation", run=name1))
head(diff)
```

| | year | DIFF index | | name | run |
|---|------|------------|------|--------------------------|-----------|
| 1 | 0 | 0.3938630 | DIFF | Diameter differentiation | reference |
| 2 | 1 | 0.3825122 | DIFF | Diameter differentiation | reference |
| 3 | 2 | 0.3765717 | DIFF | Diameter differentiation | reference |
| 4 | 3 | 0.3749870 | DIFF | Diameter differentiation | reference |
| 5 | 4 | 0.3681887 | DIFF | Diameter differentiation | reference |
| 6 | 5 | 0.3639637 | DIFF | Diameter differentiation | reference |

```
ming <- data.frame(treespat::MING(tree1, .x = x, .y = y, .species = species,
                                xmax = 100, ymax = 100, max.k = 4, shape='square', .groups=c('year'))) |>
  dplyr::mutate(index="MING", name="Mingling", run=name1))

indices1<-rbind(diff |> dplyr::rename(value=DIFF),
ming |> dplyr::rename(value=MINGLING ) )
```

We calculated each index as a separate variable and then merged them into `indices1`. Here I renamed the column names to have it all “value”, for easier plotting later on.

2 Process-based modeling

(each line has the information on which run and which index is the value) We do the same for the scenario simulation, we merge them together and make the plotting.

```
diff <- data.frame(treespat::DIFF(tree2, .x = x, .y = y, .mark = dbh,
                                xmax = 100, ymax = 100, max.k = 4,
                                shape = 'square', .groups = c('year')) |>
  dplyr::mutate(index = "DIFF", name = "Diameter differentiation",
               run = name2))

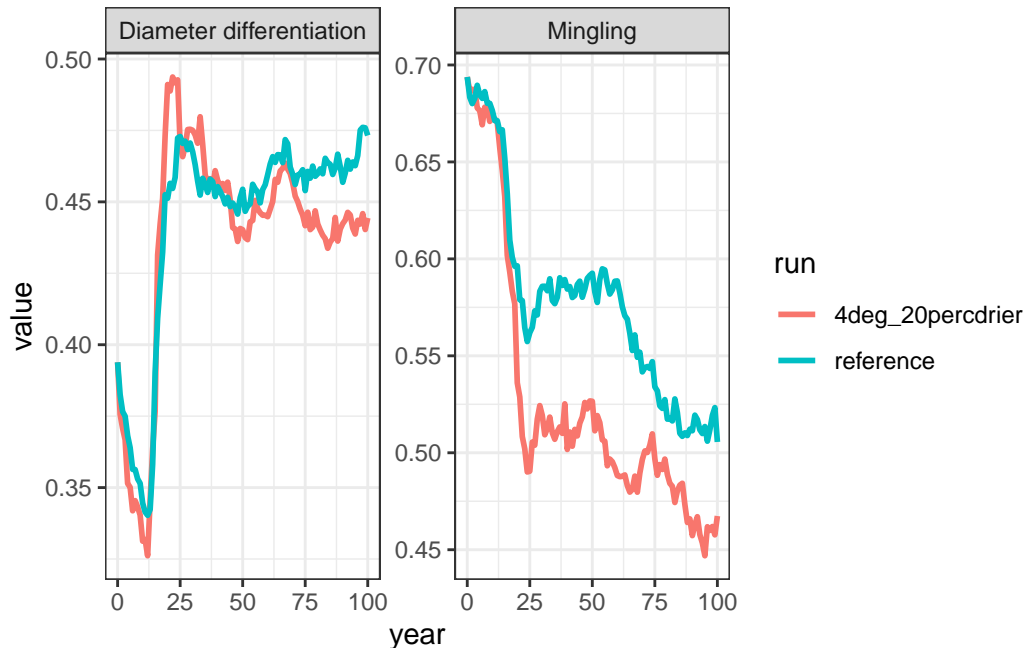
ming <- data.frame(treespat::MING(tree2, .x = x, .y = y,
                                .species = species,
                                xmax = 100, ymax = 100, max.k = 4,
                                shape = 'square', .groups=c('year')) |>
  dplyr::mutate(index = "MING", name = "Mingling",
               run = name2))

indices2 <- rbind(diff |> dplyr::rename(value = DIFF),
                 ming |> dplyr::rename(value = MINGLING))

indices <- rbind(indices1, indices2)

ggplot2::ggplot(indices, ggplot2::aes(x = year, y = value, color = run)) +
  ggplot2::geom_line(lwd = 1) +
  ggplot2::facet_wrap(~ name, ncol = 2, scales = "free") +
  ggplot2::theme_bw()
```

2 Process-based modeling



The diameter differentiation increases with the increasing average difference in diameter between neighboring trees. The value 0 indicates that neighboring trees have equal diameters. The development shows that the index values decrease during the first circa 12 years, after which it steeply increases due to the occurrence of ingrowth and then the values are stabilized. The values of Shannon index differed between the scenarios only at the end of the simulation period, when the calculated Shannon index under the climate change scenario was slightly lower than under the reference climate. The mingling index is studying the neighboring trees regarding their species. In both development there is a decrease in the index after the occurrence of regeneration, because the number of trees increased four times. Using the climate change scenario the index shows greater decrease since the spruce share was substantially reduced (see Figures in Question B - Group 3, Section 2.2.12.2).

2.2.12 Group 3 - Question B

- How are the species distribution and total living biomass C content changing in time on Plot 3? Compare 0 year and 100 year status in the reference case and in the case of your scenario(s)

Run the model as it is described in the previous chapters Section 2.2.3, Section 2.2.5 and Section 2.2.4 to have at least 2 simulations completed: one with reference conditions and one scenario with some changes in the environment. Check if you have the output files in the output folder: *iLand_simulations/output/*. We show all of the solutions

on the example of one reference and one alternative scenario output file. Open the *summerSchoolExercise.Rproj* project in R studio and start working there.

2.2.12.1 Read the landscape output table

Read in the *landscape* output table from two outputs you have for your plot:

```
path1 <- "model/iLand_simulations/output/Output_plot3.sqlite"
path2 <-
  "model/iLand_simulations/output/Output_plot3_4deg_20percdrier.sqlite"

file1 <- here::here(path1)
file2 <- here::here(path2)

# Give some name for the three simulations.
name1 <- "reference"
name2 <- "4deg_20percdrier"

# Read in data using the RSQLite package
sqlite.driver <- RSQLite::dbDriver("SQLite")

# We will work with "landscape" table and tree-scale data:
db1 <-
  RSQLite::dbConnect(sqlite.driver, dbname = file1) # connect to the file1
landscape1 <- RSQLite::dbReadTable(db1, "landscape")
RSQLite::dbDisconnect(db1) # disconnect to the file1

db2 <-
  RSQLite::dbConnect(sqlite.driver, dbname = file2) # connect to the file2
landscape2 <- RSQLite::dbReadTable(db2, "landscape")
RSQLite::dbDisconnect(db2)
```

Merge the data from the two files together and make a column caller run which tells which comes from which simulation, and study the table. The column “run” will support the plotting where we can use facets in ggplot.

```
landscape <- rbind(landscape1 |> dplyr::mutate(run = name1) ,
  landscape2 |> dplyr::mutate(run = name2))

head(landscape)
```

```
year area area_100m species count_ha dbh_avg_cm height_avg_m volume_m3
```

2 Process-based modeling

| | | | | | | | | | |
|-----------------|----------|--------|-----------|---------------|-----------|----------|-------------|--------------------|--|
| 1 | 0 | 1 | 1 | acps | 113 | 21.62995 | 18.52183 | 41.57766 | |
| 2 | 0 | 1 | 1 | fasy | 67 | 52.05965 | 29.58422 | 218.19995 | |
| 3 | 0 | 1 | 1 | piab | 49 | 50.26190 | 33.79384 | 182.14630 | |
| 4 | 0 | 1 | 1 | tico | 32 | 30.63841 | 23.38127 | 21.38005 | |
| 5 | 1 | 1 | 1 | acps | 110 | 22.55262 | 19.19236 | 43.91456 | |
| 6 | 1 | 1 | 1 | fasy | 67 | 53.02260 | 30.03274 | 226.37490 | |
| total_carbon_kg | | gwl_m3 | | basal_area_m2 | | NPP_kg | NPPabove_kg | LAI | |
| 1 | 19316.78 | | 41.57766 | | 4.693063 | | 0.000 | 0.000 0.4800021 | |
| 2 | 74974.41 | | 218.19995 | | 15.193077 | | 0.000 | 0.000 1.3766679 | |
| 3 | 45666.89 | | 182.14630 | | 10.724078 | | 0.000 | 0.000 0.9377907 | |
| 4 | 11816.98 | | 21.38005 | | 2.379258 | | 0.000 | 0.000 0.2673509 | |
| 5 | 20284.37 | | 44.17968 | | 4.895663 | | 3936.955 | 2581.190 0.4935337 | |
| 6 | 79317.75 | | 226.37490 | | 15.670265 | | 12642.176 | 8302.325 1.4294626 | |
| cohort_count_ha | | run | | | | | | | |
| 1 | 0 | | reference | | | | | | |
| 2 | 0 | | reference | | | | | | |
| 3 | 0 | | reference | | | | | | |
| 4 | 0 | | reference | | | | | | |
| 5 | 27 | | reference | | | | | | |
| 6 | 49 | | reference | | | | | | |

2.2.12.2 Visualize changes in time

We can see that the output is given for each year and each species in our 1ha area. Plot the living carbon (total_carbon_kg) in time, coloring by species. We give a unified species coloring in the beginning. Plot number of trees and mean diameter. Carbon and number of trees can be plotted in an additive way, but for mean dbh we do line plot per species.

```
cols.all=c( "rops"="#e0e0e0","acpl"="#A9A9A9","alin"="#696969","alvi"="#2e2e2e",
  "bepe"="#fADFAD","casa"="#7eeadf","coav"="#20c6b6","tipl"="#645394",
  "ulgl"="#311432","saca"="#D8BFD8","soar"="#DDA0DD","soau"="#BA55D3",
  "pice"="#D27D2D","pini"="#a81c07","algl"="#2ECBE9","tico"="#128FC8",
  "potr"="#00468B","poni"="#5BAEB7","frex"="#fe9cb5","cabe"="#fe6181",
  "acps"="#fe223e","lade"="#FFFE71","abal"="#FFD800","pisy"="#A4DE02",
  "fasy"="#76BA1B","piab"="#006600","quro"="#FF7F00","qupe"="#FF9900",
  "qupu"="#CC9900")

# We set here the order of the run categories for the table, to have the first
#run first and then the second. (left-right of the plots)
landscape$run <- factor(landscape$run, levels = c(name1, name2))
```

2 Process-based modeling

```
# Plot the living carbon content, to have tonnes/ha, we divide total_carbon_kg by 1000.
g1 <-
  ggplot2::ggplot(landscape, ggplot2::aes(year, total_carbon_kg / 1000 ,
                                           fill = factor(species))) +

  ggplot2::geom_area() +
  ggplot2::scale_fill_manual(values = cols.all,
                             guide = ggplot2::guide_legend(reverse = TRUE)) +

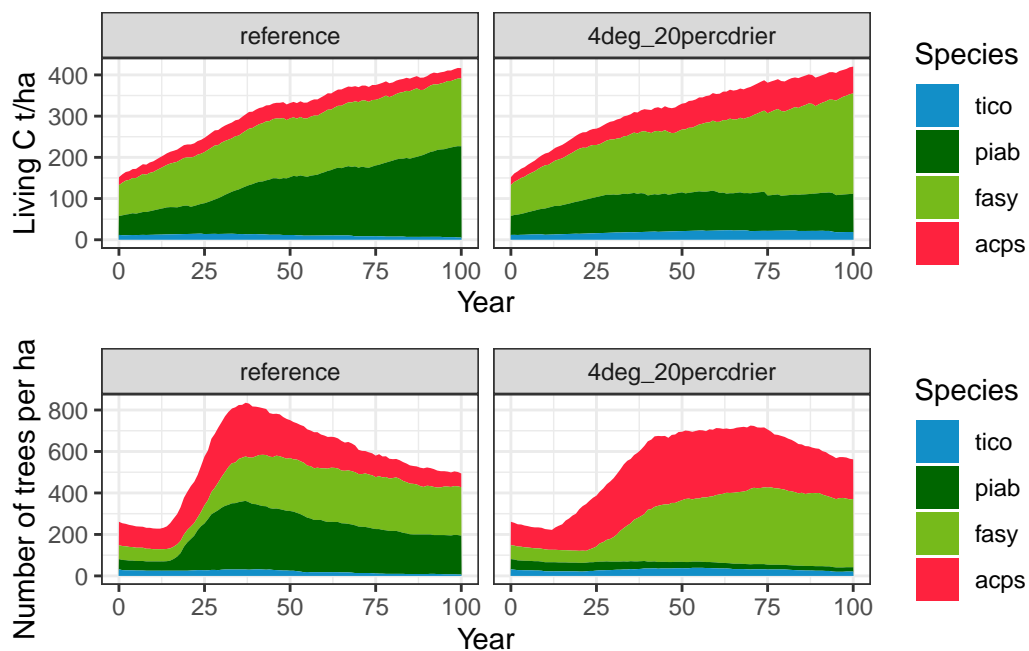
  ggplot2::facet_wrap( ~ run, nrow = 1) +
  ggplot2::labs(x = "Year", y = "Living C t/ha", fill = "Species") +
  ggplot2::theme_bw()

g2 <-
  ggplot2::ggplot(landscape, ggplot2::aes(year, count_ha,
                                           fill = factor(species))) +

  ggplot2::geom_area() +
  ggplot2::scale_fill_manual(values = cols.all,
                             guide = ggplot2::guide_legend(reverse = TRUE)) +

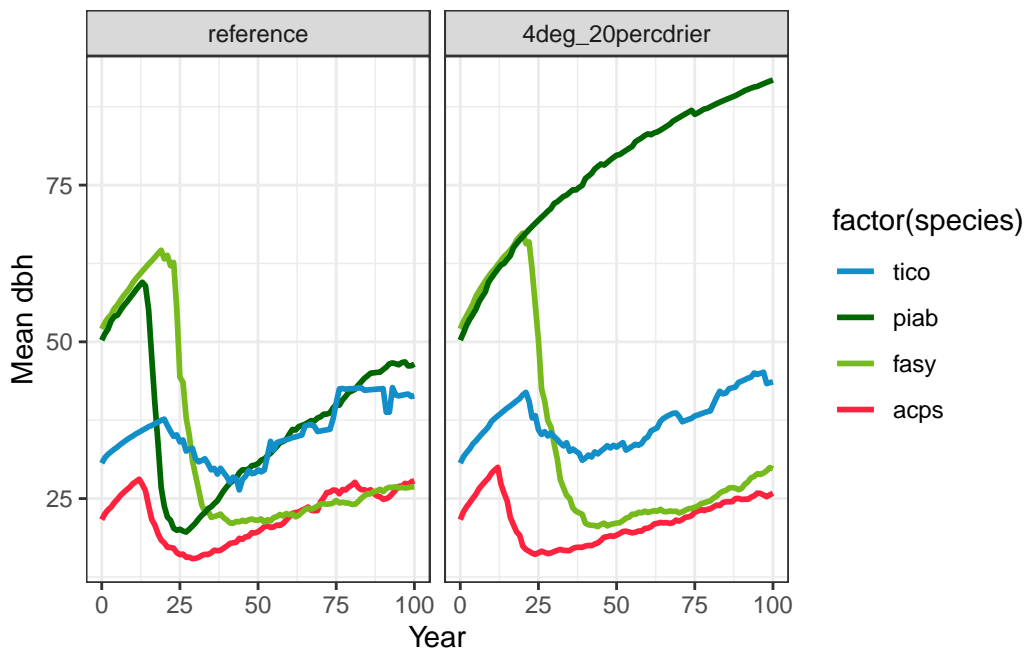
  ggplot2::facet_wrap( ~ run, nrow = 1) +
  ggplot2::labs(x = "Year", y = "Number of trees per ha",
               fill = "Species") +
  ggplot2::theme_bw()

gridExtra::grid.arrange(g1, g2, ncol = 1)
```



2 Process-based modeling

```
g3 <-
  ggplot2::ggplot(landscape, ggplot2::aes(year, dbh_avg_cm ,
                                           color = factor(species))) +
  ggplot2::geom_line(lwd = 1) +
  ggplot2::scale_color_manual(values = cols.all,
                             guide = ggplot2::guide_legend(reverse = TRUE)) +
  ggplot2::facet_wrap( ~ run, nrow = 1) +
  ggplot2::labs(x = "Year", y = "Mean dbh", fill = "Species") +
  ggplot2::theme_bw()
print(g3)
```



Note that we do not have management intervention, and in the model trees shorter than 4m are not included in these outputs. However as they grow taller than 4m, model starts to handle them as individual trees and including in these outputs which we are looking now.

Beech profited from drier and warmer conditions at the expense of spruce. *Acer pseudo-platanus* and *Tilia cordata* also slightly increased their proportion in the living C stock and number of trees. The increase of the number of trees indicates the success of the regeneration under reference conditions, however this increase is much slower under the climate change scenario.

Mean dbh of individual species reflected the development of the number of trees. The increase in the number of trees caused the reduction of mean dbh, e.g. of beech under

both scenarios between 20 and 35 simulation years. The species-specific graphs for mean dbh indicates that some species do not have successful regeneration under the climate change scenario. Spruce dbh decreased only under reference scenario, when we observed the increase of the number of trees, while under climate change scenario the mean dbh of spruce was growing indicating the growth of remaining trees of the species at the plot.

2.2.12.3 Assess the stored carbon amount

Calculate the stored C amount in the initial year (year==0) and the last year (year==100)

```
livingC0 <- data.frame(
  landscape |> dplyr::filter(year == 0) |>
    dplyr::group_by(run) |>
    dplyr::summarize(sum.livingC = sum(total_carbon_kg / 1000))
)
print(livingC0)
```

| | run | sum.livingC |
|---|------------------|-------------|
| 1 | reference | 151.7751 |
| 2 | 4deg_20percdrier | 151.7751 |

```
livingC100 <- data.frame(
  landscape |> dplyr::filter(year == 100) |>
    dplyr::group_by(run) |>
    dplyr::summarize(sum.livingC = sum(total_carbon_kg / 1000))
)
print(livingC100)
```

| | run | sum.livingC |
|---|------------------|-------------|
| 1 | reference | 416.3909 |
| 2 | 4deg_20percdrier | 420.1472 |

The initial conditions are same for the runs, but they are ending up at different C levels.

Calculate the stored C amount PER SPECIES in the initial year (year==0) and the last year (year==100)

2 Process-based modeling

```
species.livingC0 <-  
  data.frame(  
    landscape |> dplyr::filter(year == 0) |>  
    dplyr::group_by(run, species) |>  
    dplyr::summarize(livingC = sum(total_carbon_kg / 1000))  
  )  
print(species.livingC0)
```

| | run | species | livingC |
|---|------------------|---------|----------|
| 1 | reference | acps | 19.31678 |
| 2 | reference | fasy | 74.97441 |
| 3 | reference | piab | 45.66689 |
| 4 | reference | tico | 11.81698 |
| 5 | 4deg_20percdrier | acps | 19.31678 |
| 6 | 4deg_20percdrier | fasy | 74.97441 |
| 7 | 4deg_20percdrier | piab | 45.66689 |
| 8 | 4deg_20percdrier | tico | 11.81698 |

```
species.livingC100 <-  
  data.frame(  
    landscape |> dplyr::filter(year == 100) |>  
    dplyr::group_by(run, species) |>  
    dplyr::summarize(livingC = sum(total_carbon_kg / 1000))  
  )  
print(species.livingC100)
```

| | run | species | livingC |
|---|------------------|---------|------------|
| 1 | reference | acps | 25.042637 |
| 2 | reference | fasy | 164.555979 |
| 3 | reference | piab | 221.267535 |
| 4 | reference | tico | 5.524713 |
| 5 | 4deg_20percdrier | acps | 65.167214 |
| 6 | 4deg_20percdrier | fasy | 243.374438 |
| 7 | 4deg_20percdrier | piab | 92.649456 |
| 8 | 4deg_20percdrier | tico | 18.956110 |

2.2.12.4 Assess the species proportions

Calculate the species proportions based on the stored C amount in the initial year (year==0) and the last year (year==100) For this we need the total C amount and the species-specific C amount.

2 Process-based modeling

```
LC0 <- dplyr::left_join(species.livingC0, livingC0, by = "run")
LC0 <-
  data.frame(LC0 |> dplyr::mutate(spec.prop = livingC / sum.livingC,
                                year = 0))
print(LC0)
```

| | run | species | livingC | sum.livingC | spec.prop | year |
|---|------------------|---------|----------|-------------|-----------|------|
| 1 | reference | acps | 19.31678 | 151.7751 | 0.1272724 | 0 |
| 2 | reference | fasy | 74.97441 | 151.7751 | 0.4939837 | 0 |
| 3 | reference | piab | 45.66689 | 151.7751 | 0.3008854 | 0 |
| 4 | reference | tico | 11.81698 | 151.7751 | 0.0778585 | 0 |
| 5 | 4deg_20percdrier | acps | 19.31678 | 151.7751 | 0.1272724 | 0 |
| 6 | 4deg_20percdrier | fasy | 74.97441 | 151.7751 | 0.4939837 | 0 |
| 7 | 4deg_20percdrier | piab | 45.66689 | 151.7751 | 0.3008854 | 0 |
| 8 | 4deg_20percdrier | tico | 11.81698 | 151.7751 | 0.0778585 | 0 |

```
LC100 <-
  dplyr::left_join(species.livingC100, livingC100, by = "run")
LC100 <-
  data.frame(LC100 |> dplyr::mutate(spec.prop = livingC / sum.livingC,
                                   year = 100))
print(LC100)
```

| | run | species | livingC | sum.livingC | spec.prop | year |
|---|------------------|---------|------------|-------------|------------|------|
| 1 | reference | acps | 25.042637 | 416.3909 | 0.06014214 | 100 |
| 2 | reference | fasy | 164.555979 | 416.3909 | 0.39519594 | 100 |
| 3 | reference | piab | 221.267535 | 416.3909 | 0.53139383 | 100 |
| 4 | reference | tico | 5.524713 | 416.3909 | 0.01326809 | 100 |
| 5 | 4deg_20percdrier | acps | 65.167214 | 420.1472 | 0.15510567 | 100 |
| 6 | 4deg_20percdrier | fasy | 243.374438 | 420.1472 | 0.57925991 | 100 |
| 7 | 4deg_20percdrier | piab | 92.649456 | 420.1472 | 0.22051665 | 100 |
| 8 | 4deg_20percdrier | tico | 18.956110 | 420.1472 | 0.04511778 | 100 |

Put the two tables together and visualize the results

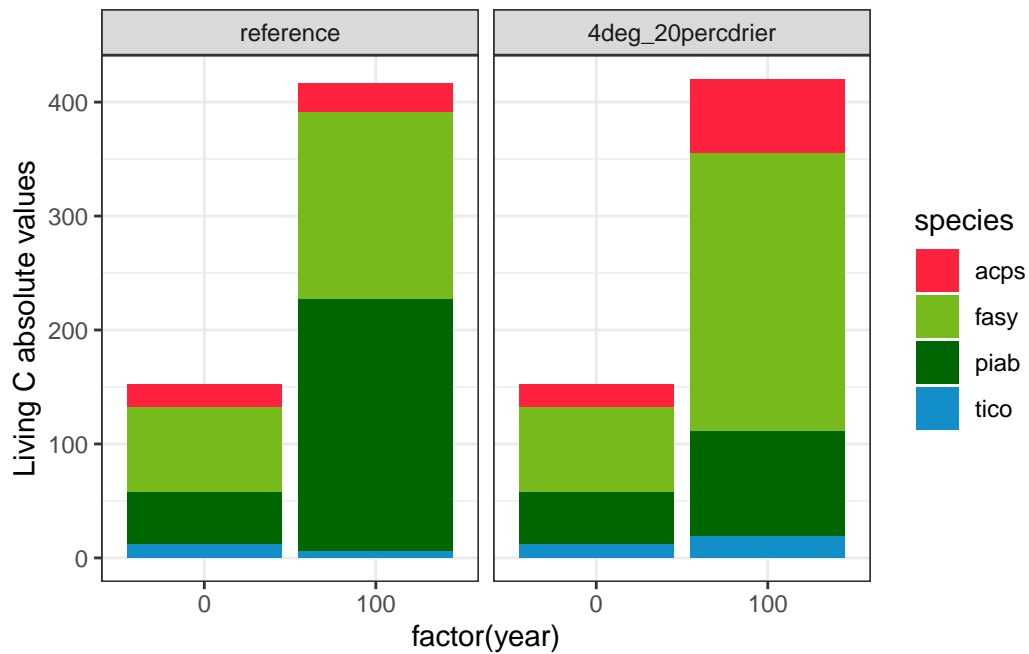
```
LC <- rbind(LC0, LC100)

LC$run <- factor(LC$run, levels = c(name1, name2))

ggplot2::ggplot(LC, ggplot2::aes(fill = species, y = livingC,
                                x = factor(year))) +
```

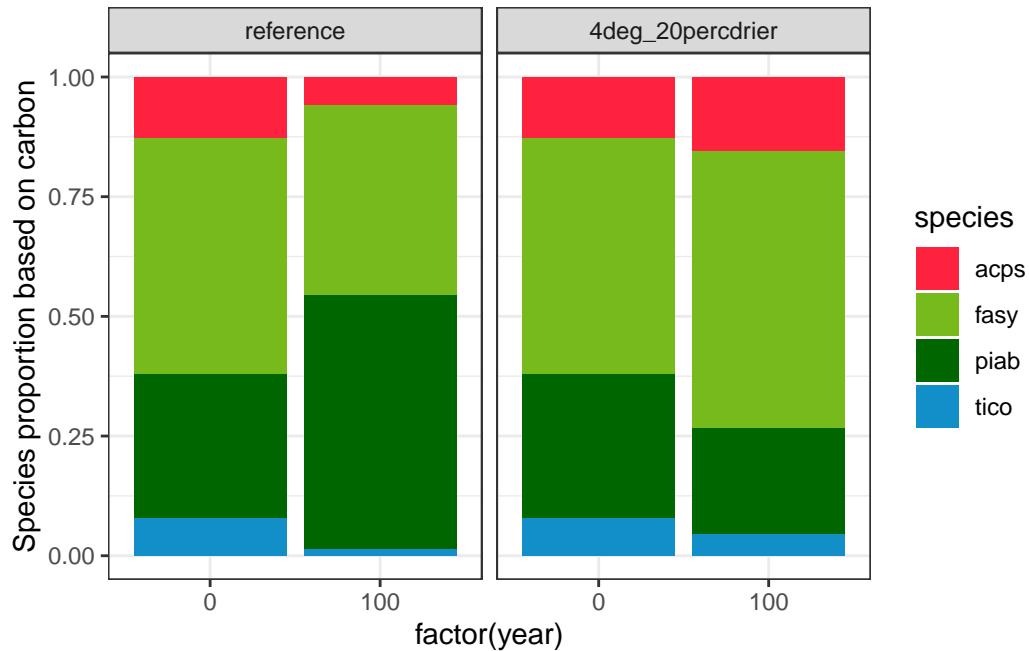
2 Process-based modeling

```
ggplot2::geom_bar(position = "stack", stat = "identity") +
ggplot2::scale_fill_manual(values = cols.all) +
ggplot2::facet_wrap( ~ run) +
ggplot2::ylab("Living C absolute values") +
ggplot2::theme_bw()
```



```
ggplot2::ggplot(LC, ggplot2::aes(fill = species, y = spec.prop,
                                   x = factor(year))) +
ggplot2::geom_bar(position = "stack", stat = "identity") +
ggplot2::scale_fill_manual(values = cols.all) +
ggplot2::facet_wrap( ~ run) +
ggplot2::ylab("Species proportion based on carbon") +
ggplot2::theme_bw()
```

2 Process-based modeling



The living C stock more than doubled over 100 years due to the accumulation of biomass in trees and no management interventions. Moreover, the proportion of individual tree species changed depending on the driving climatic conditions. Under reference conditions the proportion of spruce has grown, under climate change the proportion of beech.

2.2.13 Group 4 - Question A

- How are biodiversity indices changing in time and across the simulated scenario(s) on Plot 4?

Run the model as it is described in the previous chapters Section 2.2.3, Section 2.2.5 and Section 2.2.4 to have at least 2 simulations completed: one with reference conditions and one scenario with some changes in the environment. Check if you have the output files in the output folder: *iLand_simulations/output/*. We show all of the solutions on the example of one reference and one alternative scenario output file. Open the *summerSchoolExercise.Rproj* project in R studio and start working there.

Read in the *tree* output table from two outputs you have for your plot:

```
path1 <- "model/iLand_simulations/output/Output_plot4.sqlite"
path2 <- "model/iLand_simulations/output/Output_plot4_4deg_20percldrier.sqlite"
```

2 Process-based modeling

```
file1 <- here::here(path1)
file2 <- here::here(path2)

# Give some name for the three simulations.
name1 <- "reference"
name2 <- "4deg_20percdrier"

# Read in data using the RSQLite package
sqlite.driver <- RSQLite::dbDriver("SQLite")
db1 <-
  RSQLite::dbConnect(sqlite.driver, dbname = file1) # connect to the file1

tables.in.the.file <-
  RSQLite::dbListTables(db1) # explore the tables in the file1
print(tables.in.the.file)
```

```
[1] "carbon"           "carbonflow"       "dynamicstand"
[4] "landscape"        "landscape_removed" "runinfo"
[7] "stand"            "tree"
```

```
# We will work with "tree" table and tree-scale data:
tree1 <- RSQLite::dbReadTable(db1, "tree")
RSQLite::dbDisconnect(db1) # disconnect to the file1

# READ IN DATA FROM THE SECOND FILE: -----
db2 <-
  RSQLite::dbConnect(sqlite.driver, dbname = file2) # connect to the file2
tree2 <- RSQLite::dbReadTable(db2, "tree")
RSQLite::dbDisconnect(db2)
```

Merge the data from the two files together and make a column caller run which tells which comes from which simulation, and study the table. The column “run” will support the plotting where we can use facets in ggplot.

```
tree <- rbind(tree1 |> dplyr::mutate(run = name1) ,
              tree2 |> dplyr::mutate(run = name2))

head(tree)
```

```
year ru rid species id x y dbh height basalArea volume_m3 age
```

2 Process-based modeling

| | | | | | | | | | | | | |
|---|-----------|----------|----------|----------|----------|----|----|----------|----------|-----------|----------|-----|
| 1 | 0 | 0 | 1 | fasy | 1 | 49 | 65 | 98.48459 | 55.96636 | 0.7617745 | 18.46041 | 699 |
| 2 | 0 | 0 | 1 | fasy | 2 | 51 | 15 | 94.27415 | 53.57367 | 0.6980316 | 16.19252 | 669 |
| 3 | 0 | 0 | 1 | fasy | 3 | 97 | 47 | 94.07941 | 53.46301 | 0.6951508 | 16.09238 | 668 |
| 4 | 0 | 0 | 1 | fasy | 4 | 63 | 7 | 91.67390 | 52.09602 | 0.6600568 | 14.88928 | 651 |
| 5 | 0 | 0 | 1 | fasy | 5 | 53 | 57 | 90.70000 | 51.54258 | 0.6461070 | 14.41977 | 644 |
| 6 | 0 | 0 | 1 | fasy | 6 | 13 | 95 | 89.37351 | 50.78876 | 0.6273466 | 13.79631 | 634 |
| leafArea_m2 foliageMass stemMass branchMass fineRootMass coarseRootMass | | | | | | | | | | | | |
| 1 | 584.4382 | 53.13074 | 6802.456 | 845.6093 | 39.84806 | | | | | | 758.3801 | |
| 2 | 542.6002 | 49.32729 | 6165.430 | 764.7609 | 36.99547 | | | | | | 685.2726 | |
| 3 | 540.6961 | 49.15419 | 6136.807 | 761.1324 | 36.86565 | | | | | | 681.9930 | |
| 4 | 517.4045 | 47.03678 | 5789.331 | 717.1134 | 35.27758 | | | | | | 642.2182 | |
| 5 | 508.0949 | 46.19045 | 5651.843 | 699.7122 | 34.64284 | | | | | | 626.5004 | |
| 6 | 495.5272 | 45.04793 | 5467.530 | 676.3990 | 33.78595 | | | | | | 605.4482 | |
| lri lightResponse stressIndex reserve_kg treeFlags run | | | | | | | | | | | | |
| 1 | 0.6396535 | | 0 | 0 | 92.97880 | | | | 0 | reference | | |
| 2 | 0.4253728 | | 0 | 0 | 86.32275 | | | | 0 | reference | | |
| 3 | 1.0000000 | | 0 | 0 | 86.01984 | | | | 0 | reference | | |
| 4 | 0.4545080 | | 0 | 0 | 82.31436 | | | | 0 | reference | | |
| 5 | 0.6055760 | | 0 | 0 | 80.83328 | | | | 0 | reference | | |
| 6 | 1.0000000 | | 0 | 0 | 78.83388 | | | | 0 | reference | | |

2.2.13.1 Visualize trees in year 0 and year 100

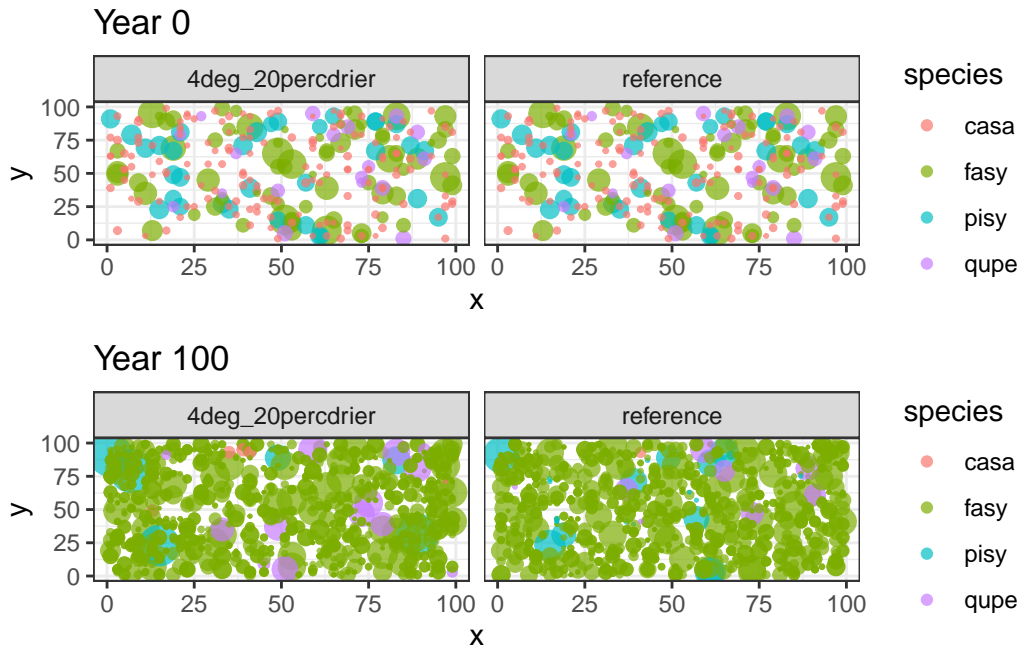
To explore a bit the simulation, plot the tree locations at the beginning and the end of the simulation. For plotting we use the colors for the species, and the size of a circles to show dbh differences. Here we divided dbh with the value 20 just for visualization, not to have too huge circles shading each others completely, but still see the trees.

```
tree0 <- tree |> dplyr::filter(year == 0)
g1 <-
  ggplot2::ggplot(tree0, ggplot2::aes(x = x, y = y, color = species)) +
  ggplot2::geom_point(size = tree0$dbh / 20, alpha = 0.7) +
  ggplot2::ggtitle("Year 0") +
  ggplot2::facet_wrap(~ run) + ggplot2::theme_bw()

tree100 <- tree |> dplyr::filter(year == 100)
g2 <-
  ggplot2::ggplot(tree100, ggplot2::aes(x = x, y = y, color = species)) +
  ggplot2::geom_point(size = tree100$dbh / 20, alpha = 0.7) +
  ggplot2::ggtitle("Year 100") +
  ggplot2::facet_wrap(~ run) + ggplot2::theme_bw()
```

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```
gridExtra::grid.arrange(g1, g2, ncol = 1)
```



We can see that the species composition is somewhat changed and the forest become more dense. We can even identify the same trees at the same location.

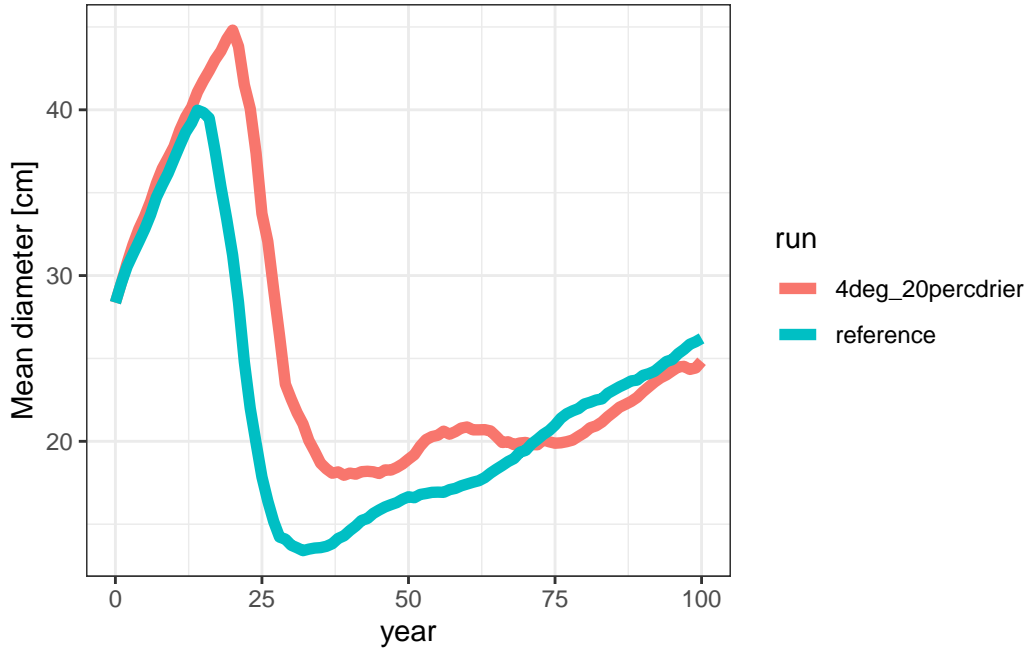
2.2.13.2 Visualize some changes in time

Visualize some changes in time, for example the mean diameter of the trees

```
sum.table <- tree |> dplyr::group_by(year, run) |>
  dplyr::summarise(
    N = dplyr::n(),
    MD = mean(dbh, na.rm = TRUE), #mean diameter
    BA = sum(basalArea)#basal area
  )

ggplot2::ggplot(sum.table, ggplot2::aes(x = year, y = MD, color = run)) +
  ggplot2::geom_line(lwd = 2) +
  ggplot2::ylab("Mean diameter [cm]") + ggplot2::theme_bw()
```

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We can see that there is an initial increase in mean dbh, then a drop after 15/20 years followed by a less steep increase until the end of the simulation period. This is due to the growing regeneration layer that is produced by the seeds of the existing trees. In the initial year we do not have regeneration layer in the simulations (it is possible to put there, but we do not have it now). And until the small trees are less than 4 m tall, they do not appear in the individual *tree* output as they are handled in cohorts. When the canopy closes around the age 30/40, no more massive ingrowth occurs and mean DBH starts to grow again.

2.2.13.3 Species diversity

To study biodiversity aspects, we can calculate biodiversity indicators. Let's use the *adiv* package for species diversity. First we need to change the database structure to have the number of trees for each species in different columns (`pivot_wider`) without any additional columns for the *adiv* package *speciesdiv* function. We work first only with tree data from one simulation (*tree1*). You can find the documentation of the *adiv* package here: "[documents/adiv.pdf](#)"

Shannon index is calculated as follows:

$$S = - \sum (p_i * \log(p_i))$$

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Where p_i is the relative abundance of the species i , calculated as the ratio of the abundance of the species i and the abundance of all species. Shannon-index is 0 when we have only one species at the stand. Here we calculate the abundance based on the number of trees, but can be calculate based on the volume to give more weight to larger trees. We add N as the number of records in the summarizing process below, but we can sum up the volume_m3 column and prepare the table for the speciesdiv function based on the volume (or any other variable, e.g. basal area).

```
# First we need to change the
tlong1 <- tree1 |>
  dplyr::group_by(year, species) |> dplyr::summarise(N = dplyr::n()) |>
  tidyr::pivot_wider(
    id_cols = 'year',
    names_from = 'species',
    values_from = 'N',
    values_fill = 0
  ) |>
  dplyr::ungroup() |>
  dplyr::select(-year)

head(tlong1)
```

```
# A tibble: 6 x 4
   casa fasy pisy qupe
<int> <int> <int> <int>
1   152    70    33    18
2   147    70    32    18
3   143    69    32    18
4   139    68    30    18
5   139    68    30    18
6   137    68    30    18
```

Then we apply the “speciesdiv” function and we add back the year and run columns to have the information.

```
div1 <- data.frame(adiv::speciesdiv(tlong1)) |>
  dplyr::mutate(year = unique(tree1$year), run = name1)
head(div1)
```

```
   richness GiniSimpson  Simpson  Shannon  Margalef Menhinick  McIntosh year
1         4    0.6052946 2.533535 1.109706 0.5348097 0.2420910 0.3956925    0
2         4    0.6092385 2.559105 1.115644 0.5369369 0.2447960 0.3993293    1
```


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```
3      4      0.6131053 2.584683 1.122656 0.5387598 0.2471208 0.4028815      2
4      4      0.6129335 2.583535 1.122122 0.5413928 0.2504897 0.4030962      3
5      4      0.6129335 2.583535 1.122122 0.5413928 0.2504897 0.4030962      4
6      4      0.6154135 2.600195 1.126170 0.5421632 0.2514778 0.4053326      5
      run
1 reference
2 reference
3 reference
4 reference
5 reference
6 reference
```

We make the same steps for the other simulation results (tree2).

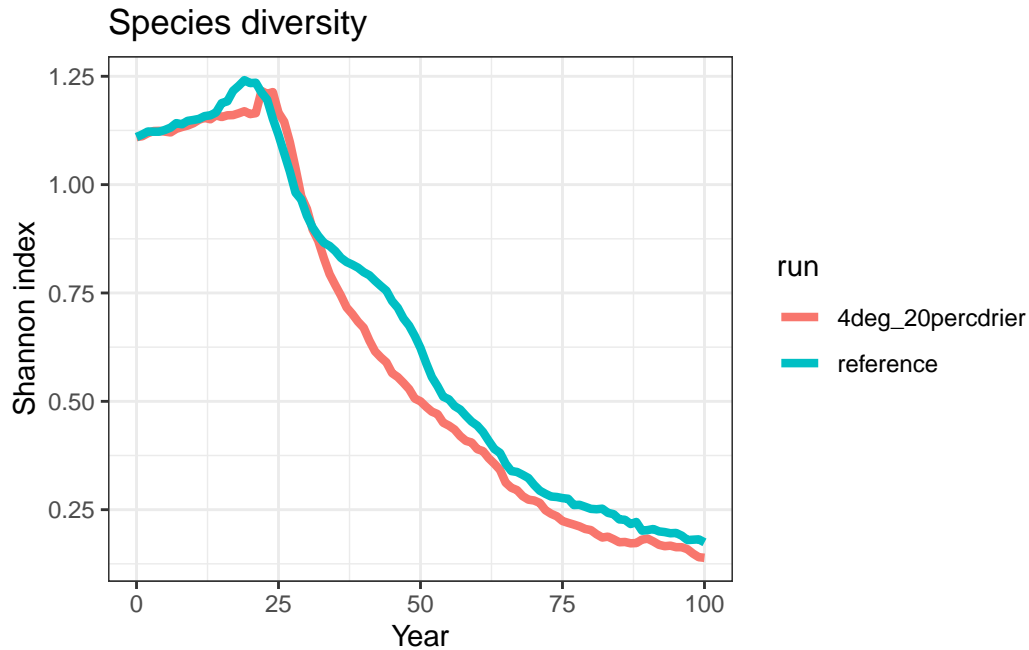
```
tlong2 <- tree2 |>
  dplyr::group_by(year, species) |> dplyr::summarise(N = dplyr::n()) |>
  tidyr::pivot_wider(
    id_cols = 'year',
    names_from = 'species',
    values_from = 'N',
    values_fill = 0
  ) |>
  dplyr::ungroup() |>
  dplyr::select(-year)

div2 <- data.frame(adiv::speciesdiv(tlong2)) |>
  dplyr::mutate(year = unique(tree2$year), run = name2)
```

We merge them all together and make a plot based on Shannon index.

```
div <- rbind(div1, div2)

ggplot2::ggplot(div, ggplot2::aes(year, Shannon , color = run)) +
  ggplot2::geom_line(lwd = 1.5) +
  ggplot2::ggtitle("Species diversity") +
  ggplot2::labs(x = "Year", y = "Shannon index") +
  ggplot2::theme_bw()
```



We see that the values of Shannon index are first stable and then tend to decrease, while the reduction under the *4deg_20percdrrier* scenario is slightly greater than under the reference scenario due to the more pronounced dominance of beech (see Figures in Question B - Group 4, Section 2.2.14.2).

2.2.13.4 Spatial diversity

We can calculate some additional biodiversity indices targeting spatial diversity using the *treespac* package developed by Francesco Chianucci (fchianucci@gmail.com). You can find a short description of the package here: “[documents/treespac_package.pdf](#)”

You can install the package using devtools:

```
devtools::install_gitlab('fchianucci/treespac')
```

Then, we are ready to use it Let's calculate these two indices:

- Diameter differentiation (Gadow, 1993): Spatial size inequality defined as the mean of the ratio of smaller and larger plant sizes in the nearest neighbors of a tree. The value of the index increases with increasing average size difference between neighboring trees. 0 is implying that neighboring trees have equal size.

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- Mingling (Aguirre et al., 2003): One very intuitive extension of taxonomic species diversity (either richness or abundance) is considering spatial mingling, namely how plants of the same (con-specific neighbors) or different (hetero-specific neighbors) species are arranged in space. The mingling index calculates the proportion of the k nearest neighbors that do not belong to the same species as the reference tree. For example, with four neighbors, the mingling attribute can assume five values, ranging from 0 (all trees are of the same species) to 1 (all trees belong to different species).

Calculate the indices based on the reference run, then based on the scenario. For each index we add extra columns with the index name, and run name for further analyses. The `max.k` parameter is telling how many neighboring trees we want to account for.

```
# diameter differentiation:
# mingling

diff <- data.frame(treespat::DIFF(tree1, .x = x, .y = y, .mark = dbh, xmax = 100,
                                ymax = 100, max.k = 4, shape='square', .groups=c('year')) |>
  dplyr::mutate(index="DIFF", name="Diameter differentiation", run=name1))
head(diff)
```

| | year | | DIFF index | | name | run |
|---|------|-----------|------------|----------|-----------------|-----------|
| 1 | 0 | 0.4874231 | DIFF | Diameter | differentiation | reference |
| 2 | 1 | 0.4752327 | DIFF | Diameter | differentiation | reference |
| 3 | 2 | 0.4665189 | DIFF | Diameter | differentiation | reference |
| 4 | 3 | 0.4701394 | DIFF | Diameter | differentiation | reference |
| 5 | 4 | 0.4668349 | DIFF | Diameter | differentiation | reference |
| 6 | 5 | 0.4663594 | DIFF | Diameter | differentiation | reference |

```
ming <- data.frame(treespat::MING(tree1, .x = x, .y = y, .species = species,
                                xmax = 100, ymax = 100, max.k = 4, shape='square', .groups=c('year')) |>
  dplyr::mutate(index="MING", name="Mingling", run=name1))

indices1<-rbind(diff |> dplyr::rename(value=DIFF),
  ming |> dplyr::rename(value=MINGLING ) )
```

We calculated each index as a separate variable and then merged them into `indices1`. Here I renamed the column names to have it all “value”, for easier plotting later on. (each line has the information on which run and which index is the value) We do the same for the scenario simulation, we merge them together and make the plotting.

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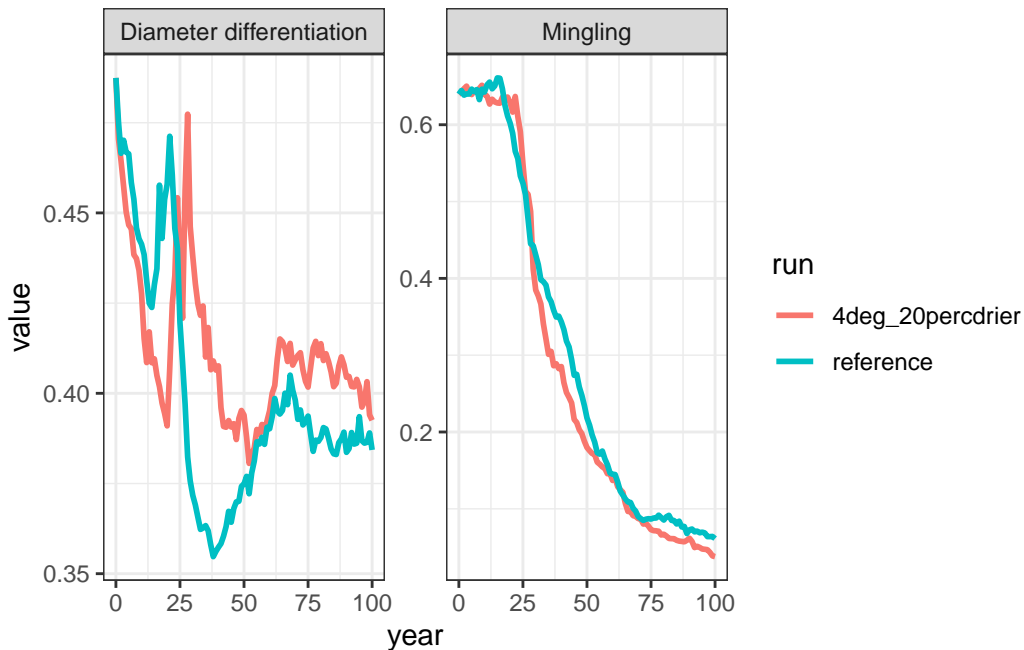
```
diff <- data.frame(treespat::DIFF(tree2, .x = x, .y = y, .mark = dbh,
  xmax = 100, ymax = 100, max.k = 4, shape = 'square',
  .groups = c('year')) |>
  dplyr::mutate(index = "DIFF", name = "Diameter differentiation",
    run = name2))

ming <- data.frame(treespat::MING(tree2, .x = x, .y = y, .species = species,
  xmax = 100, ymax = 100, max.k = 4, shape = 'square',
  .groups = c('year')) |>
  dplyr::mutate(index = "MING", name = "Mingling", run = name2))

indices2 <- rbind(diff |> dplyr::rename(value = DIFF),
  ming |> dplyr::rename(value = MINGLING))

indices <- rbind(indices1, indices2)

ggplot2::ggplot(indices, ggplot2::aes(x = year, y = value, color = run)) +
  ggplot2::geom_line(lwd = 1) +
  ggplot2::facet_wrap(~ name, ncol = 2, scales = "free") +
  ggplot2::theme_bw()
```



The diameter differentiation increases with the increasing average difference in diameter between neighboring trees. The value 0 indicates that neighboring trees have equal

diameters. The development shows that the index values decrease during the first 15/20 years, after which increase due to the occurrence of ingrowth and then the values are reduced again to their minima in 37/50 years, after which they again slightly increase. The values for the reference climate scenario are slightly lower than for the climate change scenario indicating slower growth. The mingling index is studying the neighboring trees regarding their species. No substantial difference in species mingling between scenarios was detected.

2.2.14 Group 4 - Question B

- How are the species distribution and total living biomass C content changing in time on Plot 4? Compare 0 year and 100 year status in the reference case and in the case of your scenario(s)

Run the model as it is described in the previous chapters Section 2.2.3, Section 2.2.5 and Section 2.2.4 to have at least 2 simulations completed: one with reference conditions and one scenario with some changes in the environment. Check if you have the output files in the output folder: *iLand_simulations/output/*. We show all of the solutions on the example of one reference and one alternative scenario output file. Open the *summerSchoolExercise.Rproj* project in R studio and start working there.

2.2.14.1 Read the landscape output table

Read in the *landscape* output table from two outputs you have for your plot:

```
path1 <- "model/iLand_simulations/output/Output_plot4.sqlite"
path2 <-
  "model/iLand_simulations/output/Output_plot4_4deg_20percdrier.sqlite"

file1 <- here::here(path1)
file2 <- here::here(path2)

# Give some name for the three simulations.
name1 <- "reference"
name2 <- "4deg_20percdrier"

# Read in data using the RSQLite package
sqlite.driver <- RSQLite::dbDriver("SQLite")

# We will work with "landscape" table and tree-scale data:
db1 <-
  RSQLite::dbConnect(sqlite.driver, dbname = file1) # connect to the file1
```

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```
landscape1 <- RSQLite::dbReadTable(db1, "landscape")
RSQLite::dbDisconnect(db1) # disconnect to the file1

db2 <-
  RSQLite::dbConnect(sqlite.driver, dbname = file2) # connect to the file2
landscape2 <- RSQLite::dbReadTable(db2, "landscape")
RSQLite::dbDisconnect(db2)
```

Merge the data from the two files together and make a column caller run which tells which comes from which simulation, and study the table. The column “run” will support the plotting where we can use facets in ggplot.

```
landscape <- rbind(landscape1 |> dplyr::mutate(run = name1),
  landscape2 |> dplyr::mutate(run = name2))

head(landscape)
```

| | year | area | area_100m | species | count_ha | dbh_avg_cm | height_avg_m | volume_m3 | | |
|---|-----------------|------|------------|---------------|----------|------------|--------------|------------|--|--|
| 1 | 0 | 1 | 1 | casa | 152 | 12.96761 | 10.77155 | 9.465222 | | |
| 2 | 0 | 1 | 1 | fasy | 70 | 48.97035 | 27.82864 | 260.513423 | | |
| 3 | 0 | 1 | 1 | pisu | 33 | 52.05737 | 29.57999 | 91.870356 | | |
| 4 | 0 | 1 | 1 | qupe | 18 | 34.83232 | 17.83572 | 15.683124 | | |
| 5 | 1 | 1 | 1 | casa | 147 | 13.72713 | 11.31040 | 10.643544 | | |
| 6 | 1 | 1 | 1 | fasy | 70 | 50.20535 | 28.46379 | 268.968996 | | |
| | total_carbon_kg | | gwl_m3 | basal_area_m2 | | NPP_kg | NPPabove_kg | LAI | | |
| 1 | 8041.268 | | 9.465222 | 2.099428 | | 0.000 | 0.00 | 0.3009711 | | |
| 2 | 80391.775 | | 260.513423 | 15.847768 | | 0.000 | 0.00 | 1.3974759 | | |
| 3 | 30694.307 | | 91.870356 | 7.063300 | | 0.000 | 0.00 | 0.8112550 | | |
| 4 | 10327.265 | | 15.683124 | 1.791511 | | 0.000 | 0.00 | 0.1830485 | | |
| 5 | 8550.914 | | 10.987314 | 2.266547 | | 2834.498 | 1765.12 | 0.3118849 | | |
| 6 | 84739.791 | | 268.968996 | 16.383716 | | 13024.190 | 8553.20 | 1.4546398 | | |
| | cohort_count_ha | | run | | | | | | | |
| 1 | 0 | | reference | | | | | | | |
| 2 | 0 | | reference | | | | | | | |
| 3 | 0 | | reference | | | | | | | |
| 4 | 0 | | reference | | | | | | | |
| 5 | 0 | | reference | | | | | | | |
| 6 | 229 | | reference | | | | | | | |

2.2.14.2 Visualize changes in time

We can see that the output is given for each year and each species in our 1ha area. Plot the living carbon (total_carbon_kg) in time, coloring by species. We give a unified species coloring in the beginning. Plot number of trees and mean diameter. Carbon and number of trees can be plotted in an additive way, but for mean dbh we do line plot per species.

```
cols.all=c( "rops"="#e0e0e0", "acpl"="#A9A9A9", "alin"="#696969", "alvi"="#2e2e2e",
  "bepe"="#fadbaf", "casa"="#7eeadf", "coav"="#20c6b6", "tipl"="#645394",
  "ulgl"="#311432", "saca"="#D8BFD8", "soar"="#DDA0DD", "soau"="#BA55D3",
  "pice"="#D27D2D", "pini"="#a81c07", "algl"="#2ECBE9", "tico"="#128FC8",
  "potr"="#00468B", "poni"="#5BAEB7", "frex"="#fe9cb5", "cabe"="#fe6181",
  "acps"="#fe223e", "lade"="#FFFE71", "abal"="#FFD800", "pisy"="#A4DE02",
  "fasy"="#76BA1B", "piab"="#006600", "quro"="#FF7F00", "qupe"="#FF9900",
  "qupu"="#CC9900")

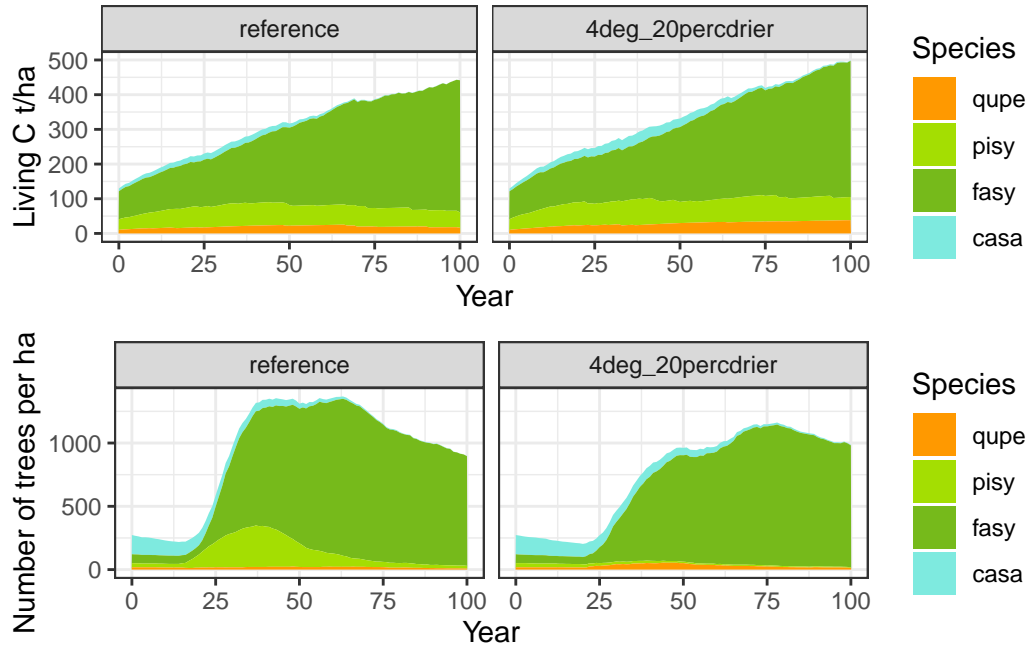
# We set here the order of the run categories for the table, to have the first
#run first and then the second. (left-right of the plots)
landscape$run <- factor(landscape$run, levels = c(name1, name2))

# Plot the living carbon content, to have tonnes/ha, we divide total_carbon_kg by 1000.
g1 <-
  ggplot2::ggplot(landscape, ggplot2::aes(year, total_carbon_kg / 1000,
                                           fill = factor(species))) +
    ggplot2::geom_area() +
    ggplot2::scale_fill_manual(values = cols.all,
                              guide = ggplot2::guide_legend(reverse = TRUE)) +
    ggplot2::facet_wrap( ~ run, nrow = 1) +
    ggplot2::labs(x = "Year", y = "Living C t/ha", fill = "Species") +
    ggplot2::theme_bw()

g2 <-
  ggplot2::ggplot(landscape, ggplot2::aes(year, count_ha,
                                           fill = factor(species))) +
    ggplot2::geom_area() +
    ggplot2::scale_fill_manual(values = cols.all,
                              guide = ggplot2::guide_legend(reverse =
                                                                TRUE)) +
    ggplot2::facet_wrap( ~ run, nrow = 1) +
    ggplot2::labs(x = "Year", y = "Number of trees per ha", fill = "Species") +
    ggplot2::theme_bw()
```

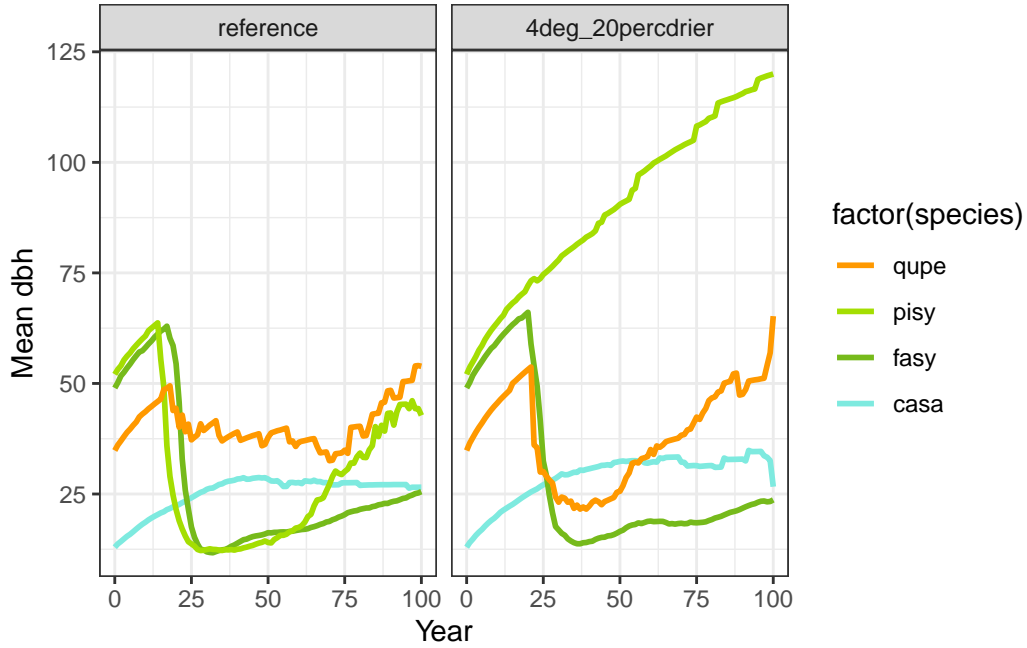
2 Process-based modeling

```
gridExtra::grid.arrange(g1, g2, ncol = 1)
```



```
g3 <-
  ggplot2::ggplot(landscape, ggplot2::aes(year, dbh_avg_cm,
                                            color = factor(species))) +
  ggplot2::geom_line(lwd = 1) +
  ggplot2::scale_color_manual(values = cols.all,
                              guide = ggplot2::guide_legend(reverse =
                                                                TRUE)) +
  ggplot2::facet_wrap(~ run, nrow = 1) +
  ggplot2::labs(x = "Year", y = "Mean dbh", fill = "Species") +
  ggplot2::theme_bw()
print(g3)
```


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Note that we do not have management intervention, and in the model trees shorter than 4m are not included in these outputs. However as they grow taller than 4m, model starts to handle them as individual trees and including in these outputs which we are looking now.

At the end of the simulated 100 years, the total simulated carbon stock in living biomass under climate change scenario was slightly higher than under the reference climate. The proportion of beech has increased under both simulations. The number of trees increased in both cases after circa 25 years, but the increase was steeper under reference conditions. This increase was caused by the regeneration. However, at the end of the simulation period, the number of remaining trees was slightly higher under climate change scenario than the reference one, indicating much higher tree mortality.

Mean dbh of individual species reflected the development of the number of trees. The increase in the number of trees caused the reduction of mean dbh, e.g. of beech under both scenarios between 20 and 35 simulation years. The species-specific graphs for mean dbh indicates that some species do not have successful regeneration under the climate change scenario. Pine dbh decreased only under reference scenario, when we observed the increase of the number of trees, while under climate change scenario the mean dbh of pine was growing indicating the growth of remaining trees of the species at the plot. The small proportion of chestnut almost decrease to 0 under both scenarios, its dbh development does not show any successful regeneration processes.

2.2.14.3 Assess the stored carbon amount

Calculate the stored C amount in the initial year (year==0) and the last year (year==100)

```
livingC0 <- data.frame(
  landscape |> dplyr::filter(year == 0) |>
    dplyr::group_by(run) |>
    dplyr::summarize(sum.livingC = sum(total_carbon_kg / 1000))
)
print(livingC0)
```

| | run | sum.livingC |
|---|------------------|-------------|
| 1 | reference | 129.4546 |
| 2 | 4deg_20percdrier | 129.4546 |

```
livingC100 <- data.frame(
  landscape |> dplyr::filter(year == 100) |>
    dplyr::group_by(run) |>
    dplyr::summarize(sum.livingC = sum(total_carbon_kg / 1000))
)
print(livingC100)
```

| | run | sum.livingC |
|---|------------------|-------------|
| 1 | reference | 441.6930 |
| 2 | 4deg_20percdrier | 499.1578 |

The initial conditions are same for the runs, but they are ending up at different C levels.

Calculate the stored C amount PER SPECIES in the initial year (year==0) and the last year (year==100)

```
species.livingC0 <- data.frame(
  landscape |> dplyr::filter(year == 0) |>
    dplyr::group_by(run, species) |>
    dplyr::summarize(livingC = sum(total_carbon_kg / 1000))
)
print(species.livingC0)
```

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| | run | species | livingC |
|---|------------------|---------|-----------|
| 1 | reference | casa | 8.041268 |
| 2 | reference | fasy | 80.391775 |
| 3 | reference | pisy | 30.694307 |
| 4 | reference | qupe | 10.327265 |
| 5 | 4deg_20percdrier | casa | 8.041268 |
| 6 | 4deg_20percdrier | fasy | 80.391775 |
| 7 | 4deg_20percdrier | pisy | 30.694307 |
| 8 | 4deg_20percdrier | qupe | 10.327265 |

```
species.livingC100 <-  
  data.frame(  
    landscape |> dplyr::filter(year == 100) |>  
    dplyr::group_by(run, species) |>  
    dplyr::summarize(livingC = sum(total_carbon_kg / 1000))  
  )  
print(species.livingC100)
```

| | run | species | livingC |
|---|------------------|---------|-------------|
| 1 | reference | casa | 0.2319933 |
| 2 | reference | fasy | 380.6997702 |
| 3 | reference | pisy | 44.2202121 |
| 4 | reference | qupe | 16.5410152 |
| 5 | 4deg_20percdrier | casa | 1.5847763 |
| 6 | 4deg_20percdrier | fasy | 392.4993454 |
| 7 | 4deg_20percdrier | pisy | 66.8578057 |
| 8 | 4deg_20percdrier | qupe | 38.2158285 |

2.2.14.4 Assess the species proportions

Calculate the species proportions based on the stored C amount in the initial year (year==0) and the last year (year==100) For this we need the total C amount and the species-specific C amount.

```
LC0 <- dplyr::left_join(species.livingC0, livingC0, by = "run")  
LC0 <-  
  data.frame(LC0 |> dplyr::mutate(spec.prop = livingC / sum.livingC, year =  
                                0))  
print(LC0)
```

| run | species | livingC | sum.livingC | spec.prop | year |
|-----|---------|---------|-------------|-----------|------|
|-----|---------|---------|-------------|-----------|------|

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| | | | | | | |
|---|------------------|-------|-----------|----------|------------|---|
| 1 | reference | casa | 8.041268 | 129.4546 | 0.06211650 | 0 |
| 2 | reference | fasy | 80.391775 | 129.4546 | 0.62100355 | 0 |
| 3 | reference | pisys | 30.694307 | 129.4546 | 0.23710477 | 0 |
| 4 | reference | qupe | 10.327265 | 129.4546 | 0.07977518 | 0 |
| 5 | 4deg_20percdrier | casa | 8.041268 | 129.4546 | 0.06211650 | 0 |
| 6 | 4deg_20percdrier | fasy | 80.391775 | 129.4546 | 0.62100355 | 0 |
| 7 | 4deg_20percdrier | pisys | 30.694307 | 129.4546 | 0.23710477 | 0 |
| 8 | 4deg_20percdrier | qupe | 10.327265 | 129.4546 | 0.07977518 | 0 |

```
LC100 <- dplyr::left_join(species.livingC100, livingC100, by = "run")
LC100 <-
  data.frame(LC100 |> dplyr::mutate(spec.prop = livingC / sum.livingC, year =
    100))
print(LC100)
```

| | run | species | livingC | sum.livingC | spec.prop | year |
|---|------------------|---------|-------------|-------------|--------------|------|
| 1 | reference | casa | 0.2319933 | 441.6930 | 0.0005252366 | 100 |
| 2 | reference | fasy | 380.6997702 | 441.6930 | 0.8619103723 | 100 |
| 3 | reference | pisys | 44.2202121 | 441.6930 | 0.1001152679 | 100 |
| 4 | reference | qupe | 16.5410152 | 441.6930 | 0.0374491232 | 100 |
| 5 | 4deg_20percdrier | casa | 1.5847763 | 499.1578 | 0.0031749006 | 100 |
| 6 | 4deg_20percdrier | fasy | 392.4993454 | 499.1578 | 0.7863232430 | 100 |
| 7 | 4deg_20percdrier | pisys | 66.8578057 | 499.1578 | 0.1339412339 | 100 |
| 8 | 4deg_20percdrier | qupe | 38.2158285 | 499.1578 | 0.0765606224 | 100 |

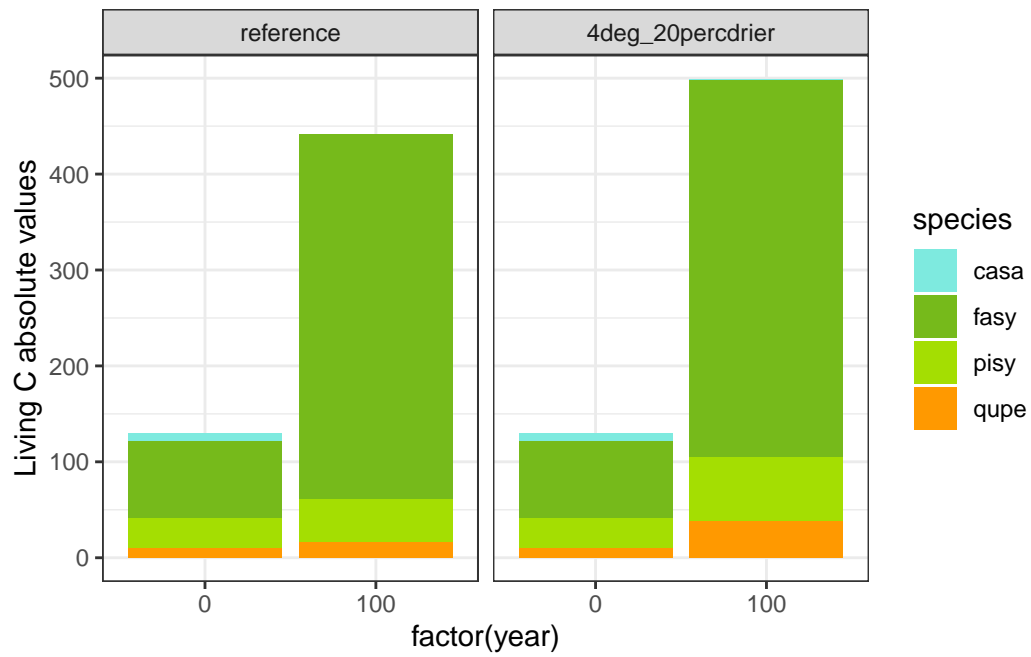
Put the two tables together and visualize the results

```
LC <- rbind(LC0, LC100)

LC$run <- factor(LC$run, levels = c(name1, name2))

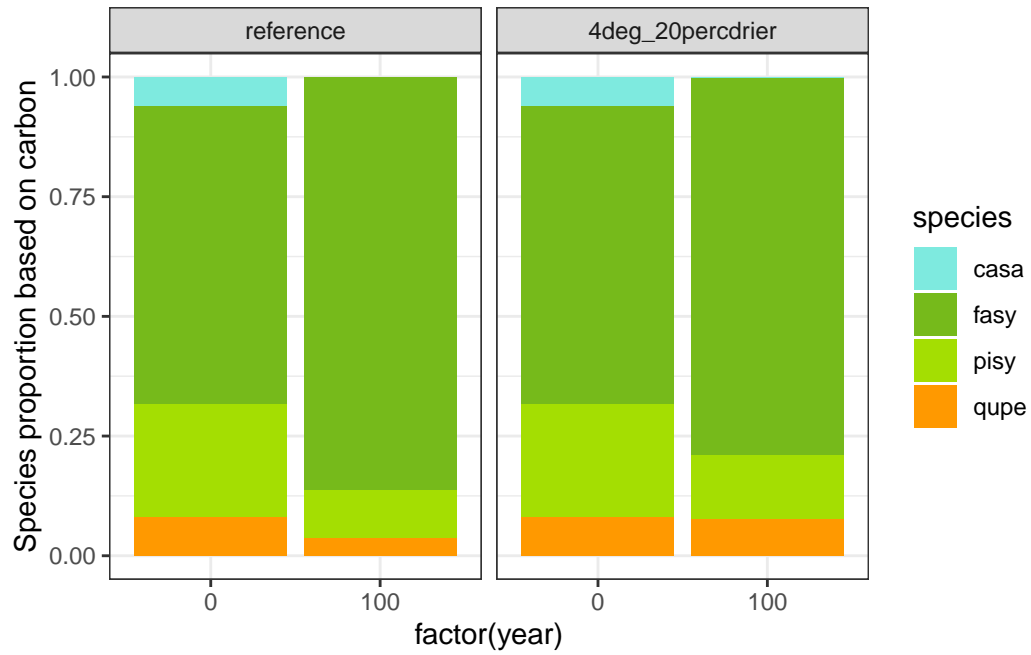
ggplot2::ggplot(LC, ggplot2::aes(fill = species, y = livingC,
                                x = factor(year))) +
  ggplot2::geom_bar(position = "stack", stat = "identity") +
  ggplot2::scale_fill_manual(values = cols.all) +
  ggplot2::facet_wrap(~ run) +
  ggplot2::ylab("Living C absolute values") +
  ggplot2::theme_bw()
```

2 Process-based modeling



```
ggplot2::ggplot(LC, ggplot2::aes(fill = species, y = spec.prop,  
                                x = factor(year))) +  
  ggplot2::geom_bar(position = "stack", stat = "identity") +  
  ggplot2::scale_fill_manual(values = cols.all) +  
  ggplot2::facet_wrap( ~ run) +  
  ggplot2::ylab("Species proportion based on carbon") +  
  ggplot2::theme_bw()
```

2 Process-based modeling



The living C stock tripled over 100 years due to the accumulation of biomass in trees and no management interventions and reached higher level under the climate change scenario. Both cases the proportion of beech increased.

3 Empirical modeling

In the empirical modelling we will cover two examples of creating two models based on observed data. We will use two approaches Generalized Linear Models (GLMs) and Boosted Regression trees (BRTs). Please take all the results with a grain of salt, we are making very generalized statements from a limited data set, and we are not getting into the details of how each of the models should be assessed; the goal here is that you learn how observed data can be used to create models that help you to understand the data and relationships better.

3.1 Data

We will work with one dataset derived from the inventory developed to assess forest structure and deadwood properties of six representative forest areas in the Czech Republic (Hošek, 2022). This dataset collects observations of the presence /absence of certain species of biodiversity importance across 99 plots.

The data was collected from square sampling plots (2500 m² each) in six forested Czech Republic regions. These regions are representative of the main bio-regions and elevation range of forests, considering their importance in territorial representation, forestry, and ecology. The inventory sampled for biodiversity variables such as the presence/absence of different species of birds, Tracheophyta, Bryophyte, fungi, lichens, and beetles.

The dataset has been generously provided by Jeňýk Hofmeister at the Czech University of Life Sciences Prague (jenyk.hofmeister@email.cz) to be used in the context of this exercise. It should not be used for other purposes or be further distributed. If you want to use this data or learn more about it, please get in touch with Jeňýk Hofmeister here: jenyk.hofmeister@email.cz.

The data you can download for this exercise is an aggregated summary of the original data, some aspects have been modified from the observed data, so the results you will obtain will only partially match the observed reality. This data is very similar in structure and observed variables to the one you collected in this summer school. The idea is to move from data collection, analysis to this part, where you use the data to create a model.

3.1.1 Data description

These are the variables available in the data

- **longitud**: longitude of the plot location
- **latitude**: latitude of the plot location
- **forestManagementType**: forest management type applied in this plot
- **forestStructure**: current forest structure in the plot
- **slope**: slope of the plot
- **A.pseudoplatanus**: proportion of this tree species in the plot in volume
- **F.sylvatica**: proportion of this tree species in the plot in volume
- **L.decidua**: proportion of this tree species in the plot in volume
- **Q.robur**: proportion of this tree species in the plot in volume
- **S.aucuparia** : proportion of this tree species in the plot in volume
- **B.pendula**: proportion of this tree species in the plot in volume
- **P.abies**: proportion of this tree species in the plot in volume
- **P.sylvestris**: proportion of this tree species in the plot in volume
- **F.excelsior**: proportion of this tree species in the plot in volume
- **A.alba**: proportion of this tree species in the plot in volume
- **A.platanoides**: proportion of this tree species in the plot in volume
- **T.cordata**: proportion of this tree species in the plot in volume
- **S.racemosa**: proportion of this tree species in the plot in volume
- **U.glabra**: proportion of this tree species in the plot in volume
- **S.nigra**: proportion of this tree species in the plot in volume
- **P.alba**: proportion of this tree species in the plot in volume
- **U.minor**: proportion of this tree species in the plot in volume
- **S.caprea**: proportion of this tree species in the plot in volume
- **C.betulus**: proportion of this tree species in the plot in volume
- **P.nigra**: proportion of this tree species in the plot in volume
- **Q.petraea**: proportion of this tree species in the plot in volume
- **S.torminalis**: proportion of this tree species in the plot in volume
- **A.campestre**: proportion of this tree species in the plot in volume
- **P.strobus**: proportion of this tree species in the plot in volume
- **Q.rubra**: proportion of this tree species in the plot in volume
- **volAllha**: total volume in the plot
- **GiniDBH**: Gini index calculated to assess the forest structural diversity in diameter sizes, higher values indicate more structural heterogeneity; lower values indicate more homogeneous stands
- **ShannonIndexTreeSpp**: The Shannon index is way to measure the diversity of tree species in the plot
- **Tracheophyta_rich**: Species richness across Tracheophyta species
- **Birds_rich**: Species richness across Birds species
- **Bryophytes_rich** : Species richness across Bryophyte species
- **Fungi_rich**: Species richness across Fungi species

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- **Lichens_rich**: Species richness across Lichens species
- **Beetles_rich**: Species richness across Beetles species
- **dendrocoposMajor**: presence / absence of Great spotted woodpecker (*Dendrocopos major*)
- **certhia**: presence / absence of Eurasian treecreeper (*Certhia familiaris*)
- **bryophyteNumObs**: number of observed Bryophyte species
- **birdNumObs**: number of observed Bird species
- **PlotID**: ID number for the plot

3.2 Species description

3.2.1 Species 1 - Bryophyte

Bryophyte constitute an important and permanent component of the forest flora and diversity. They colonize various substrates, which are unsuitable for vascular plants, because of low light intensity or low nutrient level, such as deadwood, bark, rocks, and open soil. They provide shelter habitats, food, and nest material for many animals.

In forests, different ecological guilds of Bryophyte can be distinguished by the substrate on which they are growing, including terricolous, lignicolous, corticolous and saxicolous species that occur on soil, deadwood, bark of living trees and shrubs, or rocks, respectively. As diversity and quality of these substrates is affected by forest management, Bryophyte are suitable indicators for the effect of management on forest conditions. Especially typical woodland Bryophyte, which are strictly depending on forest conditions. It is interesting to better understand the relation of forest management effects on Bryophyte and some studies have already demonstrated their sensitivity to management practices.

3.2.2 Species 2 - Great spotted woodpecker

The great spotted woodpecker (*Dendrocopos major*) is a medium-sized woodpecker with pied black and white plumage and a red patch on the lower belly. It is found in a wide variety of woodlands, broadleaf, coniferous or mixed forests. The great spotted woodpecker spends much of its time climbing trees. It is a generalist bird species.

3.2.3 Species 3 - Eurasian treecreeper

The Eurasian treecreeper (*Certhia familiaris*) is a small passerine bird. It prefers mature trees, and in most of Europe, it tends to be found mainly in coniferous forest, especially spruce and fir.

3.3 Models

3.3.1 Generalized Linear Models (GLMs)

We propose to use a generalized linear model (GLM) to understand the abundance of different Bryophyte and birds species in the 99 plots. Count data often conform to a Poisson distribution; in this case, we have a count of the number of species recorded at each plot.

Fitting a Poisson GLM in R is similar to analyzing covariance (or linear model), except that we now need to use the `glm` function. To run a GLM, we need to provide one extra piece of information beyond that required for a linear model: the family of models we want to use. In this case, we want a Poisson family, `family=poisson`.

3.3.2 Boosted regression trees (BRTs)

Boosted regression trees (BRT) are a combination of two powerful statistical techniques: boosting and regression trees. Boosting is a machine learning technique similar to model averaging, where the results of several competing models are merged. Unlike model averaging, however, boosting uses a forward, stage-wise procedure, where tree models are fitted iteratively to a subset of the training data. Subsets of the training data used at each iteration of the model fit are randomly selected without replacement, where the proportion of the training data used is determined by the modeler, this is defined with the “bag fraction” parameter. This procedure, known as stochastic gradient boosting, introduces an element of stochasticity that improves model accuracy and reduces overfitting (Elith et al., 2008).

The BRT model calibration is defined by four parameters:

- the **learning rate** (or shrinkage parameter): The learning rate determines the contribution of each new tree to the growing model, and it is always substantially lower than 1, higher values being related to faster learning.
- the **bag fraction**: The bag fraction provides information on which fraction [0-1] of the entire data should be drawn randomly to fit the new tree. This parameter includes a random probabilistic component, making each run model different, and is aimed at improving model accuracy, speed of model creation, and the reduction of overfitting (Friedman et al., 2008).
- the **tree complexity**: Tree complexity controls the number of fitted interactions among variables, and determines the number of splits in each tree; for example, a value of 1 will present only one split, meaning that the model does not consider interactions; a value of 2 will result in two splits, and two interactions.

- The `number of trees` required for optimal prediction: The optimal number of trees is selected based on the three previous parameters. The values fitted by the final model are computed as the sum of all of the predictions of the trees, multiplied by their respective learning rates.

3.4 The exercise

3.4.1 Recomendations before starting

We highly recommend that you open the `summerSchoolExercise.Rproj` from the project folder that you now you have in your computer after following the instructions in Section 1.1.1.

We also highly recommend that you storage any Rscript that you create in the folder `code`.

3.4.2 Find the data

If you followed the instructions in Section 1.1.1 you should have the file `observations.csv` inside the folder `data` of your project file:

3.4.3 Explore the data

You can load the data in R by doing:

```
observations <- read.csv(here::here("data/observations.csv"))
```

Once you have obtained the data, your next step is to explore it. It is important to carefully analyze the structure of the data and understand its meaning. Each variable must be examined closely, along with the data structure. Remember that each row in this dataset represents one plot, identified by its `PlotID`, and each column represents one variable.

You can explore each of the variables by doing:

```
str(observations)
```

3 Empirical modeling

```
'data.frame':  99 obs. of  45 variables:
 $ X                : int  1 2 3 4 5 6 7 8 9 10 ...
 $ longitud         : num  13.5 13.5 13.5 13.6 13.6 ...
 $ latitude         : num  49.5 49.5 49.5 49.5 49.5 ...
 $ forestManagementType: chr  "simple clearcutting" "simple clearcutting" "simple clearcutting" ...
 $ forestStructure   : chr  "even-aged" "even-aged" "even-aged" "even-aged" ...
 $ slope            : num  16.85 6.51 4.91 5.55 14.55 ...
 $ A.pseudoplatanus : int  0 0 0 0 0 4 1 7 16 0 ...
 $ F.sylvatica       : int  61 0 0 100 0 82 85 91 75 0 ...
 $ L.decidua         : int  38 0 0 0 4 6 0 0 0 0 ...
 $ Q.robur           : int  0 1 0 0 0 0 0 0 0 0 ...
 $ S.aucuparia       : int  0 0 0 0 0 0 0 0 0 0 ...
 $ B.pendula         : int  0 0 1 0 28 0 0 0 0 0 ...
 $ P.abies           : int  0 99 93 0 30 0 0 0 8 99 ...
 $ P.sylvestris      : int  0 0 7 0 1 0 0 0 0 0 ...
 $ F.excelisor       : int  0 0 0 0 38 0 0 0 0 0 ...
 $ A.alba            : int  0 0 0 0 0 4 0 0 0 1 ...
 $ A.platanoides     : int  0 0 0 0 0 2 2 2 0 0 ...
 $ T.cordata         : int  0 0 0 0 0 2 12 0 0 0 ...
 $ S.racemosa        : int  0 0 0 0 0 0 0 0 0 0 ...
 $ U.glabra          : int  0 0 0 0 0 0 0 0 1 0 ...
 $ S.nigra           : int  0 0 0 0 0 0 0 0 0 0 ...
 $ P.alba            : int  0 0 0 0 0 0 0 0 0 0 ...
 $ U.minor           : int  0 0 0 0 0 0 0 0 0 0 ...
 $ S.caprea          : int  0 0 0 0 0 0 0 0 0 0 ...
 $ C.betulus         : int  0 0 0 0 0 0 0 0 0 0 ...
 $ P.nigra           : int  0 0 0 0 0 0 0 0 0 0 ...
 $ Q.petraea         : int  0 0 0 0 0 0 0 0 0 0 ...
 $ S.torminalis      : int  0 0 0 0 0 0 0 0 0 0 ...
 $ A.campestre       : int  0 0 0 0 0 0 0 0 0 0 ...
 $ P.strobus         : int  0 0 0 0 0 0 0 0 0 0 ...
 $ Q.rubra           : int  0 0 0 0 0 0 0 0 0 0 ...
 $ volAllha         : num  592 377 438 615 194 ...
 $ GiniDBH           : num  0.448 0.416 0.12 0.133 0.378 ...
 $ ShannonIndexTreeSpp : num  0.68 0.07 0.28 0 1.28 0.78 0.54 0.39 0.75 0.06 ...
 $ Tracheophyta_rich  : num  0.218 0.233 0.209 0.189 0.354 ...
 $ Birds_rich        : num  0.358 0.46 0.485 0.307 0.383 ...
 $ Bryophytes_rich    : num  0.0876 0.0876 NA 0.2629 0.3505 ...
 $ Fungi_rich        : num  0.199 0.133 0.114 0.218 0.262 ...
 $ Lichens_rich       : num  0.0659 0.1976 0.1318 0.1537 0.1537 ...
 $ Beetles_rich       : num  0.16 0.16 0.234 0.258 0.221 ...
 $ dendrocoposMajor  : int  1 1 1 0 1 1 1 1 1 1 ...
 $ certhia           : int  0 0 0 0 0 0 1 0 1 0 ...
```

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```
$ bryophyteNumObs      : int   1 1 0 3 4 5 7 4 7 1 ...  
$ birdNumObs           : int   14 18 19 12 15 14 12 14 18 18 ...  
$ PlotID               : int    1 2 3 4 5 6 7 8 9 10 ...
```

You have a description of each of the variables in the section Section 3.1.1.

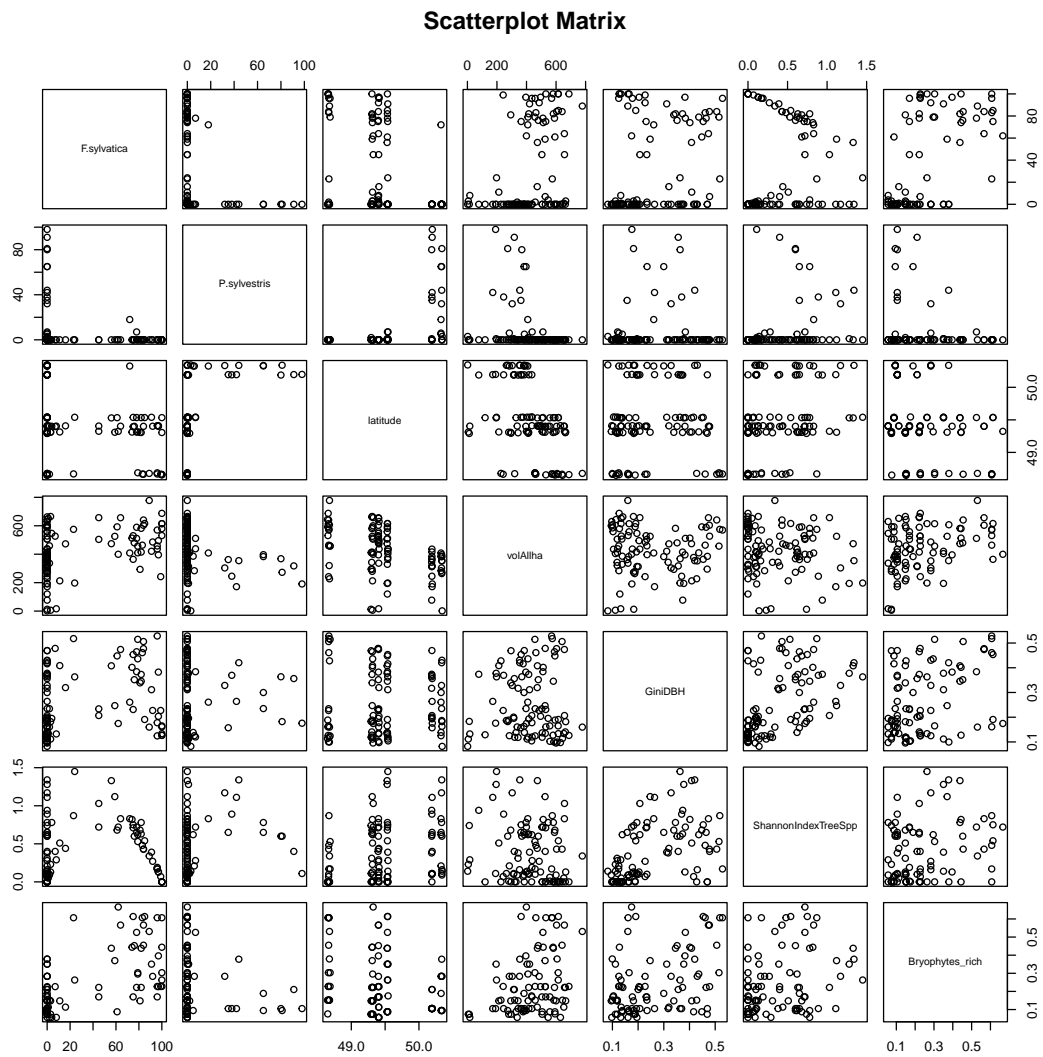
You could do further analysis by exploring the data correlations and you can even plot them to explore their values and ranges better. During this process you should start thinking:

- What am I trying to understand with this model? (your question)
- What variables are important to answer my question?

You could for example explore the behavior of the variables by plotting a scatterplot:

```
pairs(  
  ~ F.sylvatica + P.sylvestris + latitude + volAllha + GiniDBH +  
    ShannonIndexTreeSpp + Bryophytes_rich,  
  data = observations,  
  main = "Scatterplot Matrix"  
)
```

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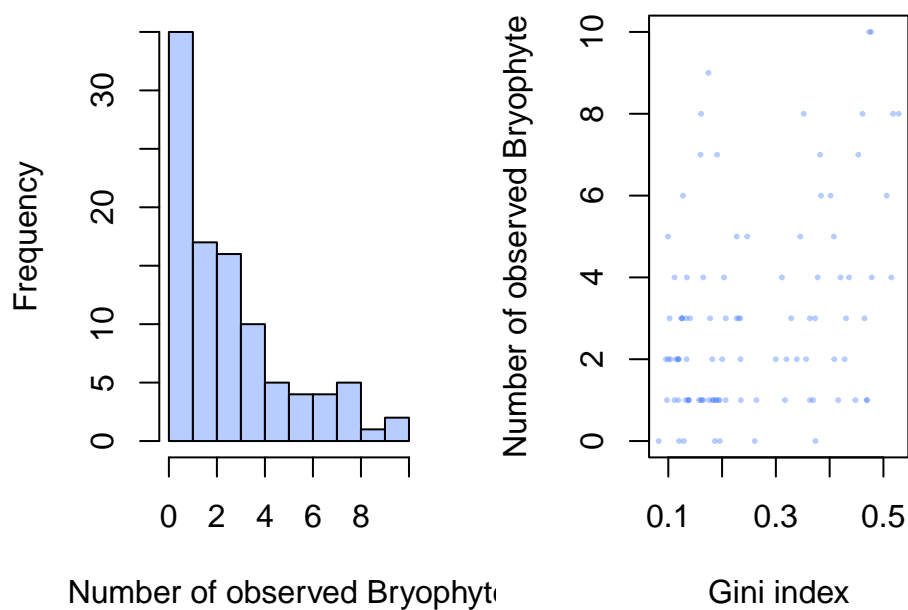
You can also create individual scatterplots or histograms for a variable of interest, for example:

```
#Divide the screen in 1 line and 3 columns
par(mfrow = c(1, 2), oma = c(0, 2, 0, 0))

#Make the margin around each graph a bit smaller
par(mar = c(4, 4, 2, 2))
# Histogram and Scatterplot
hist(
  observations$bryophyteNumObs,
```

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```
main = "",
breaks = 10,
col = rgb(0.3, 0.5, 1, 0.4) ,
xlab = "Number of observed Bryophyte"
)
plot(
  y = observations$bryophyteNumObs,
  x = observations$GiniDBH,
  main = "" ,
  pch = 20,
  cex = 0.4,
  col = rgb(0.3, 0.5, 1, 0.4),
  xlab = "Gini index",
  ylab = "Number of observed Bryophyte"
)
```



3.4.4 Group 1 - Question C

- Does a more diverse forest in structure and composition have more Bryophyte species?

3.4.4.1 Fitting a Poisson GLM in R

During your data exploration, you should have selected your response variable, `bryophyteNumObs`. In this case, since we are trying to understand forest structure and composition, you should also choose explanatory variables for that, such as `GiniDBH`, which indicates the forest structural diversity in diameter sizes; higher values indicate more structural heterogeneity, and lower values indicate more homogeneous stands, or the `ShannonIndexTreeSpp` which assesses the diversity of tree species in the plot.

We could start by only looking at how the forest structural diversity affects the number of Bryophyte species that we have in a plot. You can create a GLM model with `bryophyteNumObs` as the response variable and `GiniDBH` as an explanatory variable. You will use the function `glm` in R and the `family = poisson`. You can see how to create and see this model here:

```
bryoModel1 <- glm(bryophyteNumObs ~ GiniDBH,
                  family = poisson,
                  data = observations)

summary(bryoModel1)
```

Call:

```
glm(formula = bryophyteNumObs ~ GiniDBH, family = poisson, data = observations)
```

Coefficients:

| | Estimate | Std. Error | z value | Pr(> z) | |
|-------------|----------|------------|---------|----------|-----|
| (Intercept) | 0.4627 | 0.1388 | 3.333 | 0.000859 | *** |
| GiniDBH | 2.2797 | 0.4221 | 5.401 | 6.64e-08 | *** |

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

(Dispersion parameter for poisson family taken to be 1)

Null deviance: 188.58 on 98 degrees of freedom
 Residual deviance: 159.92 on 97 degrees of freedom
 AIC: 424.2

Number of Fisher Scoring iterations: 5

Here you can see that the coefficient table produced by a GLM is very similar to a linear model. The intercept tells us the estimated value of the response variable when the continuous explanatory variables (here, just the Gini index) has a value of 0. We

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then also have coefficients describing the slope of the relationship with our continuous explanatory variables. We can see here that the number of Bryophyte species appears to show a positive relationship with the Gini index, which means that increasing structural diversity in tree diameter sizes has a positive relationship with the number of Bryophyte species in the plot.

We are also interested in understanding the relationship of the number of Bryophyte species and the tree species diversity; we can now try to add this variable into the model and see if it helps us to understand things. You can do that by adding the variable `ShannonIndexTreeSpp` to the model:

```
bryoModel2 <- glm(bryophyteNumObs ~ GiniDBH + ShannonIndexTreeSpp,
                  family = poisson,
                  data = observations)

summary(bryoModel2)
```

Call:

```
glm(formula = bryophyteNumObs ~ GiniDBH + ShannonIndexTreeSpp,
     family = poisson, data = observations)
```

Coefficients:

| | Estimate | Std. Error | z value | Pr(> z) | |
|---------------------|----------|------------|---------|----------|-----|
| (Intercept) | 0.45277 | 0.14060 | 3.220 | 0.00128 | ** |
| GiniDBH | 2.17411 | 0.46413 | 4.684 | 2.81e-06 | *** |
| ShannonIndexTreeSpp | 0.09209 | 0.16202 | 0.568 | 0.56977 | |

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

(Dispersion parameter for poisson family taken to be 1)

Null deviance: 188.58 on 98 degrees of freedom
Residual deviance: 159.60 on 96 degrees of freedom
AIC: 425.88

Number of Fisher Scoring iterations: 5

Here we can see that the variable Shannon index also has a positive relationship with the number of Bryophyte species in the plot, but its effect is much smaller. We can also observe that this variable is not significant. This does not mean it is wrong to add this variable because we want to understand its effect, but keeping this variable in the model depends on what you're trying to do and what “reality” is. Adding variables that are

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not significant will not help your model (particularly your estimates) but also might not matter much (e.g., predictions). However, removing actual variables can create a useless model even if they don't meet significance.

Variable selection is a long and complicated topic. Some general rules of thumb include: (1) Include the variable if it is of interest, (2) Include the variable if you have some prior knowledge that it should be relevant. This can be misleading because it's a confirmation bias, but in most cases, this makes sense. (3) If you want a model that can generalize many cases, you should favor fewer variables.

3.4.4.2 Explanatory Power of the model

When we ran linear models, we used the coefficient of determination, or R^2 to assess how much of the variability in our response variable is explained by a given model. R^2 is based on the sums of squares of our model, and so cannot be calculated for GLMs. Instead, we can calculate the deviance explained by our model:

```
# Extract the null and residual deviance from the model
dev.null <- bryoModel1>null.deviance
dev.resid <- bryoModel1$deviance

# Calculate the deviance explained by the model
dev.explained <- (dev.null - dev.resid) / dev.null

# Round to 3 decimal places
dev.explained <- round(dev.explained, 3)

dev.explained
```

```
[1] 0.152
```

Variability in forest structure (Gini index) explain 15% of the variation in Bryophyte species richness in this study. That is an ok explanatory power for a very simple model of a complex ecological system (many factors determine the species richness for Bryophyte and we are attempting to explain everything with just one variable).

3.4.4.3 Model Assumptions

For Poisson GLMs, there is one further assumption that we have not encountered before. If data follow a Poisson distribution, then the mean of the distribution is equal to the variance. Accordingly, a Poisson distribution is represented by just one parameter λ , which describes both the mean and the variance of the distribution.

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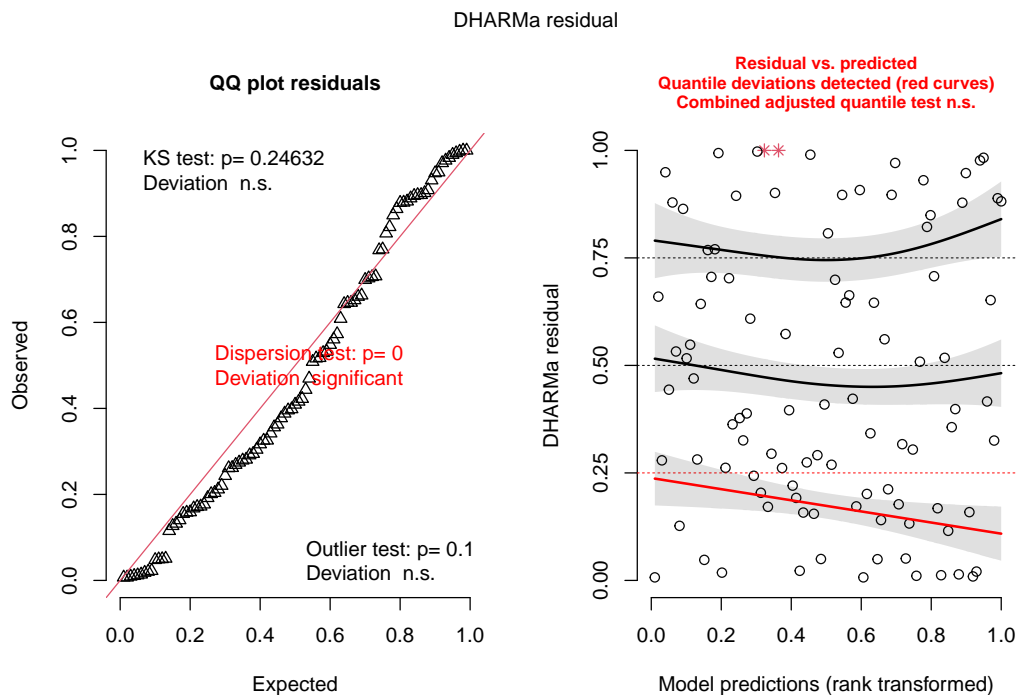
Count data in ecology are often **overdispersed**, where the variance is greater than the mean. This violates the assumption of a Poisson GLM, and means that any statistics that we calculate from the model may be unreliable.

We can get look whether a model is over-dispersed by inspecting the model summary as you did in Section 3.4.4.1. As a rule of thumb, if the response variable conforms to a true Poisson distribution, we expect the residual deviance to be approximately equal to the residual degrees of freedom. If the deviance is much greater than the degrees of freedom, this indicates over-dispersion. This is the case in our models (see outputs from running the code in Section 3.4.4.1).

To check the model assumptions in a GLM is not as straight forward as with a linear model. This is because classical residuals are not expected to behave in the same way for GLMs. We can use the DHARMA package in R for working with GLMs, which uses a simulation-based approach to compare the residuals from the actual model with the expectation if the model is behaving normally:

```
# Simulate residuals
simResids <- DHARMA::simulateResiduals(bryoModel1)

# Generate plots to compare the model residuals to expectations
plot(simResids)
```



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In these plots the outliers are highlighted in red (if they are any). To provide a visual aid in detecting deviations from uniformity in y-direction, the plot function calculates a quantile regression of the residuals, by default for the 0.25, 0.5 and 0.75 quantiles. As the residuals should be uniformly distributed for a correctly specified model, the theoretical expectations for these regressions are straight lines at 0.25, 0.5 and 0.75, which are displayed as dashed black lines on the plot. Some deviations from these expectations are to be expected by chance, however, even for a perfect model, especially if the sample size is small. The function therefore tests if deviation of the fitted quantile regression from the expectation is significant, using `testQuantiles`. If so, the significant quantile regression will be highlighted as red, and a warning will be displayed in the plot.

In these plots we can see that this model is not behaving as we would expect in terms of homogeneity of variance and distribution of residuals. A follow up to this would be to try alternatives to deal with over-dispersed count data in GLMs such as fit a quasi-Poisson GLM or a negative binomial GLM. Unfortunately we do not have time to continue in this exercise.

3.4.5 Group 1 - Question D

- Is the number of Bryophytes species affected by forest management type and the forest structural diversity?

3.4.5.1 Fitting a Poisson GLM in R

Fitting a Poisson GLM in R is very similar to fitting an analysis of covariance (or linear model), except that now we need to use the `glm` function. To run a GLM, we need to provide one extra piece of information beyond that needed for a linear model: the family of model we want to use. In this case, we want a Poisson family.

We could start by only looking at how the forest structural diversity affects the number Bryophyte species that we have in a plot. You can do this by creating a GLM model which has `bryophyteNumObs` as response variable and `GiniDBH` as explanatory variable. For that you will use the function `glm` in R and use the `family = poisson`. You can see how to create and see this model here:

```
bryoModel1 <- glm(bryophyteNumObs ~ GiniDBH,
                  family = poisson,
                  data = observations)

summary(bryoModel1)
```

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Call:

```
glm(formula = bryophyteNumObs ~ GiniDBH, family = poisson, data = observations)
```

Coefficients:

| | Estimate | Std. Error | z value | Pr(> z) |
|-------------|----------|------------|---------|--------------|
| (Intercept) | 0.4627 | 0.1388 | 3.333 | 0.000859 *** |
| GiniDBH | 2.2797 | 0.4221 | 5.401 | 6.64e-08 *** |

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

(Dispersion parameter for poisson family taken to be 1)

Null deviance: 188.58 on 98 degrees of freedom
Residual deviance: 159.92 on 97 degrees of freedom
AIC: 424.2

Number of Fisher Scoring iterations: 5

Here you can see that the coefficient table produced by a GLM is very similar to a linear model. The intercept tells us the estimated value of the response variable when the continuous explanatory variables (here just Gini index) have a value of 0. We then also have coefficients describing the slope of the relationship with our continuous explanatory variables. We can see here that the bryophyte numbers appears to show a positive relationship with Gini index, which means that increasing structural diversity in trees diameter sizes has a positive relationship with the number of Bryophyte species in the plot.

We are also interested in understanding the relationship of the number of observed Bryophyte species and forest management, we can now try create a new model considering this variable.

```
bryoModel2 <- glm(bryophyteNumObs ~ forestManagementType,  
                  family = poisson,  
                  data = observations)  
  
summary(bryoModel2)
```

Call:

```
glm(formula = bryophyteNumObs ~ forestManagementType, family = poisson,  
    data = observations)
```

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Coefficients:

| | Estimate | Std. Error | z value | Pr(> z) |
|---|----------|------------|---------|----------|
| (Intercept) | 0.9651 | 0.1543 | 6.254 | 3.99e-10 |
| forestManagementTypesimple clearcutting | -0.1335 | 0.1750 | -0.763 | 0.445 |
| forestManagementTypeunmanaged | 0.7633 | 0.1821 | 4.192 | 2.76e-05 |

| | |
|---|-----|
| (Intercept) | *** |
| forestManagementTypesimple clearcutting | |
| forestManagementTypeunmanaged | *** |

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

(Dispersion parameter for poisson family taken to be 1)

Null deviance: 188.58 on 98 degrees of freedom
Residual deviance: 141.54 on 96 degrees of freedom
AIC: 407.82

Number of Fisher Scoring iterations: 5

The intercept here tells us the estimated value of the response variable when the reference groups in our grouping (categorical) variables (here for retention clear-cutting). We can see here that number of Bryophyte species appears to show a negative relationship with simple clearcutting, and appears to have a positive relationship with unmanaged and retention clear-cutting.

The type simple clearcutting appears to be non significant, which only tells us about the pairwise differences between the levels. To test whether the categorical predictor, as a whole, is significant is equivalent to testing whether there is any heterogeneity in the means of the levels of the predictor. When there are no other predictors in the model, this is a classical ANOVA problem.

3.4.5.2 Explanatory Power of the model

When we run linear models, we use the coefficient of determination, or R^2 to assess how much of the variability in our response variable is explained by a given model. R^2 is based on the sums of squares of our model, and so it cannot be calculated for GLMs. Instead, we can calculate the the deviance explained by our model:

```
# Extract the null and residual deviance from the model
dev.null <- bryoModel1$null.deviance
dev.resid <- bryoModel1$deviance
```

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```
# Calculate the deviance explained by the model
dev.explained <- (dev.null - dev.resid) / dev.null

# Round to 3 decimal places
dev.explained <- round(dev.explained, 3)

dev.explained
```

```
[1] 0.152
```

Variability in forest structure (Gini index) explains 15% of the variation in Bryophyte species richness in this study system. That is an ok explanatory power for a very simple model of a complex ecological system (many factors determine the species richness of Bryophyte and we are attempting to explain everything with one variable).

3.4.5.3 Model Assumptions

For Poisson GLMs, there is one further assumption that we have not encountered before. If data follow a Poisson distribution, then the mean of the distribution is equal to the variance. Accordingly, a Poisson distribution is represented by just one parameter λ , which describes both the mean and the variance of the distribution.

Count data in ecology are often *overdispersed*, where the variance is greater than the mean. This violates the assumption of a Poisson GLM, and means that any statistics that we calculate from the model may be unreliable.

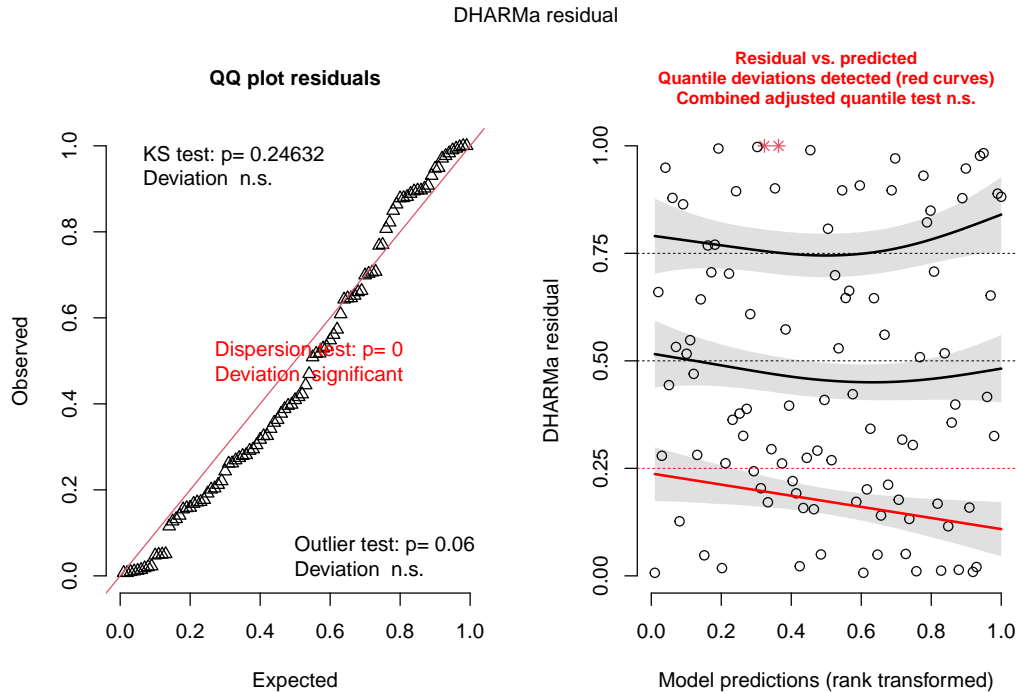
We can get look whether a model is over-dispersed by inspecting the model summary as you did in Section 3.4.5.1. As a rule of thumb, if the response variable conforms to a true Poisson distribution, we expect the residual deviance to be approximately equal to the residual degrees of freedom. If the deviance is much greater than the degrees of freedom, this indicates over-dispersion. This is the case in our models (see outputs from running the code in Section 3.4.5.1).

To check the model assumptions in a GLM is not as straight-forward as with a linear model. This is because classical residuals are not expected to behave in the same way for GLMs. We can use the DHARMA package in R for working with GLMs, which uses a simulation-based approach to compare the residuals from the actual model with the expectation if the model is behaving normally.

```
# Simulate residuals
simResids <- DHARMA::simulateResiduals(bryoModel1)
```

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```
# Generate plots to compare the model residuals to expectations
plot(simResids)
```



In these plots the outliers are highlighted in red (if they are any). To provide a visual aid in detecting deviations from uniformity in y-direction, the plot function calculates a quantile regression of the residuals, by default for the 0.25, 0.5 and 0.75 quantiles. As the residuals should be uniformly distributed for a correctly specified model, the theoretical expectations for these regressions are straight lines at 0.25, 0.5 and 0.75, which are displayed as dashed black lines on the plot. Some deviations from these expectations are to be expected by chance, however, even for a perfect model, especially if the sample size is small. The function therefore tests if deviation of the fitted quantile regression from the expectation is significant, using `testQuantiles`. If so, the significant quantile regression will be highlighted as red, and a warning will be displayed in the plot. You can find more information about this graphs in the package instructions [here](#).

These plots show us that this model is not behaving as we would expect in terms of homogeneity of variance and distribution of residuals. A follow up to this would be to try alternatives to deal with over-dispersed count data in GLMs such as fit a quasi-Poisson GLM or a negative binomial GLM. Unfortunately we do not have to continue in this exercise.

3.4.6 Group 2 - Question C

- Does a more diverse forest in structure and composition have more bird species?

3.4.6.1 Fitting a Poisson GLM in R

During your data exploration you should have selected your response variable: `birdNumObs`. In this case since we are trying to understand forest structure and composition you should also select explanatory variables for that such as `GiniDBH` which indicates the forest structural diversity in diameter sizes, higher values indicate more structural heterogeneity and lower values indicate more homogeneous stands, or the `ShannonIndexTreeSpp` which assess the diversity of tree species in the plot.

We could start by only looking at how the forest structural diversity affects the number bird species that we have in a plot. You can do this by creating a GLM model which has `birdNumObs` as response variable and `GiniDBH` as explanatory variable. For that you will use the function `glm` in R and use the `family = poisson`. You can see how to create and see this model here:

```
birdModel1 <- glm(birdNumObs ~ GiniDBH,
                  family = poisson,
                  data = observations)

summary(birdModel1)
```

Call:

```
glm(formula = birdNumObs ~ GiniDBH, family = poisson, data = observations)
```

Coefficients:

| | Estimate | Std. Error | z value | Pr(> z) |
|-------------|----------|------------|---------|------------|
| (Intercept) | 2.63827 | 0.05636 | 46.809 | <2e-16 *** |
| GiniDBH | 0.42725 | 0.19030 | 2.245 | 0.0248 * |

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

(Dispersion parameter for poisson family taken to be 1)

Null deviance: 59.277 on 98 degrees of freedom
 Residual deviance: 54.280 on 97 degrees of freedom
 AIC: 511.57

Number of Fisher Scoring iterations: 4

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Here you can see that the coefficient table produced by a GLM is very similar to a linear model. The intercept tells us the estimated value of the response variable when the continuous explanatory variables (here just Gini index) has a value of 0. We then also have coefficients describing the slope of the relationship with our continuous explanatory variables. We can see here that the number of bird species appears to show a positive relationship with Gini index, which means that increasing structural diversity in trees diameter sizes has a positive relationship with the number of bird species in the plot.

We are also interested in understanding the relationship of the number of bird species and the trees species diversity, we can now try to add this variable into the model and see if it help us to understand things. You can do that by adding the variable `ShannonIndexTreeSpp` into the model

```
birdModel2 <- glm(birdNumObs ~ GiniDBH + ShannonIndexTreeSpp,
                  family = poisson,
                  data = observations)

summary(birdModel2)
```

Call:

```
glm(formula = birdNumObs ~ GiniDBH + ShannonIndexTreeSpp, family = poisson,
     data = observations)
```

Coefficients:

| | Estimate | Std. Error | z value | Pr(> z) |
|---------------------|----------|------------|---------|------------|
| (Intercept) | 2.63499 | 0.05665 | 46.513 | <2e-16 *** |
| GiniDBH | 0.33323 | 0.21661 | 1.538 | 0.124 |
| ShannonIndexTreeSpp | 0.06923 | 0.07444 | 0.930 | 0.352 |

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

(Dispersion parameter for poisson family taken to be 1)

Null deviance: 59.277 on 98 degrees of freedom
Residual deviance: 53.419 on 96 degrees of freedom
AIC: 512.71

Number of Fisher Scoring iterations: 4

Here we can see that the variable Shannon index also has a positive relationship with the number of bird species in the plot but its effect is much smaller. We can also observe that this variable is not significant and that including this variable also made Gini index

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variable not significant. This does not mean that is wrong to add this variable, because we want to understand its effect, but keeping this variable in the model or not depends on what you're trying to do, and what "reality" is. Adding variables that are not needed will not help your model (particularly your estimates), but also might not matter much (e.g. predictions). However, removing variables that are real, even if they don't meet significance, can create a useless model.

Variable selection is a long and complicated topic. some general rules of thumb include: (1) Include the variable if it is of interest, (2) Include the variable if you have some prior knowledge that it should be relevant. This can be misleading, because it's a confirmation bias, but in most cases this makes sense. (3) If you want a model that can generalize to many cases, you should favor fewer variables.

3.4.6.2 Explanatory Power of the model

When we ran linear models, we used the coefficient of determination, or R^2 to assess how much of the variability in our response variable is explained by a given model. R^2 is based on the sums of squares of our model, and so cannot be calculated for GLMs. Instead, we can calculate the the deviance explained by our model:

```
# Extract the null and residual deviance from the model
dev.null <- birdModel1>null.deviance
dev.resid <- birdModel1$deviance

# Calculate the deviance explained by the model
dev.explained <- (dev.null - dev.resid) / dev.null

# Round to 3 decimal places
dev.explained <- round(dev.explained, 3)

dev.explained
```

```
[1] 0.084
```

Variability in forest structure (Gini index) explain 8% of the variation in bird species richness in this study. That is an ok explanatory power for a very simple model of a complex ecological system (many factors determine the species richness for birds and we are attempting to explain everything with just one variable).

3.4.6.3 Model Assumptions

For Poisson GLMs, there is one further assumption that we have not encountered before. If data follow a Poisson distribution, then the mean of the distribution is equal to the variance. Accordingly, a Poisson distribution is represented by just one parameter λ , which describes both the mean and the variance of the distribution.

Count data in ecology are often **overdispersed**, where the variance is greater than the mean. This violates the assumption of a Poisson GLM, and means that any statistics that we calculate from the model may be unreliable.

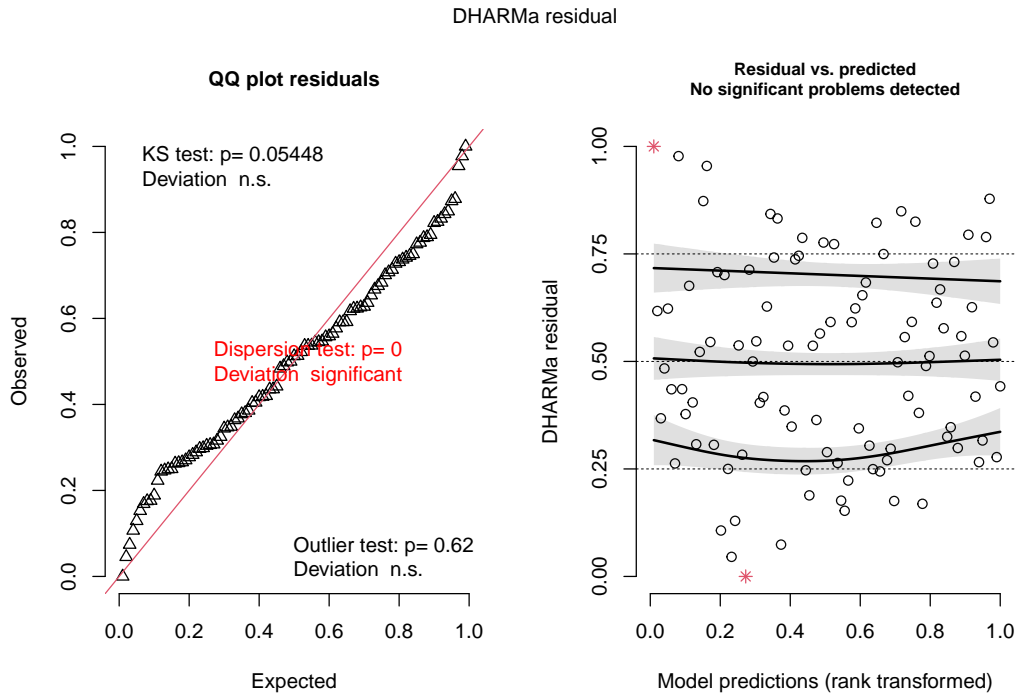
We can get look whether a model is over-dispersed by inspecting the model summary as you did in Section 3.4.6.1. As a rule of thumb, if the response variable conforms to a true Poisson distribution, we expect the residual deviance to be approximately equal to the residual degrees of freedom. If the deviance is much greater than the degrees of freedom, this indicates over-dispersion. This is the case in our models (see outputs from running the code in Section 3.4.6.1).

To check the model assumptions in a GLM is not as straight-forward as with a linear model. This is because classical residuals are not expected to behave in the same way for GLMs. We can use the DHARMA package in R for working with GLMs, which uses a simulation-based approach to compare the residuals from the actual model with the expectation if the model is behaving normally:

```
# Simulate residuals
simResids <- DHARMA::simulateResiduals(birdModel1)

# Generate plots to compare the model residuals to expectations
plot(simResids)
```

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In these plots the outliers are highlighted in red (if they are any). To provide a visual aid in detecting deviations from uniformity in y-direction, the plot function calculates a quantile regression of the residuals, by default for the 0.25, 0.5 and 0.75 quantiles. As the residuals should be uniformly distributed for a correctly specified model, the theoretical expectations for these regressions are straight lines at 0.25, 0.5 and 0.75, which are displayed as dashed black lines on the plot. Some deviations from these expectations are to be expected by chance, however, even for a perfect model, especially if the sample size is small. The function therefore tests if deviation of the fitted quantile regression from the expectation is significant, using `testQuantiles`. If so, the significant quantile regression will be highlighted as red, and a warning will be displayed in the plot. You can find more information about this graphs in the package instructions [here](#).

These plots show us that this model is not behaving as we would expect in terms of homogeneity of variance and distribution of residuals. A follow up to this would be to try alternatives to deal with over-dispersed count data in GLMs such as fit a quasi-Poisson GLM or a negative binomial GLM. Unfortunately we do not have time to continuou in this exercise.

3.4.7 Group 2 - Question D

- Is the number of bird species affected by forest management type and the forest structural diversity?

3.4.7.1 Fitting a Poisson GLM in R

Fitting a Poisson GLM in R is very similar to fitting an analysis of covariance (or linear model), except that now we need to use the `glm` function. To run a GLM, we need to provide one extra piece of information beyond that needed for a linear model: the family of model we want to use. In this case, we want a Poisson family.

We could start by only looking at how the forest structural diversity affects the number bird species that we have in a plot. You can do this by creating a GLM model which has `birdNumObs` as response variable and `GiniDBH` as explanatory variable. For that you will use the function `glm` in R and use the `family = poisson`. You can see how to create and see this model here:

```
birdModel1 <- glm(birdNumObs ~ GiniDBH,
                  family = poisson,
                  data = observations)

summary(birdModel1)
```

Call:

```
glm(formula = birdNumObs ~ GiniDBH, family = poisson, data = observations)
```

Coefficients:

| | Estimate | Std. Error | z value | Pr(> z) |
|-------------|----------|------------|---------|------------|
| (Intercept) | 2.63827 | 0.05636 | 46.809 | <2e-16 *** |
| GiniDBH | 0.42725 | 0.19030 | 2.245 | 0.0248 * |

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

(Dispersion parameter for poisson family taken to be 1)

Null deviance: 59.277 on 98 degrees of freedom
 Residual deviance: 54.280 on 97 degrees of freedom
 AIC: 511.57

Number of Fisher Scoring iterations: 4

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Here you can see that the coefficient table produced by a GLM is very similar to a linear model. The intercept tells us the estimated value of the response variable when the continuous explanatory variables (here just Gini index) have a value of 0. We then also have coefficients describing the slope of the relationship with our continuous explanatory variables. We can see here that the bird numbers appears to show a positive relationship with Gini index, which means that increasing structural diversity in trees diameter sizes has a positive relationship with the number of bird species in the plot.

We are also interested in understanding the relationship of the number of observed bird species and forest management, we can now try to create a new model with this variable.

```
birdModel2 <- glm(birdNumObs ~ forestManagementType,
                  family = poisson,
                  data = observations)

summary(birdModel2)
```

Call:

```
glm(formula = birdNumObs ~ forestManagementType, family = poisson,
     data = observations)
```

Coefficients:

| | Estimate | Std. Error | z value | Pr(> z) |
|---|----------|------------|---------|----------|
| (Intercept) | 2.83688 | 0.06052 | 46.873 | <2e-16 |
| forestManagementTypesimple clearcutting | -0.11744 | 0.06850 | -1.714 | 0.0865 |
| forestManagementTypeunmanaged | -0.06429 | 0.08338 | -0.771 | 0.4407 |

```
(Intercept) ***
forestManagementTypesimple clearcutting .
forestManagementTypeunmanaged
---
```

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

(Dispersion parameter for poisson family taken to be 1)

```
Null deviance: 59.277 on 98 degrees of freedom
Residual deviance: 56.205 on 96 degrees of freedom
AIC: 515.49
```

Number of Fisher Scoring iterations: 4

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The intercept here tells us the estimated value of the response variable when the reference groups in our grouping (categorical) variables (here for retention clear-cutting). We can see here that number of bird species appears to show a negative relationship with simple clearcutting, unmanaged and a positive relationship with retention clear-cutting.

The type simple clearcutting and unmanaged appear to be no significant, which only tell us about the pairwise differences between the levels. To test whether the categorical predictor, as a whole, is significant is equivalent to testing whether there is any heterogeneity in the means of the levels of the predictor. When there are no other predictors in the model, this is a classical ANOVA problem.

3.4.7.2 Explanatory Power of the model

When we ran linear models, we used the coefficient of determination, or R^2 to assess how much of the variability in our response variable is explained by a given model. R^2 is based on the sums of squares of our model, and so cannot be calculated for GLMs. Instead, we can calculate the the deviance explained by our model:

```
# Extract the null and residual deviance from the model
dev.null <- birdModel1$null.deviance
dev.resid <- birdModel1$deviance

# Calculate the deviance explained by the model
dev.explained <- (dev.null - dev.resid) / dev.null

# Round to 3 decimal places
dev.explained <- round(dev.explained, 3)

dev.explained
```

```
[1] 0.084
```

Variability in forest structure (Gini index) explain 8% of the variation in bird species richness in this study system. That is an ok explanatory power for a very simple model of a complex ecological system (many factors determine the species richness and we are attempting to explain everything with one variable).

3.4.7.3 Model Assumptions

For Poisson GLMs, there is one further assumption that we have not encountered before. If data follow a Poisson distribution, then the mean of the distribution is equal to the

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variance. Accordingly, a Poisson distribution is represented by just one parameter λ , which describes both the mean and the variance of the distribution.

Count data in ecology are often *overdispersed*, where the variance is greater than the mean. This violates the assumption of a Poisson GLM, and means that any statistics that we calculate from the model may be unreliable.

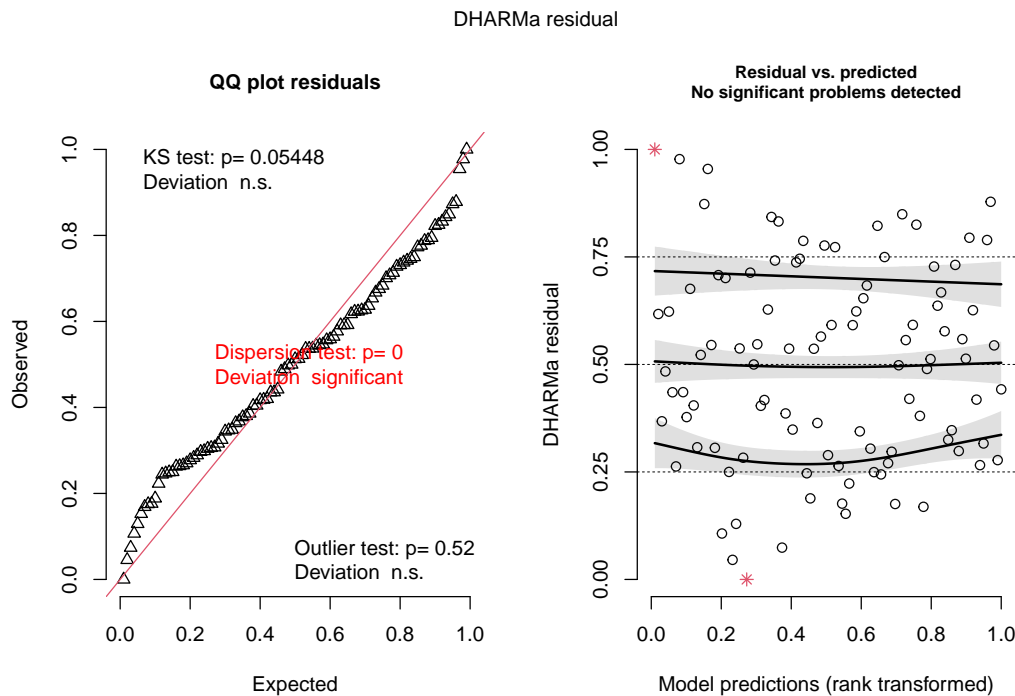
We can get look whether a model is over-dispersed by inspecting the model summary as you did in Section 3.4.7.1. As a rule of thumb, if the response variable conforms to a true Poisson distribution, we expect the residual deviance to be approximately equal to the residual degrees of freedom. If the deviance is much greater than the degrees of freedom, this indicates over-dispersion. This is the case in our models (see outputs from running the code in Section 3.4.7.1).

To check the model assumptions in a GLM is not as straight forward as with a linear model. This is because classical residuals are not expected to behave in the same way for GLMs. We can use the DHARMA package in R for working with GLMs, which uses a simulation-based approach to compare the residuals from the actual model with the expectation if the model is behaving normally.

```
# Simulate residuals
simResids <- DHARMA::simulateResiduals(birdModel1)

# Generate plots to compare the model residuals to expectations
plot(simResids)
```

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In these plots the outliers are highlighted in red (if they are any). To provide a visual aid in detecting deviations from uniformity in y-direction, the plot function calculates a quantile regression of the residuals, by default for the 0.25, 0.5 and 0.75 quantiles. As the residuals should be uniformly distributed for a correctly specified model, the theoretical expectations for these regressions are straight lines at 0.25, 0.5 and 0.75, which are displayed as dashed black lines on the plot. Some deviations from these expectations are to be expected by chance, however, even for a perfect model, especially if the sample size is small. The function therefore tests if deviation of the fitted quantile regression from the expectation is significant, using `testQuantiles`. If so, the significant quantile regression will be highlighted as red, and a warning will be displayed in the plot. You can find more information about this graphs in the package instructions [here](#).

These plots show us that this model is not behaving as we would expect in terms of homogeneity of variance and distribution of residuals. A follow up to this would be to try alternatives to deal with over-dispersed count data in GLMs such as fit a quasi-Poisson GLM or a negative binomial GLM. Unfortunately we do not have to continuou in this exercise.

3.4.8 Group 3 - Question C

- Is the presence of the Great spotted woodpecker affected by forest density?

3.4.8.1 Fitting a BRT in R

In this case we want to assess the occurrence of certain species across the plots. In other words, we want to assess what is the probability of a certain species with biodiversity interest to be present in a plot based on the variables that describe the forest of that plot. In this case the response variable is `dendrocoposMajor` that represents if the Great spotted woodpecker has been observed in this plot or not.

Then you need to select some variables of interest, after you have explored the data you can decide which variables you want to use to fit this model. We are proposing to select the following variables:

- `latitude` as proxy for plot location or/and climate
- `forestManagementType` to assess if different management types have different impact in the presence / absence of Great spotted woodpecker.
- `volAllha` that is the total volume in the plot, as a proxy of how dense the plot is. Higher volumes will mean that the forest is more dense.
- `GiniDBH` showing how homogeneous the plot is in trees diameters. A value closer to 1 indicate a more structural heterogeneity, lower values indicate more homogeneous plots.

You can create a vector `selVar` in which you add the names of the selected variables. Then you only take those variables from the data that you will use to create the model.

```
# Select variables from the dataset for the model
selVar <- c(
  "dendrocoposMajor",
  "latitude",
  "forestManagementType",
  "volAllha",
  "GiniDBH",
  "ShannonIndexTreeSpp"
)

# Filter the dataset to the selected variables
modelDataSel <- observations[, colnames(observations) %in% selVar]
```

Unfortunately the amount of observations that we have in this dataset it is not enough to fit a BRT model for these variables. We are going to do an obviously wrong thing for the sake of being able to demonstrate how to fit a BRT model. In the next code you are going to repeat the same dataset multiple times:

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```
modelDataSel <- rbind(modelDataSel, modelDataSel, modelDataSel,  
                      modelDataSel, modelDataSel)
```

Now it is important to assess if the variables have the right categories. Variables should be type numeric or factor.

```
summary(modelDataSel)
```

| latitude | forestManagementType | volAllha | GiniDBH |
|--------------------------------------|----------------------|-----------------|-----------------|
| Min. :48.65 | Length:495 | Min. : 1.681 | Min. :0.08209 |
| 1st Qu.:49.31 | Class :character | 1st Qu.:319.920 | 1st Qu.:0.13684 |
| Median :49.40 | Mode :character | Median :434.729 | Median :0.20358 |
| Mean :49.49 | | Mean :425.694 | Mean :0.25683 |
| 3rd Qu.:50.19 | | 3rd Qu.:558.355 | 3rd Qu.:0.37368 |
| Max. :50.34 | | Max. :777.882 | Max. :0.52852 |
| ShannonIndexTreeSpp dendrocoposMajor | | | |
| Min. :0.000 | Min. :0.0000 | | |
| 1st Qu.:0.060 | 1st Qu.:0.0000 | | |
| Median :0.280 | Median :1.0000 | | |
| Mean :0.392 | Mean :0.7071 | | |
| 3rd Qu.:0.680 | 3rd Qu.:1.0000 | | |
| Max. :1.450 | Max. :1.0000 | | |

```
# One variables is a character, we assign to factor instead:  
modelDataSel$forestManagementType <-  
  as.factor(modelDataSel$forestManagementType)
```

In the next step you can see how you can run the model with the selected variables and model parameters. You have a description of the models parameters in the Section 3.3.2 . In this example we are going to use the default parameters for the calibration, where learning rate = 0.01 and tree complexity = 1 and cross-validation = 10-fold. However, the bag fraction is changed from the default value, 0.75, to 0.5. As a family we used the Bernoulli family, because we are predicting presence/absence per plot. These data have 495 plots, comprising 350 presence records for the Great spotted woodpecker. You can check these numbers by doing:

```
table(modelDataSel$dendrocoposMajor)
```

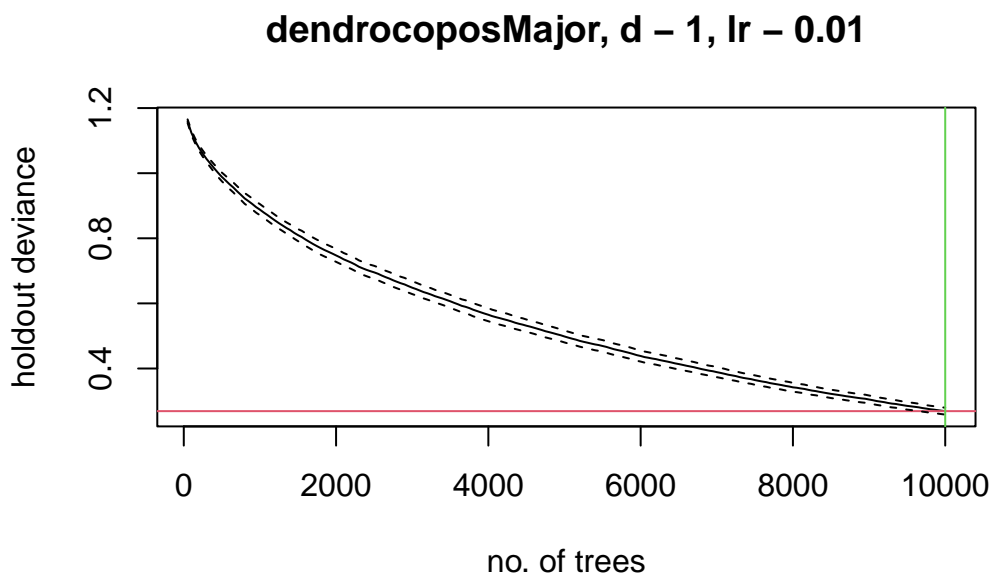
```
0 1  
145 350
```

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As a first guess you could decide there are enough data to model interactions of reasonable complexity, and a lr of about 0.01 could be a reasonable starting point. You can use the model creation function that steps forward and identifies the optimal number of trees (nt) by doing this:

```
family <- "bernoulli"
tc = 1    # tree complexity
lr = 0.01 # learning rate-shrinkage
bag = 0.5 # bag fraction

modelBRT <- dismo::gbm.step(
  data = modelDataSel,
  #indices of predictor variables in data
  gbm.x = 1:5,
  #index of response variable in data:
  gbm.y = 6,
  family = family,
  tree.complexity = tc,
  learning.rate = lr,
  bag.fraction = bag
)
```



Running a model such as that described above writes progress reports to the screen,

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makes a graph, and returns an object containing a number of components. The R console reports a brief model summary, all the model summary values are retained in the model object.

The model is built with the default 10-fold cross-validation (CV). In the plotted graph the solid black curve is the mean, and the dotted curves 1 standard error, for the changes in predictive deviance (i.e., as measured on the excluded folds of the CV). The red line shows the minimum of the mean, and the green line the number of trees at which that occurs. The final model that is returned in the model object is built on the full data set, using the number of trees identified as optimal.

Ideally, you should invest time in modifying the parameters and find the parameters that provide the models with the minimum deviance resulting from the best combination of bag, tree complexity and learning rate values. For the sake of limited timing, we will only test here the default values.

3.4.8.2 Model behaviour

You can summarize the model parameters used and the cross validation statistics from the fitted model by doing this:

```
# We make a table with the summary statistics
results <- data.frame(
  # Model parameters
  Tree.Complexity = modelBRT$gbm.call$tree.complexity,
  Learning.Rate = modelBRT$gbm.call$learning.rate,
  Bag.Fraction = modelBRT$gbm.call$bag.fraction,
  Interaction.depth = modelBRT$interaction.depth,
  Shrinkage = modelBRT$shrinkage,
  N.trees = modelBRT$n.trees,

  # Cross validation statistics

  ## mean total deviance
  Deviance = modelBRT$self.statistics$mean.resid,
  # mean residual deviance

  AUC = modelBRT$self.statistics$discrimination,
  # training data AUC score

  Corr = modelBRT$self.statistics$correlation,
  # training data correlation

  ## Cross Validation statistics
```

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```
# We calculate each statistic within each fold (at the identified optimal number
# of trees that is calculated on the mean change in predictive deviance over all fol
#then present here the mean and standard error of those fold-based statistics.

devianceCV = modelBRT$cv.statistics$deviance.mean,
# estimated cv deviance
devianceCVse = modelBRT$cv.statistics$deviance.se,
# estimated cv deviance se

CorrCV = modelBRT$cv.statistics$correlation.mean,
#cv correlation
CorrCVse = modelBRT$cv.statistics$correlation.se,
#cv correlation se

AUCcv = modelBRT$cv.statistics$discrimination.mean,
# cv AUC score
AUCcvSE = modelBRT$cv.statistics$discrimination.se
) # cv AUC score se

print(t(results))
```

| | [,1] |
|-------------------|--------------|
| Tree.Complexity | 1.000000e+00 |
| Learning.Rate | 1.000000e-02 |
| Bag.Fraction | 5.000000e-01 |
| Interaction.depth | 1.000000e+00 |
| Shrinkage | 1.000000e-02 |
| N.trees | 1.000000e+04 |
| Deviance | 2.179161e-01 |
| AUC | 1.000000e+00 |
| Corr | 9.751182e-01 |
| devianceCV | 2.690397e-01 |
| devianceCVse | 1.061444e-02 |
| CorrCV | 9.538085e-01 |
| CorrCVse | 6.109263e-03 |
| AUCcv | 1.000000e+00 |
| AUCcvSE | 0.000000e+00 |

3.4.8.3 Model output analysis

We can look at the relative contribution of each of the predictor variables. The measures are based on the number of times the variable is selected for splitting, weighted by the improvement of the model as a result of each split averaged across all trees. The relative contribution of each of the variables is scaled so the sum is 100%, with higher numbers indicating stronger influence in the response.

```
# Variables contribution
modelBRT$contributions
```

| | var | rel.inf |
|----------------------|----------------------|-----------|
| latitude | latitude | 33.373521 |
| GiniDBH | GiniDBH | 24.587996 |
| volAllha | volAllha | 24.553325 |
| ShannonIndexTreeSpp | ShannonIndexTreeSpp | 12.771539 |
| forestManagementType | forestManagementType | 4.713619 |

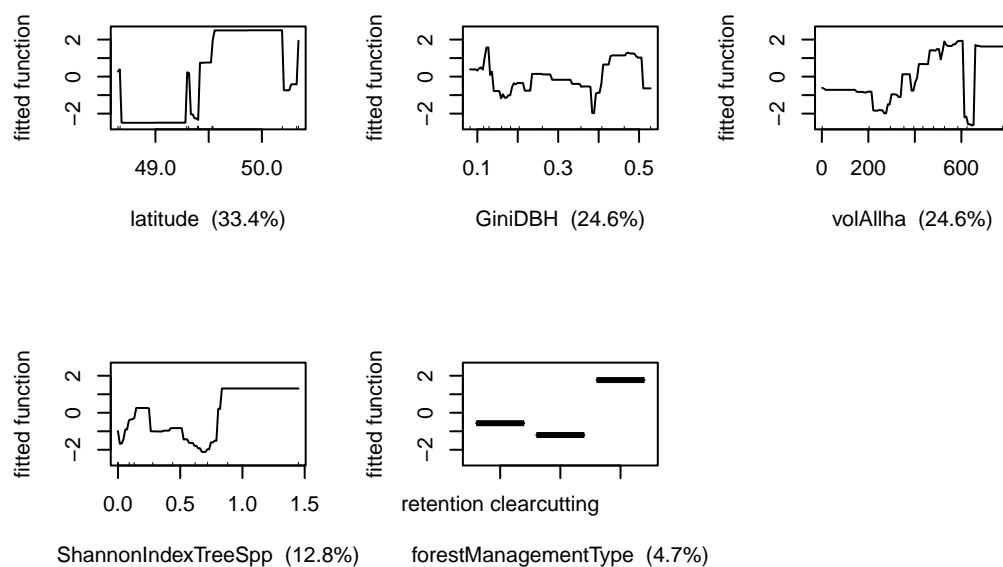
Here we can see that the two variables with the highest influence in the response are `latitude`, and `volAllhsa`.

Now we can evaluate the model behavior via partial dependence plots, showing the effect of each of the variables on the response by accounting for the average effects of all other predictors in the model:

```
dismo::gbm.plot(
  modelBRT,
  n.plots = 6,
  plot.layout = c(2, 3),
  write.title = F
)
```

Warning in `dismo::gbm.plot(modelBRT, n.plots = 6, plot.layout = c(2, 3), :`
reducing no of plotted predictors to maximum available (5)

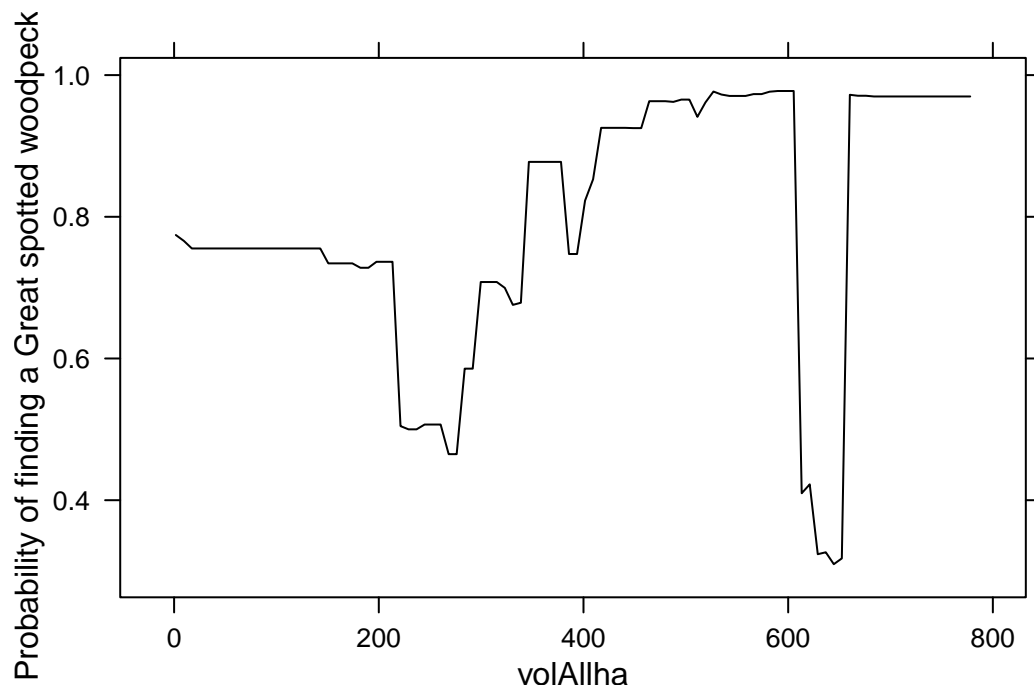
3 Empirical modeling



In partial dependence plots the predictions are on the scale of $f(x)$. In this case, for the Bernoulli loss the returned value is on the log odds scale. You can see how this plot will look by plotting with the function from the package `gbm` and using the type “response”. Since we are interested in finding out if the forest density has an impact on the presence of the Great spotted woodpecker we can have a look to the plot density variable `volAllha` :

```
gbm::plot.gbm(modelBRT, i.var = 3, type = "response",
               ylab = "Probability of finding a Great spotted woodpecker ")
```

3 Empirical modeling

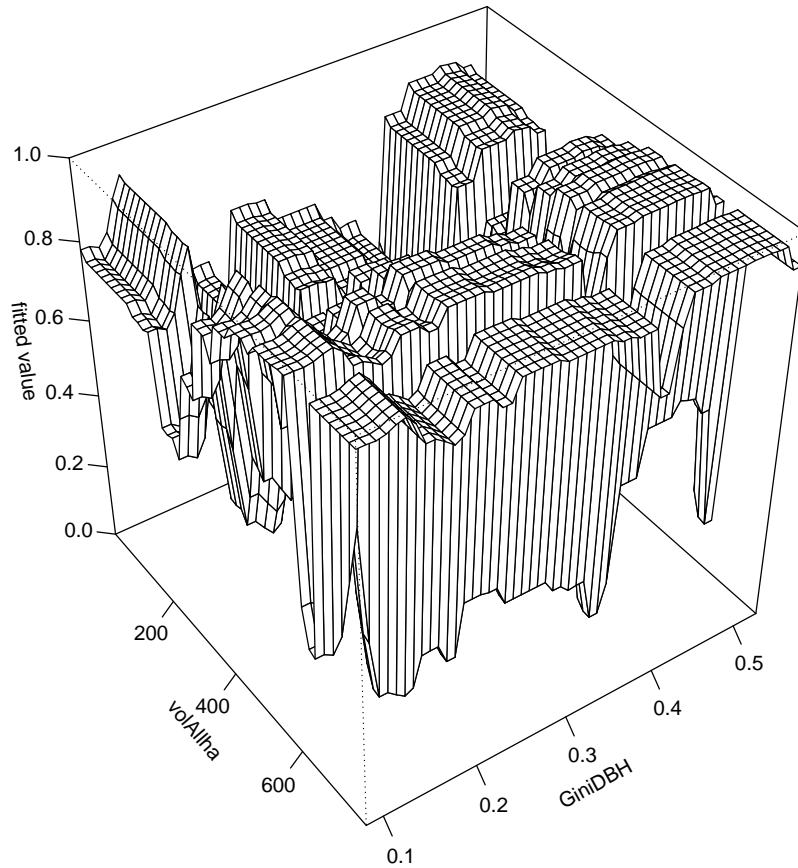


It seems that there is an increase in probability of finding a Great spotted woodpecker with higher forest densities, but the trend it is not very clear. We could also analyse the interaction effects, of density and for example the Gini index. The model predictions can be obtained for each pair of predictor variables, setting all other predictors to their means.

To plot this pairwise interactions we have to do:

```
dismo::gbm.perspec(modelBRT, 3, 4)
```

3 Empirical modeling



Here we can see that both increasing bird diversity and forest density provides the highest probabilities for finding the Great spotted woodpecker.

3.4.9 Group 3 - Question D

- Is the presence of the Great spotted woodpecker affected by forest diversity?

3.4.9.1 Fitting a BRT in R

In this case we want to assess the occurrence of certain species across the plots. In other words, we want to assess what is the probability of a certain species with biodiversity interest to be present in a plot based on the variables that describe the forest of that plot. In this case the response variable is `dendrocoposMajor` that represents if the Great spotted woodpecker has been observed in this plot or not.

Then you need to select some variables of interest, after you have explored the data you can decide which variables you want to use to fit this model. We are proposing to select the following variables:

- `latitude` as proxy for plot location or/and climate
- `forestManagementType` to assess if different management types have different impact in the presence / absence of Great spotted woodpecker.
- `volAllha` that is the total volume in the plot, as a proxy of how dense the plot is. Higher volumes will mean that the forest is more dense.
- `GiniDBH` showing how homogeneous the plot is in trees diameters. A value closer to 1 will mean that indicate more structural heterogeneity, lower values indicate more homogeneous plots.

You can create a vector `selVar` in which you add the names of the selected variables. Then you only take those variables from the data that you will use to create the model.

```
# Select variables from the dataset for the model
selVar <- c(
  "dendrocoposMajor",
  "latitude",
  "forestManagementType",
  "volAllha",
  "GiniDBH",
  "ShannonIndexTreeSpp"
)

# Filter the dataset to the selected variables
modelDataSel <- observations[, colnames(observations) %in% selVar]
```

Unfortunately the amount of observations that we have in this dataset it is not enough to fit a BRT model for these variables. We are going to do an obviously wrong thing for the sake of being able to demonstrate how to fit a BRT model. In the next code you are going to repeat the same dataset multiple times:

3 Empirical modeling

```
modelDataSel <- rbind(modelDataSel, modelDataSel, modelDataSel, modelDataSel,
                      modelDataSel)
```

Now it is important to assess if the variables have the right categories. Variables should be type numeric or factor.

```
summary(modelDataSel)
```

| latitude | forestManagementType | volAllha | GiniDBH |
|--------------------------------------|----------------------|-----------------|-----------------|
| Min. :48.65 | Length:495 | Min. : 1.681 | Min. :0.08209 |
| 1st Qu.:49.31 | Class :character | 1st Qu.:319.920 | 1st Qu.:0.13684 |
| Median :49.40 | Mode :character | Median :434.729 | Median :0.20358 |
| Mean :49.49 | | Mean :425.694 | Mean :0.25683 |
| 3rd Qu.:50.19 | | 3rd Qu.:558.355 | 3rd Qu.:0.37368 |
| Max. :50.34 | | Max. :777.882 | Max. :0.52852 |
| ShannonIndexTreeSpp dendrocoposMajor | | | |
| Min. :0.000 | Min. :0.0000 | | |
| 1st Qu.:0.060 | 1st Qu.:0.0000 | | |
| Median :0.280 | Median :1.0000 | | |
| Mean :0.392 | Mean :0.7071 | | |
| 3rd Qu.:0.680 | 3rd Qu.:1.0000 | | |
| Max. :1.450 | Max. :1.0000 | | |

```
# One variable are character, we assign to factor instead:
modelDataSel$forestManagementType <-
  as.factor(modelDataSel$forestManagementType)
```

In the next step you can see how you can run the model with the selected variables and model parameters. You have a description of the models parameters in the Section 3.3.2 . In this example we are going to use the default parameters for the calibration, where learning rate = 0.01 and tree complexity = 1 and cross-validation = 10-fold. However, the bag fraction is changed from the default value, 0.75, to 0.5. As a family we used the Bernoulli family, because we are predicting presence/absence per plot. These data have 495 plots, comprising 350 presence records for the Great spotted woodpecker. You can check these numbers by doing:

```
table(modelDataSel$dendrocoposMajor)
```

```
0 1
145 350
```

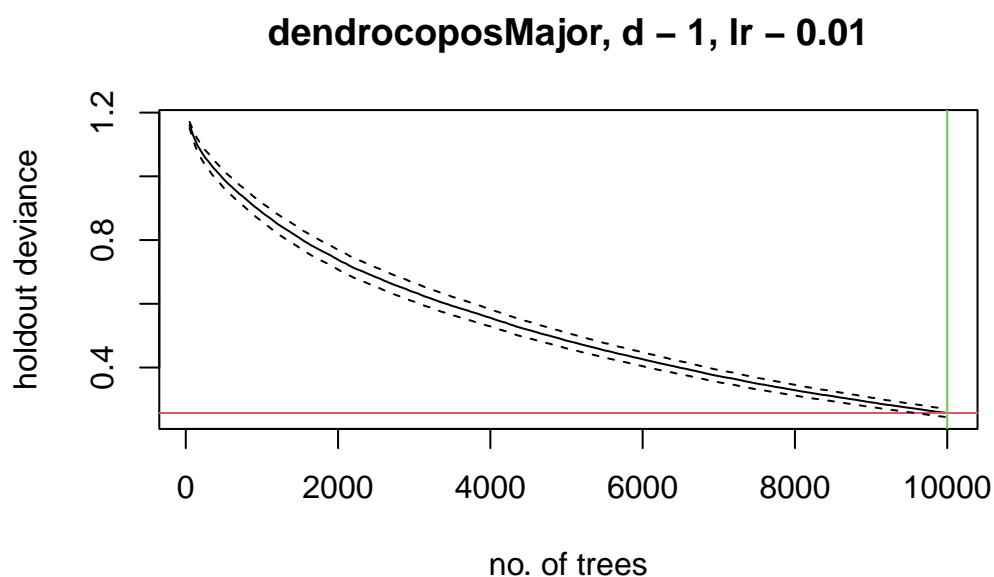
3 Empirical modeling

As a first guess you could decide there are enough data to model interactions of reasonable complexity, and a lr of about 0.01 could be a reasonable starting point. You can use the model creation function that steps forward and identifies the optimal number of trees (nt) by doing this:

```
family <- "bernoulli"

tc = 1    # tree complexity
lr = 0.01 # learning rate-shrinkage
bag = 0.5 # bag fraction

modelBRT <- dismo::gbm.step(
  data = modelDataSel,
  #indices of predictor variables in data
  gbm.x = 1:5,
  #index of response variable in data:
  gbm.y = 6,
  family = family,
  tree.complexity = tc,
  learning.rate = lr,
  bag.fraction = bag
)
```



3 Empirical modeling

Running a model such as that described above writes progress reports to the screen, makes a graph, and returns an object containing a number of components. The R console reports a brief model summary, all the model summary values are retained in the model object.

The model is built with the default 10-fold cross-validation (CV). In the plotted graph the solid black curve is the mean, and the dotted curves 1 standard error, for the changes in predictive deviance (i.e., as measured on the excluded folds of the CV). The red line shows the minimum of the mean, and the green line the number of trees at which that occurs. The final model that is returned in the model object is built on the full data set, using the number of trees identified as optimal.

Ideally, you should invest time in modifying the parameters and find the parameters that provide the models with the minimum deviance resulting from the best combination of bag, tree complexity and learning rate values. For the sake of limited timing, we will only test here the default values.

3.4.9.2 Model behaviour

You can summarize the model parameters used and the cross validation statistics from the fitted model by doing this:

```
# We make a table with the summary statistics
results <- data.frame(
  # Model parameters
  Tree.Complexity = modelBRT$gbm.call$tree.complexity,
  Learning.Rate = modelBRT$gbm.call$learning.rate,
  Bag.Fraction = modelBRT$gbm.call$bag.fraction,
  Interaction.depth = modelBRT$interaction.depth,
  Shrinkage = modelBRT$shrinkage,
  N.trees = modelBRT$n.trees,

  # Cross validation statistics

  ## mean total deviance
  Deviance = modelBRT$self.statistics$mean.resid,
  # mean residual deviance

  AUC = modelBRT$self.statistics$discrimination,
  # training data AUC score

  Corr = modelBRT$self.statistics$correlation,
  # training data correlation
```

3 Empirical modeling

```
## Cross Validation statistics

# We calculate each statistic within each fold (at the identified optimal number
# of trees that is calculated on the mean change in predictive deviance over all folds)
# then present here the mean and standard error of those fold-based statistics.

devianceCV = modelBRT$cv.statistics$deviance.mean,
# estimated cv deviance
devianceCVse = modelBRT$cv.statistics$deviance.se,
# estimated cv deviance se

CorrCV = modelBRT$cv.statistics$correlation.mean,
# cv correlation
CorrCVse = modelBRT$cv.statistics$correlation.se,
# cv correlation se

AUCcv = modelBRT$cv.statistics$discrimination.mean,
# cv AUC score
AUCcvSE = modelBRT$cv.statistics$discrimination.se
) # cv AUC score se

print(t(results))
```

```
          [,1]
Tree.Complexity  1.000000e+00
Learning.Rate    1.000000e-02
Bag.Fraction     5.000000e-01
Interaction.depth 1.000000e+00
Shrinkage        1.000000e-02
N.trees          1.000000e+04
Deviance         2.166324e-01
AUC              1.000000e+00
Corr             9.751772e-01
devianceCV       2.572895e-01
devianceCVse     1.299783e-02
CorrCV           9.616284e-01
CorrCVse         3.435403e-03
AUCcv            1.000000e+00
AUCcvSE          0.000000e+00
```


3.4.9.3 Model output analysis

We can look at the relative contribution of each of the predictor variables. The measures are based on the number of times the variable is selected for splitting, weighted by the improvement of the model as a result of each split averaged across all trees. The relative contribution of each of the variables is scaled so the sum is 100%, with higher numbers indicating stronger influence in the response.

```
# Variables contribution
modelBRT$contributions
```

| | var | rel.inf |
|----------------------|----------------------|-----------|
| latitude | latitude | 33.165957 |
| volAllha | volAllha | 25.045954 |
| GiniDBH | GiniDBH | 24.519899 |
| ShannonIndexTreeSpp | ShannonIndexTreeSpp | 12.480518 |
| forestManagementType | forestManagementType | 4.787673 |

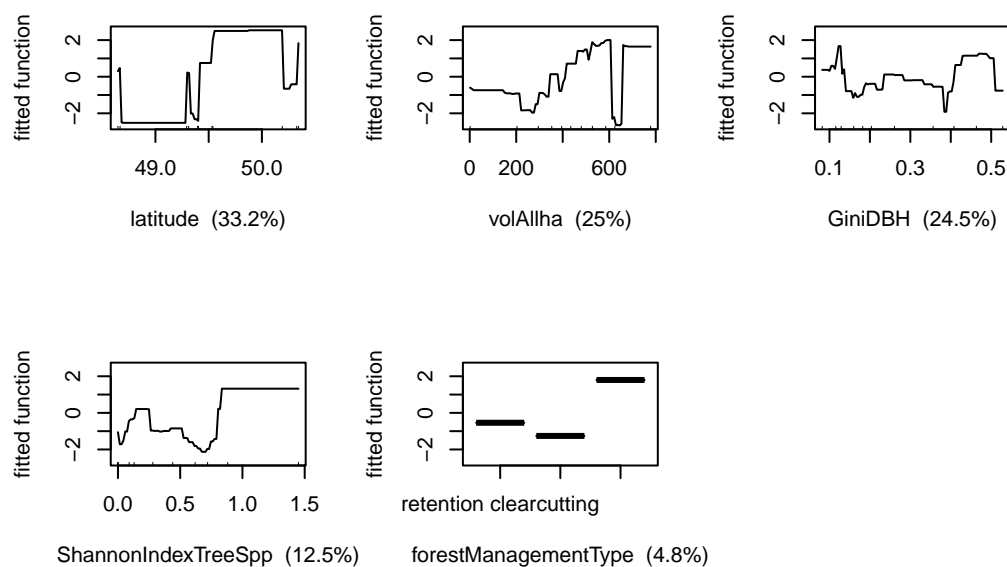
Here we can see that the two variables with the highest influence in the response are `latitude`, and `volAllha`.

Now we can evaluate the model behavior via partial dependence plots, showing the effect of each of the variables on the response by accounting for the average effects of all other predictors in the model:

```
dismo::gbm.plot(
  modelBRT,
  n.plots = 6,
  plot.layout = c(2, 3),
  write.title = F
)
```

```
Warning in dismo::gbm.plot(modelBRT, n.plots = 6, plot.layout = c(2, 3), :
reducing no of plotted predictors to maximum available (5)
```

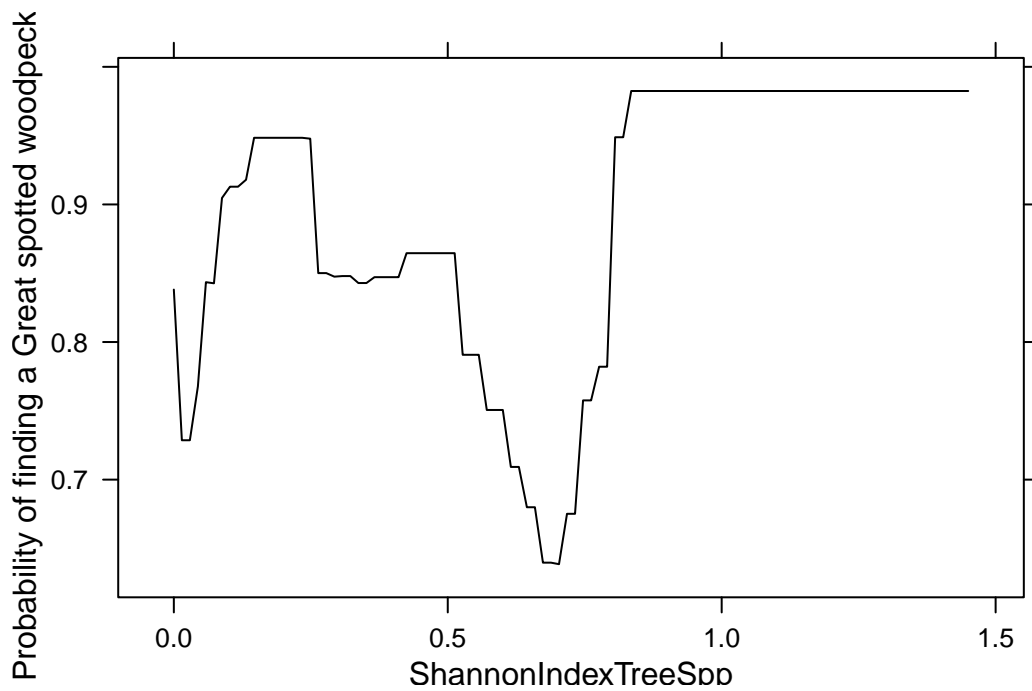
3 Empirical modeling



In this partial dependence plots the predictions are on the scale of $f(x)$. In this case, for the Bernoulli loss the returned value is on the log odds scale. You can see how this plot will look by plotting with the function from the package `gbm` and using the type “response”. Since we are interesting in finding out if the forest diversity has an impact in the presence of the Great spotted woodpecker we can have a look to the plot density variable `Shannon index` :

```
gbm::plot.gbm(modelBRT,  
  i.var = 5,  
  type = "response",  
  ylab = "Probability of finding a Great spotted woodpecker ")
```

3 Empirical modeling

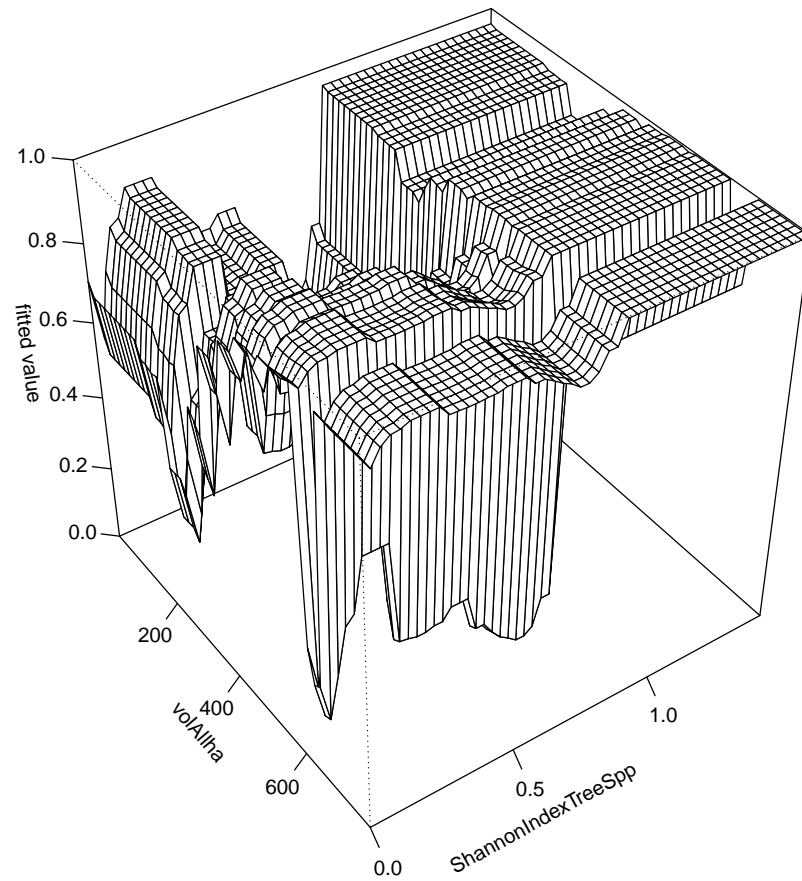


It seems that there is an increase in probability of finding a Great spotted woodpecker with higher forest densities, but the trend it is not very clear. We could also analyse the interaction effects, of forest diversity and for example forest density. The model predictions can be obtained for each pair of predictor variables, setting all other predictors to their means.

To plot this pairwise interactions we have to do:

```
dismo::gbm.perspec(modelBRT, 3, 5)
```

3 Empirical modeling



Here we can not see a very clear combined behavior between forest diversity and forest structural diversity in respect to the probabilities for finding the Great spotted woodpecker.

3.4.10 Group 4 - Question C

- Is the presence of the Eurasian treecreeper affected by forest density?

3.4.10.1 Fitting a BRT in R

In this case we want to assess the occurrence of certain species across the plots. In other words, we want to assess what is the probability of a certain species with biodiversity interest to be present in a plot based on the variables that describe the forest of that plot. In this case the response variable is `certhia` that represents if the Eurasian treecreeper has been observed in this plot or not.

Then you need to select some variables of interest, after you have explored the data you can decide which variables you want to use to fit this model. We are proposing to select the following variables:

- `latitude` as proxy for plot location or/and climate
- `forestManagementType` to assess if different management types have different impact in the presence / absence of Great spotted woodpecker.
- `volAllha` that is the total volume in the plot, as a proxy of how dense the plot is. Higher volumes will mean that the forest is more dense.
- `GiniDBH` showing how homogeneous the plot is in trees diameters. A value closer to 1 will mean that indicate more structural heterogeneity, lower values indicate more homogeneous plots.

You can create a vector `selVar` in which you add the names of the selected variables. Then you only take those variables from the data that you will use to create the model.

```
# Select variables from the dataset for the model
selVar <- c(
  "certhia",
  "latitude",
  "forestManagementType",
  "volAllha",
  "GiniDBH",
  "ShannonIndexTreeSpp"
)

# Filter the dataset to the selected variables
modelDataSel <- observations[, colnames(observations) %in% selVar]
```

Unfortunately the amount of observations that we have in this dataset it is not enough to fit a BRT model for these variables. We are going to do an obviously wrong thing for the sake of being able to demonstrate how to fit a BRT model. In the next code you are going to repeat the same dataset multiple times:

3 Empirical modeling

```
modelDataSel <- rbind(modelDataSel, modelDataSel, modelDataSel, modelDataSel,  
                      modelDataSel)
```

Now it is important to assess if the variables have the right categories. Variables should be type numeric or factor.

```
summary(modelDataSel)
```

| latitude | forestManagementType | volAllha | GiniDBH |
|---------------------|----------------------|-----------------|-----------------|
| Min. :48.65 | Length:495 | Min. : 1.681 | Min. :0.08209 |
| 1st Qu.:49.31 | Class :character | 1st Qu.:319.920 | 1st Qu.:0.13684 |
| Median :49.40 | Mode :character | Median :434.729 | Median :0.20358 |
| Mean :49.49 | | Mean :425.694 | Mean :0.25683 |
| 3rd Qu.:50.19 | | 3rd Qu.:558.355 | 3rd Qu.:0.37368 |
| Max. :50.34 | | Max. :777.882 | Max. :0.52852 |
| ShannonIndexTreeSpp | certhia | | |
| Min. :0.000 | Min. :0.0000 | | |
| 1st Qu.:0.060 | 1st Qu.:0.0000 | | |
| Median :0.280 | Median :1.0000 | | |
| Mean :0.392 | Mean :0.5859 | | |
| 3rd Qu.:0.680 | 3rd Qu.:1.0000 | | |
| Max. :1.450 | Max. :1.0000 | | |

```
# One variable is a character, we assign to factor instead:  
modelDataSel$forestManagementType <-  
  as.factor(modelDataSel$forestManagementType)
```

In the next step you can see how you can run the model with the selected variables and model parameters. You have a description of the models parameters in the Section 3.3.2 . In this example we are going to use the default parameters for the calibration, where learning rate = 0.01 and tree complexity = 1 and cross-validation = 10-fold. However, the bag fraction is changed from the default value, 0.75, to 0.5. As a family we used the Bernoulli family, because we are predicting presence/absence per plot. These data have 495 plots, comprising 290 presence records for the Eurasian treecreeper. You can check these numbers by doing:

```
table(modelDataSel$certhia)
```

```
0 1  
205 290
```

3 Empirical modeling

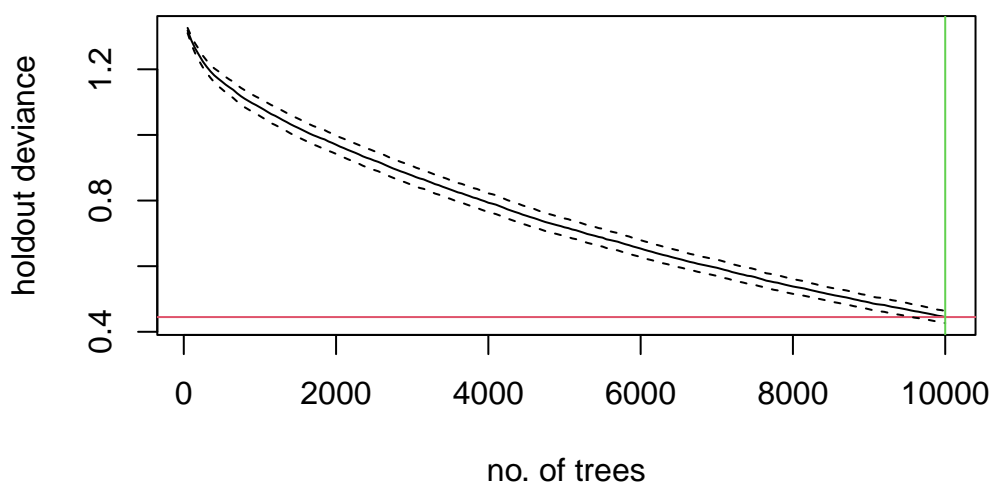
As a first guess you could decide there are enough data to model interactions of reasonable complexity, and a lr of about 0.01 could be a reasonable starting point. You can use the model creation function that steps forward and identifies the optimal number of trees (nt) by doing this:

```
family <- "bernoulli"

tc = 1    # tree complexity
lr = 0.01 # learning rate-shrinkage
bag = 0.5 # bag fraction

modelBRT <- dismo::gbm.step(
  data = modelDataSel,
  #indices of predictor variables in data
  gbm.x = 1:5,
  #index of response variable in data:
  gbm.y = 6,
  family = family,
  tree.complexity = tc,
  learning.rate = lr,
  bag.fraction = bag
)
```

certhia, d – 1, lr – 0.01



3 Empirical modeling

Running a model such as that described above writes progress reports to the screen, makes a graph, and returns an object containing a number of components. The R console reports a brief model summary, all the model summary values are retained in the model object.

The model is built with the default 10-fold cross-validation (CV). In the plotted graph the solid black curve is the mean, and the dotted curves 1 standard error, for the changes in predictive deviance (i.e., as measured on the excluded folds of the CV). The red line shows the minimum of the mean, and the green line the number of trees at which that occurs. The final model that is returned in the model object is built on the full data set, using the number of trees identified as optimal.

Ideally, you should invest time in modifying the parameters and find the parameters that provide the models with the minimum deviance resulting from the best combination of bag, tree complexity and learning rate values. For the sake of limited timing, we will only test here the default values.

3.4.10.2 Model behaviour

You can summarize the model parameters used and the cross validation statistics from the fitted model by doing this:

```
# We make a table with the summary statistics
results <- data.frame(
  # Model parameters
  Tree.Complexity = modelBRT$gbm.call$tree.complexity,
  Learning.Rate = modelBRT$gbm.call$learning.rate,
  Bag.Fraction = modelBRT$gbm.call$bag.fraction,
  Interaction.depth = modelBRT$interaction.depth,
  Shrinkage = modelBRT$shrinkage,
  N.trees = modelBRT$n.trees,

  # Cross validation statistics

  ## mean total deviance
  Deviance = modelBRT$self.statistics$mean.resid,
  # mean residual deviance

  AUC = modelBRT$self.statistics$discrimination,
  # training data AUC score

  Corr = modelBRT$self.statistics$correlation,
  # training data correlation
```


3 Empirical modeling

```
## Cross Validation statistics

# We calculate each statistic within each fold (at the identified optimal number
# of trees that is calculated on the mean change in predictive deviance over all folds)
# then present here the mean and standard error of those fold-based statistics.

devianceCV = modelBRT$cv.statistics$deviance.mean,
# estimated cv deviance
devianceCVse = modelBRT$cv.statistics$deviance.se,
# estimated cv deviance se

CorrCV = modelBRT$cv.statistics$correlation.mean,
# cv correlation
CorrCVse = modelBRT$cv.statistics$correlation.se,
# cv correlation se

AUCcv = modelBRT$cv.statistics$discrimination.mean,
# cv AUC score
AUCcvSE = modelBRT$cv.statistics$discrimination.se
) # cv AUC score se

print(t(results))
```

```
          [,1]
Tree.Complexity 1.000000e+00
Learning.Rate   1.000000e-02
Bag.Fraction    5.000000e-01
Interaction.depth 1.000000e+00
Shrinkage       1.000000e-02
N.trees         1.000000e+04
Deviance        3.645867e-01
AUC             1.000000e+00
Corr            9.532179e-01
devianceCV      4.448820e-01
devianceCVse    1.846562e-02
CorrCV          9.172424e-01
CorrCVse        9.027005e-03
AUCcv           9.955700e-01
AUCcvSE         4.430000e-03
```

3.4.10.3 Model output analysis

We can look at the relative contribution of each of the predictor variables. The measures are based on the number of times the variable is selected for splitting, weighted by the improvement of the model as a result of each split averaged across all trees. The relative contribution of each of the variables is scaled so the sum is 100%, with higher numbers indicating stronger influence in the response.

```
# Variables contribution
modelBRT$contributions
```

| | var | rel.inf |
|----------------------|----------------------|-----------|
| GiniDBH | GiniDBH | 31.157096 |
| latitude | latitude | 24.773697 |
| volAllha | volAllha | 23.776977 |
| ShannonIndexTreeSpp | ShannonIndexTreeSpp | 19.006940 |
| forestManagementType | forestManagementType | 1.285291 |

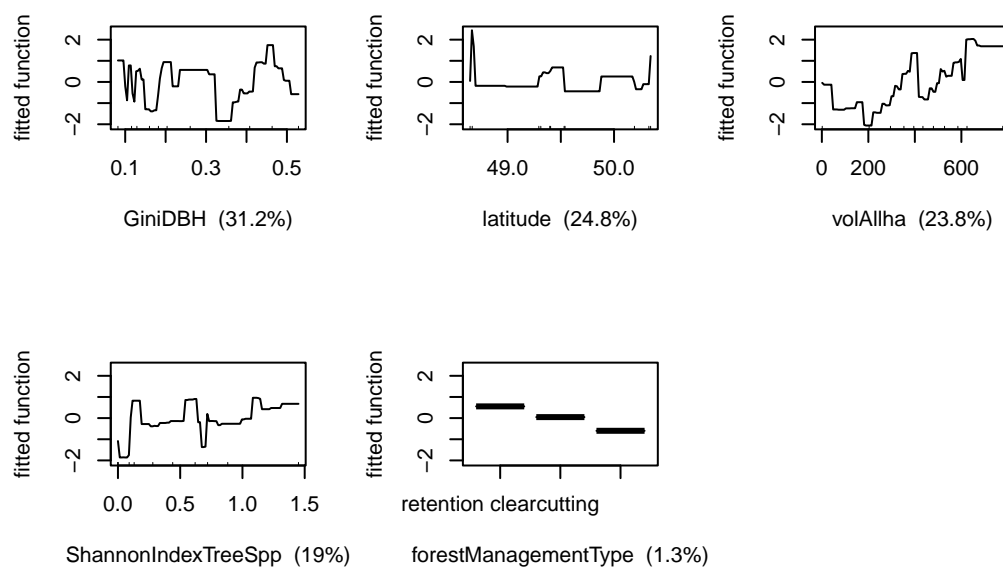
Here we can see that the two variables with the highest influence in the response are `GiniDBH` and `latitude`.

Now we can evaluate the model behavior via partial dependence plots, showing the effect of each of the variables on the response by accounting for the average effects of all other predictors in the model:

```
dismo::gbm.plot(
  modelBRT,
  n.plots = 6,
  plot.layout = c(2, 3),
  write.title = F
)
```

Warning in `dismo::gbm.plot(modelBRT, n.plots = 6, plot.layout = c(2, 3), :`
reducing no of plotted predictors to maximum available (5)

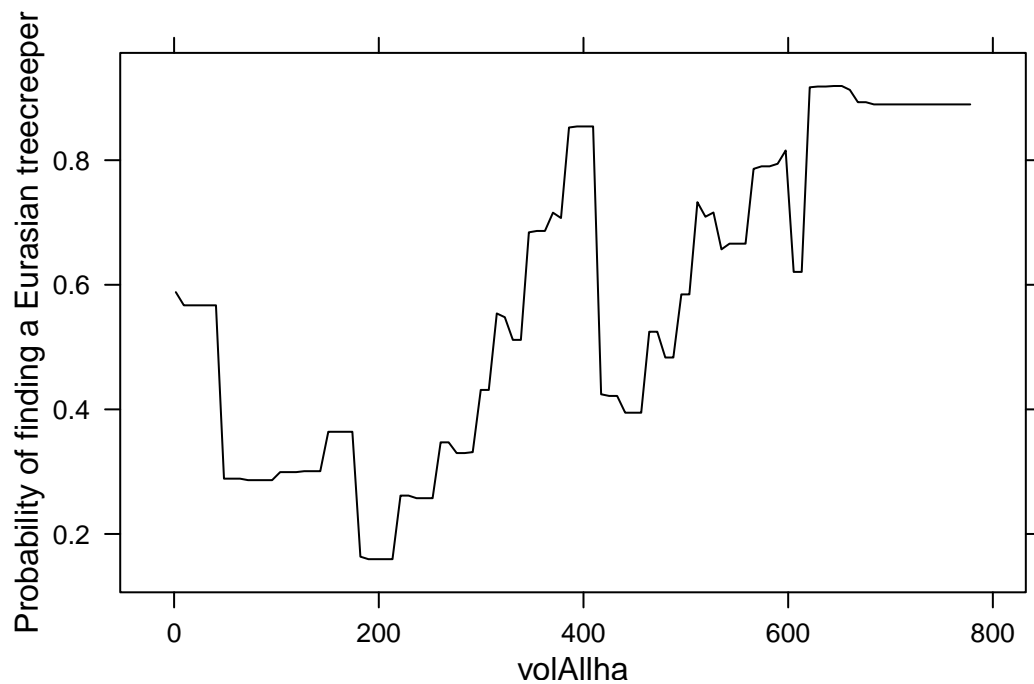
3 Empirical modeling



In this partial dependence plots the predictions are on the scale of $f(x)$. In this case, for the Bernoulli loss the returned value is on the log odds scale. You can see how this plot will look by plotting with the function from the package `gbm` and using the type “response”. Since we are interesting in finding out if the forest management type has an impact in the presence of the Eurasian treecreeper affected we can have a look to the plot density variable `forestManagementType` :

```
gbm::plot.gbm(modelBRT,  
  i.var = 3,  
  type = "response",  
  ylab = "Probability of finding a Eurasian treecreeper")
```

3 Empirical modeling

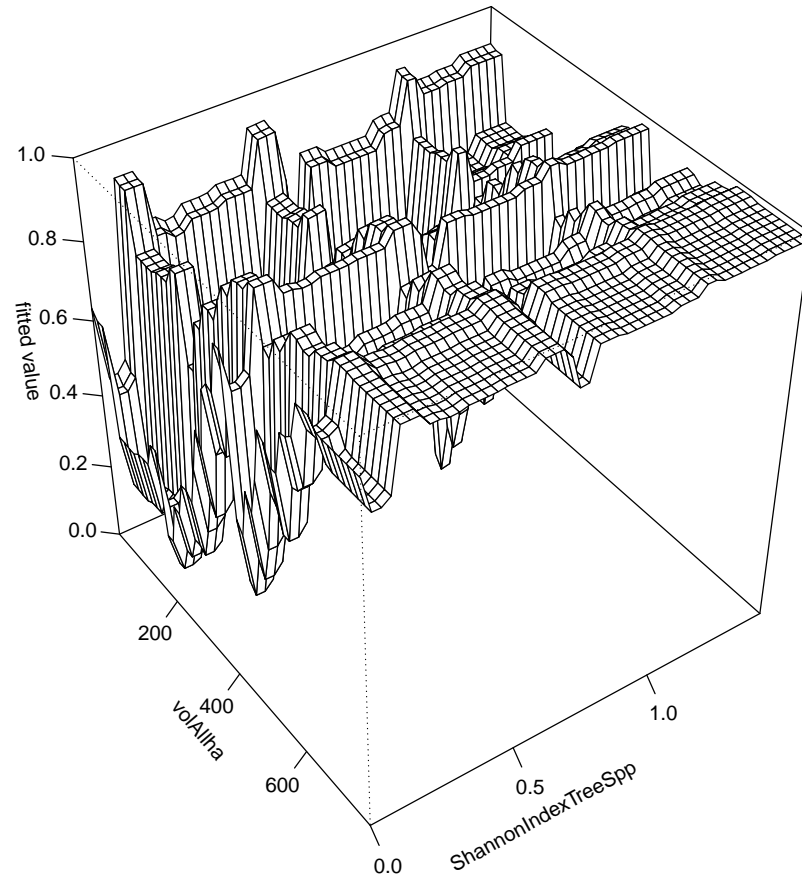


It seems that there is an increase in probability of finding a Eurasian treecreeper with higher forest densities. We could also analyse the interaction effects, of forest diversity and for example forest density. The model predictions can be obtained for each pair of predictor variables, setting all other predictors to their means.

To plot this pairwise interactions we have to do:

```
dismo::gbm.perspec(modelBRT, 3, 5)
```

3 Empirical modeling



It seems that the highest chances to see a Eurasian treecreeper is in dense forests with highest tree diversity.

3.4.11 Group 4 - Question D

- Is the presence of the Eurasian treecreeper affected by forest management?

3.4.11.1 Fitting a BRT in R

In this case we want to assess the occurrence of certain species across the plots. In other words, we want to assess what is the probability of a certain species with biodiversity interest to be present in a plot based on the variables that describe the forest of that plot. In this case the response variable is `certhia` that represents if the Eurasian treecreeper has been observed in this plot or not.

Then you need to select some variables of interest, after you have explored the data you can decide which variables you want to use to fit this model. We are proposing to select the following variables:

- `latitude` as proxy for plot location or/and climate
- `forestManagementType` to assess if different management types have different impact in the presence / absence of Great spotted woodpecker.
- `volAllha` that is the total volume in the plot, as a proxy of how dense the plot is. Higher volumes will mean that the forest is more dense.
- `GiniDBH` showing how homogeneous the plot is in trees diameters. A value closer to 1 will mean that indicate more structural heterogeneity, lower values indicate more homogeneous plots.

You can create a vector `selVar` in which you add the names of the selected variables. Then you only take those variables from the data that you will use to create the model.

```
# Select variables from the dataset for the model
selVar <- c(
  "certhia",
  "latitude",
  "forestManagementType",
  "volAllha",
  "GiniDBH",
  "ShannonIndexTreeSpp"
)

# Filter the dataset to the selected variables
modelDataSel <- observations[, colnames(observations) %in% selVar]
```

Unfortunately the amount of observations that we have in this dataset it is not enough to fit a BRT model for these variables. We are going to do an obviously wrong thing for the sake of being able to demonstrate how to fit a BRT model. In the next code you are going to repeat the same dataset multiple times:

3 Empirical modeling

```
modelDataSel <- rbind(modelDataSel, modelDataSel, modelDataSel, modelDataSel,  
                      modelDataSel)
```

Now it is important to assess if the variables have the right categories. Variables should be type numeric or factor.

```
summary(modelDataSel)
```

| latitude | forestManagementType | volAllha | GiniDBH |
|---------------------|----------------------|-----------------|-----------------|
| Min. :48.65 | Length:495 | Min. : 1.681 | Min. :0.08209 |
| 1st Qu.:49.31 | Class :character | 1st Qu.:319.920 | 1st Qu.:0.13684 |
| Median :49.40 | Mode :character | Median :434.729 | Median :0.20358 |
| Mean :49.49 | | Mean :425.694 | Mean :0.25683 |
| 3rd Qu.:50.19 | | 3rd Qu.:558.355 | 3rd Qu.:0.37368 |
| Max. :50.34 | | Max. :777.882 | Max. :0.52852 |
| ShannonIndexTreeSpp | certhia | | |
| Min. :0.000 | Min. :0.0000 | | |
| 1st Qu.:0.060 | 1st Qu.:0.0000 | | |
| Median :0.280 | Median :1.0000 | | |
| Mean :0.392 | Mean :0.5859 | | |
| 3rd Qu.:0.680 | 3rd Qu.:1.0000 | | |
| Max. :1.450 | Max. :1.0000 | | |

```
# One variable is a character, we assign to factor instead:  
modelDataSel$forestManagementType <-  
  as.factor(modelDataSel$forestManagementType)
```

In the next step you can see how you can run the model with the selected variables and model parameters. You have a description of the models parameters in the Section 3.3.2 . In this example we are going to use the default parameters for the calibration, where learning rate = 0.01 and tree complexity = 1 and cross-validation = 10-fold. However, the bag fraction is changed from the default value, 0.75, to 0.5. As a family we used the Bernoulli family, because we are predicting presence/absence per plot. These data have 495 plots, comprising 290 presence records for the Eurasian treecreeper. You can check these numbers by doing:

```
table(modelDataSel$certhia)
```

```
0 1  
205 290
```

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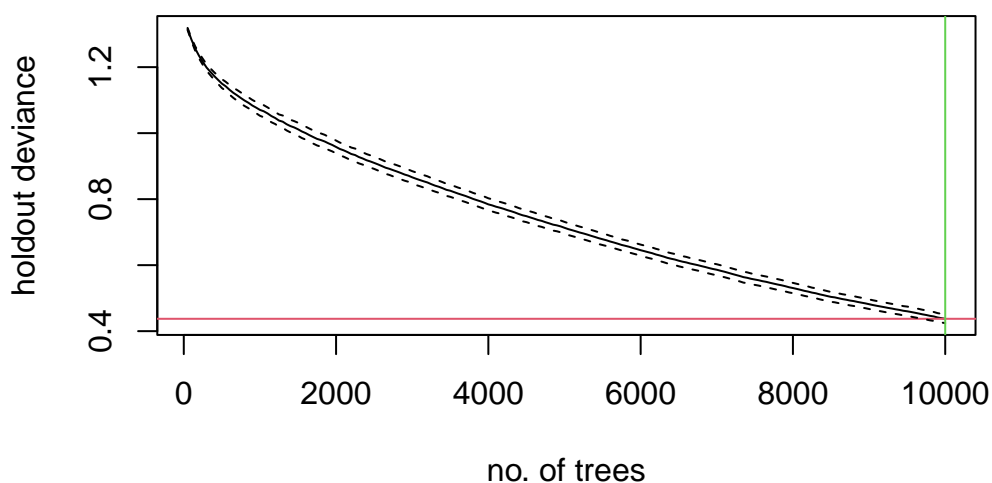
As a first guess you could decide there are enough data to model interactions of reasonable complexity, and a lr of about 0.01 could be a reasonable starting point. You can use the model creation function that steps forward and identifies the optimal number of trees (nt) by doing this:

```
family <- "bernoulli"

tc = 1    # tree complexity
lr = 0.01 # learning rate-shrinkage
bag = 0.5 # bag fraction

modelBRT <- dismo::gbm.step(
  data = modelDataSel,
  #indices of predictor variables in data
  gbm.x = 1:5,
  #index of response variable in data:
  gbm.y = 6,
  family = family,
  tree.complexity = tc,
  learning.rate = lr,
  bag.fraction = bag
)
```

certhia, d – 1, lr – 0.01



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Running a model such as that described above writes progress reports to the screen, makes a graph, and returns an object containing a number of components. The R console reports a brief model summary, all the model summary values are retained in the model object.

The model is built with the default 10-fold cross-validation (CV). In the plotted graph the solid black curve is the mean, and the dotted curves 1 standard error, for the changes in predictive deviance (i.e., as measured on the excluded folds of the CV). The red line shows the minimum of the mean, and the green line the number of trees at which that occurs. The final model that is returned in the model object is built on the full data set, using the number of trees identified as optimal.

Ideally, you should invest time in modifying the parameters and find the parameters that provide the models with the minimum deviance resulting from the best combination of bag, tree complexity and learning rate values. For the sake of limited timing, we will only test here the default values.

3.4.11.2 Model behaviour

You can summarize the model parameters used and the cross validation statistics from the fitted model by doing this:

```
# We make a table with the summary statistics
results <- data.frame(
  # Model parameters
  Tree.Complexity = modelBRT$gbm.call$tree.complexity,
  Learning.Rate = modelBRT$gbm.call$learning.rate,
  Bag.Fraction = modelBRT$gbm.call$bag.fraction,
  Interaction.depth = modelBRT$interaction.depth,
  Shrinkage = modelBRT$shrinkage,
  N.trees = modelBRT$n.trees,

  # Cross validation statistics

  ## mean total deviance
  Deviance = modelBRT$self.statistics$mean.resid,
  # mean residual deviance

  AUC = modelBRT$self.statistics$discrimination,
  # training data AUC score

  Corr = modelBRT$self.statistics$correlation,
  # training data correlation
```

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```
## Cross Validation statistics

# We calculate each statistic within each fold (at the identified optimal number
# of trees that is calculated on the mean change in predictive deviance over all folds)
# then present here the mean and standard error of those fold-based statistics.

devianceCV = modelBRT$cv.statistics$deviance.mean,
# estimated cv deviance
devianceCVse = modelBRT$cv.statistics$deviance.se,
# estimated cv deviance se

CorrCV = modelBRT$cv.statistics$correlation.mean,
# cv correlation
CorrCVse = modelBRT$cv.statistics$correlation.se,
# cv correlation se

AUCcv = modelBRT$cv.statistics$discrimination.mean,
# cv AUC score
AUCcvSE = modelBRT$cv.statistics$discrimination.se
) # cv AUC score se

print(t(results))
```

```
          [,1]
Tree.Complexity  1.000000e+00
Learning.Rate    1.000000e-02
Bag.Fraction     5.000000e-01
Interaction.depth 1.000000e+00
Shrinkage        1.000000e-02
N.trees          1.000000e+04
Deviance         3.649073e-01
AUC              1.000000e+00
Corr             9.533777e-01
devianceCV       4.373848e-01
devianceCVse     1.311274e-02
CorrCV           9.206644e-01
CorrCVse         5.962036e-03
AUCcv            9.991500e-01
AUCcvSE          5.840947e-04
```

3.4.11.3 Model output analysis

We can look at the relative contribution of each of the predictor variables. The measures are based on the number of times the variable is selected for splitting, weighted by the improvement of the model as a result of each split averaged across all trees. The relative contribution of each of the variables is scaled so the sum is 100%, with higher numbers indicating stronger influence in the response.

```
# Variables contribution
modelBRT$contributions
```

| | var | rel.inf |
|----------------------|----------------------|-----------|
| GiniDBH | GiniDBH | 30.831090 |
| latitude | latitude | 25.010315 |
| volAllha | volAllha | 23.813300 |
| ShannonIndexTreeSpp | ShannonIndexTreeSpp | 19.091659 |
| forestManagementType | forestManagementType | 1.253636 |

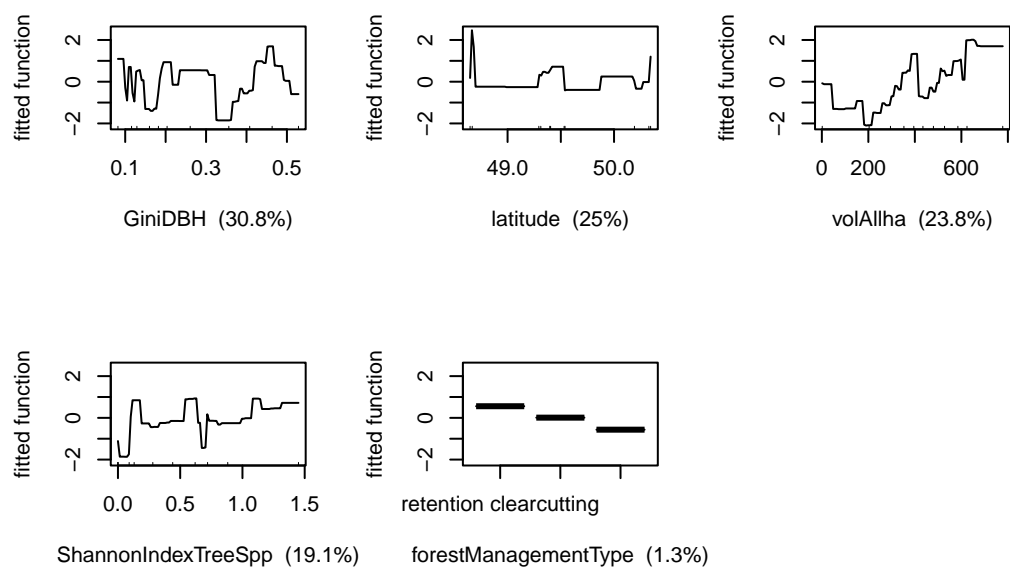
Here we can see that the two variables with the highest influence in the response are GiniDBH and volAllha.

Now we can evaluate the model behavior via partial dependence plots, showing the effect of each of the variables on the response by accounting for the average effects of all other predictors in the model:

```
dismo::gbm.plot(
  modelBRT,
  n.plots = 6,
  plot.layout = c(2, 3),
  write.title = F
)
```

```
Warning in dismo::gbm.plot(modelBRT, n.plots = 6, plot.layout = c(2, 3), :
reducing no of plotted predictors to maximum available (5)
```

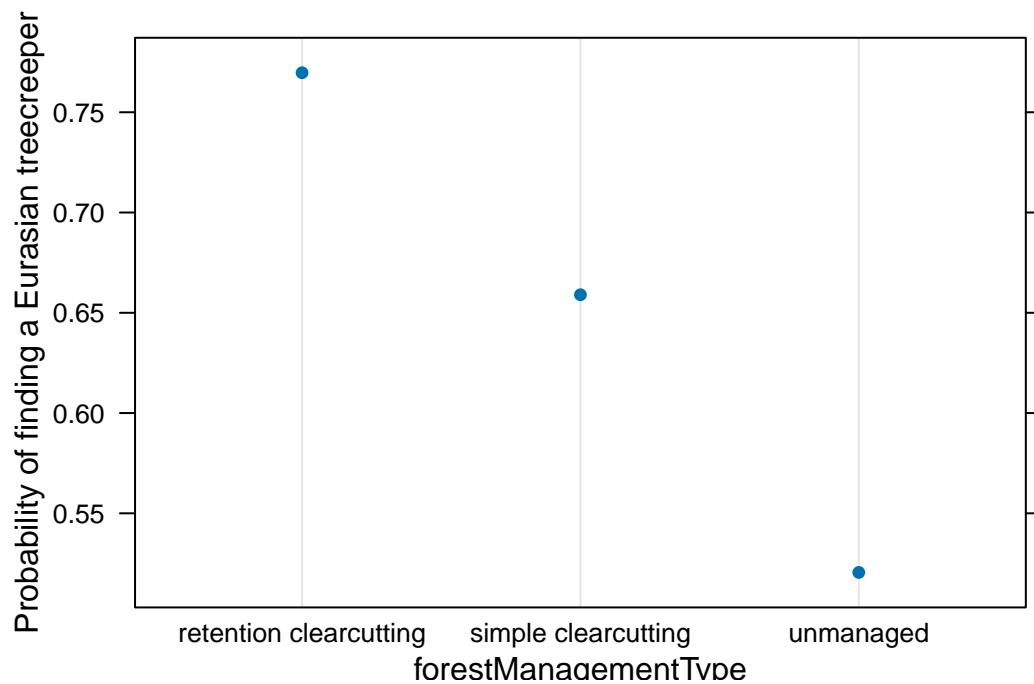
3 Empirical modeling



In this partial dependence plots the predictions are on the scale of $f(x)$. In this case, for the Bernoulli loss the returned value is on the log odds scale. You can see how this plot will look by plotting with the function from the package `gbm` and using the type “response”. Since we are interested in finding out if the forest density has an impact in the presence of the Eurasian treecreeper affected we can have a look to the plot density variable `volAllha` :

```
gbm::plot.gbm(modelBRT,  
  i.var = 2,  
  type = "response",  
  ylab = "Probability of finding a Eurasian treecreeper")
```

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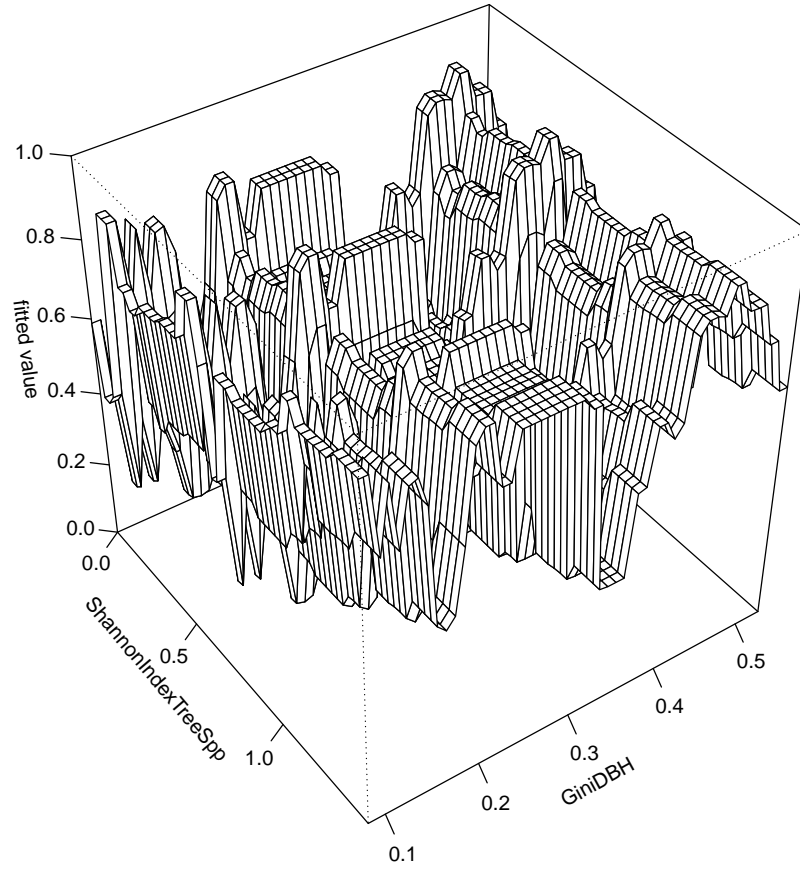


It seems that there is a small difference in the probability of finding the Eurasian treecreeper different management strategies. We could also analyse the interaction effects, of forest diversity and forest structural diversity. The model predictions can be obtained for each pair of predictor variables, setting all other predictors to their means.

To plot this pairwise interactions we have to do:

```
dismo::gbm.perspec(modelBRT, 5, 4)
```

3 Empirical modeling



It seems that there are not clear patterns in the combined effect of forest structure diversity and forest tree species diversity.

4 References and further reading

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4 References and further reading

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- Honkaniemi, J., Rammer, W., & Seidl, R. (2020). Norway spruce at the trailing edge: the effect of landscape configuration and composition on climate resilience. *Landscape Ecology*, 35(3), 591–606.
- Sommerfeld, A., Rammer, W., Heurich, M., Hilmers, T., Müller, J., & Seidl, R. (2020). Do bark beetle outbreaks amplify or dampen future bark beetle disturbances in Central Europe? *Journal of Ecology*, July, 1–13.

5 Appendix - Initialize trees for the model based on inventory data

5.1 Inventory data

We had inventory data prior the summer school. These plots were established in 2007 for monitoring of urban forest Rožnik. Those four plots were already remeasured by NFI teams (for yearly training) at the beginning of April 2023. The radius of the plots is 13.8m and trees $dbh \geq 10\text{cm}$ were measured.

The original number of these plots are 3, 4, 8, 9 but in this exercise this are respectively: plot 1, plot 2, plot 3 and plot 4.

5.2 iLand needs

We need to produce tree list with tree positions, species, dbh and height for a 1ha area, that is the smallest unit in the model that can be individually simulated. We will use a so called “torus” when the simulation space is treated as a torus, where any influence (e.g. a light influence pattern) leaving on one side again enters at the opposite site. This is especially useful for small simulated areas to provide a continuous environment without edge effects.

Idea: use the measured trees as the middle of our 1ha area, keep the trees and locations as they are, but populate the rest of the 1ha randomly based on the characteristics of the measured plot.

This script is using these input files which are placed here: `iLand_simulations/init/trees/ -testPlot_data_Roznik.xlsx -species_names.csv`

And making outputs as text files for each four plots with tree lists that are directly can go into model iLand as initialization file.

5.2.1 Read in the inventory data to R visualize it. Read also a table with species latin names and short names in iLand.

```
a <-
  openxlsx::read.xlsx(here::here("model/iLand_simulations/init/trees/testPlot_data_Rozi"),
  head(a)
```

| | plotID | treeID | treeSp | dbh | azimuth | h_dist.(dm) | X | Y |
|---|--------|--------|------------------|------|---------|-------------|-----------|-------------|
| 1 | 3 | 1 | Fagus sylvatica | 65.8 | 29.0 | 118.3 | 5.736914 | 10.3496665 |
| 2 | 3 | 2 | Pinus sylvestris | 56.7 | 91.5 | 66.0 | 6.597738 | -0.1727679 |
| 3 | 3 | 3 | Pinus sylvestris | 46.2 | 151.5 | 122.0 | 5.821337 | -10.7215688 |
| 4 | 3 | 4 | Pinus sylvestris | 48.6 | 165.0 | 78.3 | 2.025259 | -7.5583696 |
| 5 | 3 | 5 | Fagus sylvatica | 41.5 | 192.7 | 85.0 | -1.863868 | -8.2931294 |
| 6 | 3 | 6 | Fagus sylvatica | 50.5 | 197.0 | 83.7 | -2.446177 | -8.0010831 |

| | height.(dm) |
|---|-------------|
| 1 | 338.0 |
| 2 | 309.3 |
| 3 | 289.3 |
| 4 | 294.5 |
| 5 | 338.8 |
| 6 | 332.0 |

```
# read table with latin and iLand names:
sp <-
  utils::read.table(
    here::here("model/iLand_simulations/init/trees/species_names.csv"),
    header = T,
    sep = ";"
  )

# change the column names to have the latin name column similar name as in "a"
colnames(sp) <- c("id", "iLand_name", "treeSp")

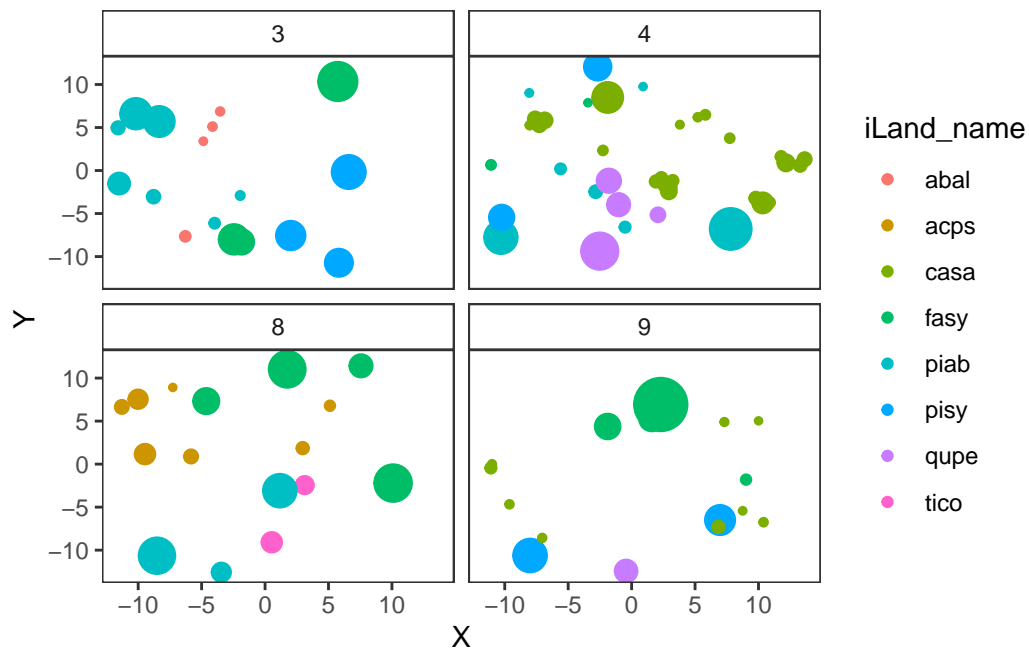
# add iLand names as a new column:
a <- dplyr::left_join(a, sp, by = "treeSp")

g1 <- ggplot2::ggplot(a, ggplot2::aes(X, Y, color = iLand_name)) +
  ggplot2::geom_point(size = a$dbh / 10) +
  ggplot2::facet_wrap( ~ plotID, nrow = 2) +
  ggplot2::theme_bw() +
```

5 Appendix - Initialize trees for the model based on inventory data

```
ggplot2::theme(
  panel.grid.major = ggplot2::element_blank(),
  panel.grid.minor = ggplot2::element_blank(),
  panel.background = ggplot2::element_blank(),
  strip.background = ggplot2::element_rect(fill = "white")
)

print(g1)
```



5.2.2 Calculate some statistics for populating remaining areas

Not all records have height, so we calculate H:D ratios for each tree that has.

```
# Area of the plots:
r <- 13.82 #m, radius of the circular plot
plot.area <- r * r * pi #m2

tree.stats <- a |> dplyr::group_by(plotID, treeSp, iLand_name) |>
  dplyr::summarize(
    mean.dbh = mean(dbh),
    min.dbh = min(dbh),
```

5 Appendix - Initialize trees for the model based on inventory data

```

    max.dbh = max(dbh),
    sd.dbh = sd(dbh) ,
    n = dplyr::n()
  ) |>
  dplyr::mutate(n.perha = n * 10000 / plot.area)

tree.stats$sd.dbh[is.na(tree.stats$sd.dbh) == T] <- 10

# Look the H:D ratio for each trees:
a <- a |> dplyr::mutate(hdratio = 10 * `height.(dm)` / dbh)

# Species specific H:D ratio ranges (to calculate height for trees which are not
#given:
hdratios <- a |> dplyr::group_by(treeSp, iLand_name) |>
  dplyr::summarize(
    mean.hdratio = mean(hdratio, na.rm = T),
    min.hdratio = min(hdratio, na.rm = T),
    max.hdratio = max(hdratio, na.rm = T),
    n = dplyr::n()
  )

# abies alba was missing hd ratios, there were no height for any abal trees:
hdratios$mean.hdratio[hdratios$iLand_name == "abal"] <- 80

print(hdratios)

```

```

# A tibble: 8 x 6
# Groups:   treeSp [8]
  treeSp          iLand_name mean.hdratio min.hdratio max.hdratio      n
  <chr>          <chr>          <dbl>         <dbl>         <dbl> <int>
1 Abies alba      abal             80           Inf           -Inf      4
2 Acer pseudoplatanus acps          85.6          78.2          98.4      7
3 Castanea sativa  casa          83.1          62.6         109.     32
4 Fagus sylvatica  fasy          56.8          31.4          81.6     13
5 Picea abies      piab          67.2          46.2          85.5     17
6 Pinus sylvestris pisy          56.8          49.8          62.6      7
7 Quercus petraea  qupe          51.2          43.3          59.1      5
8 Tilia cordata    tico          76.3          70.2          82.4      2

```

5.2.3 Generate trees for each plot

- Using the number of trees/ha
- Generate dbh of individual trees based on a normal distribution using mean dbh and stdev
- Randomly placed: x,y coordinates -50m -> 50m. (inventory data had 0,0 coordinate in the middle, so we kept this “coordinate system” for now)

```
ids <- unique(a$plotID)
tree.list <- c()
for (i in 1:4) {
  # go on plots

  a1 <- tree.stats |> dplyr::filter(plotID == ids[i])

  for (j in 1:length(a1$treeSp)) {
    # go on species
    spec1 <- a1[j, ]
    ntree <- round(spec1$n.perha)
    print(paste(
      "We need ",
      ntree,
      spec1$iLand_name ,
      "trees per ha,for plot id: ",
      ids[i]
    ))

    # tree list for one species:

    trees <- data.frame(
      plotID = rep(ids[i], ntree),
      species = rep(spec1$iLand_name, ntree),
      dbh = truncnorm::rtruncnorm(ntree, 5, 100,
                                   spec1$mean.dbh, spec1$sd.dbh),
      X = runif(ntree) * 100 - 50,
      Y = runif(ntree) * 100 - 50
    )

    tree.list <- rbind(tree.list, trees)
  }
}
```

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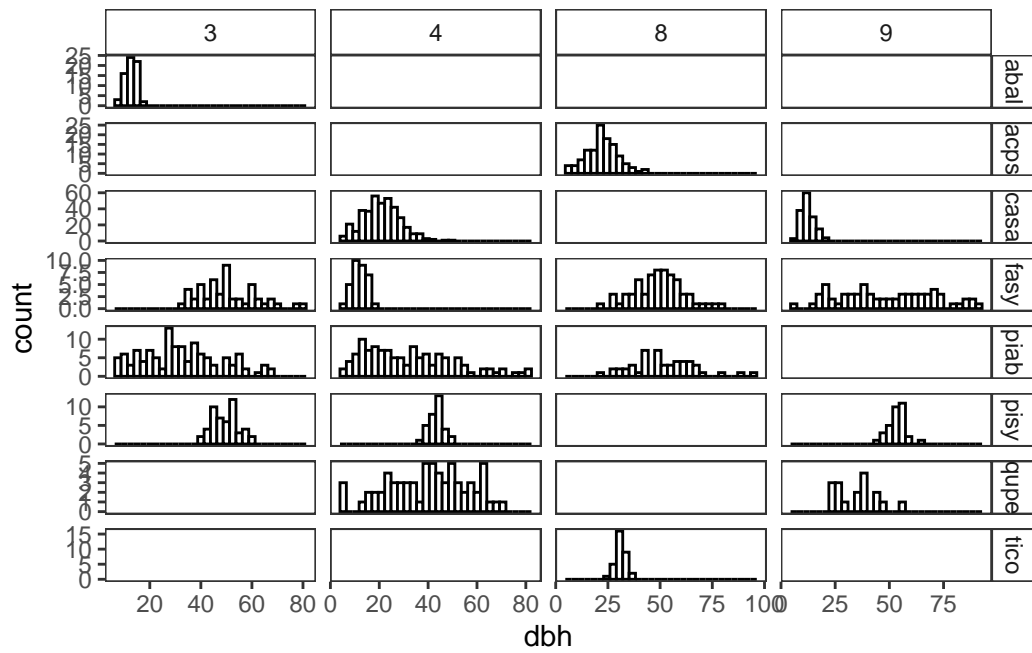
```
[1] "We need 67 abal trees per ha,for plot id: 3"
[1] "We need 50 fasy trees per ha,for plot id: 3"
[1] "We need 117 piab trees per ha,for plot id: 3"
[1] "We need 50 pisy trees per ha,for plot id: 3"
[1] "We need 383 casa trees per ha,for plot id: 4"
[1] "We need 33 fasy trees per ha,for plot id: 4"
[1] "We need 117 piab trees per ha,for plot id: 4"
[1] "We need 33 pisy trees per ha,for plot id: 4"
[1] "We need 67 qupe trees per ha,for plot id: 4"
[1] "We need 117 acps trees per ha,for plot id: 8"
[1] "We need 67 fasy trees per ha,for plot id: 8"
[1] "We need 50 piab trees per ha,for plot id: 8"
[1] "We need 33 tico trees per ha,for plot id: 8"
[1] "We need 150 casa trees per ha,for plot id: 9"
[1] "We need 67 fasy trees per ha,for plot id: 9"
[1] "We need 33 pisy trees per ha,for plot id: 9"
[1] "We need 17 qupe trees per ha,for plot id: 9"
```

```
g2 <- ggplot2::ggplot(tree.list, ggplot2::aes(dbh)) +
  ggplot2::geom_histogram(color = "black", fill = "white") +
  ggplot2::facet_grid(species ~ plotID, scales = "free") +
  ggplot2::theme_bw() + ggplot2::theme(
    panel.grid.major = ggplot2::element_blank(),
    panel.grid.minor = ggplot2::element_blank(),
    panel.background = ggplot2::element_blank(),
    strip.background = ggplot2::element_rect(fill = "white")
  )

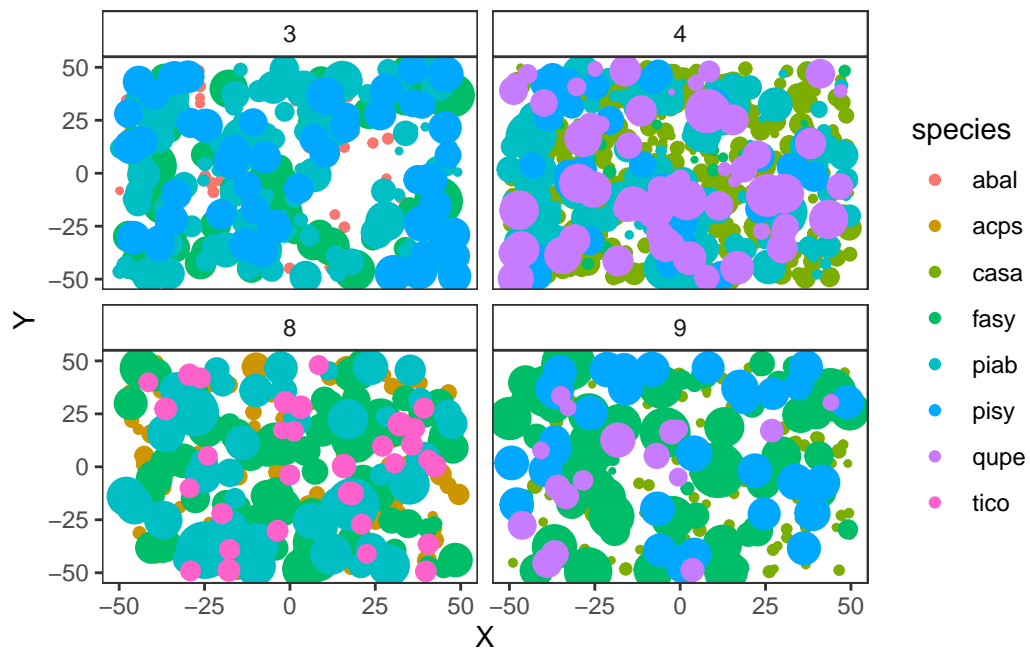
g3 <- ggplot2::ggplot(tree.list, ggplot2::aes(X, Y, color = species)) +
  ggplot2::geom_point(size = tree.list$dbh / 10) +
  ggplot2::facet_wrap(~ plotID, nrow = 2) +
  ggplot2::xlim(-50, 50) + ggplot2::ylim(-50, 50) +
  ggplot2::theme_bw() + ggplot2::theme(
    panel.grid.major = ggplot2::element_blank(),
    panel.grid.minor = ggplot2::element_blank(),
    panel.background = ggplot2::element_blank(),
    strip.background = ggplot2::element_rect(fill = "white")
  )

print(g2)
```

5 Appendix - Initialize trees for the model based on inventory data



```
print(g3)
```



5.2.4 Lets remove the trees in the middle, and put back the real trees from the inventory

```
# Calculate the distance for each tree from the center point:
tree.list <- tree.list |> dplyr::mutate(distance = sqrt(X * X + Y * Y))

# Look which we want to keep: where distance is larger than the plot radius was:
cutted.tree.list <- tree.list |> dplyr::filter(distance > r)

g4 <- ggplot2::ggplot(cutted.tree.list,
                      ggplot2::aes(X, Y, color = species)) +
  ggplot2::geom_point(size = cutted.tree.list$dbh / 10) +
  ggplot2::facet_wrap(~ plotID, nrow = 2) +
  ggplot2::xlim(-50, 50) + ggplot2::ylim(-50, 50) +
  ggplot2::theme_bw() + ggplot2::theme(
    panel.grid.major = ggplot2::element_blank(),
    panel.grid.minor = ggplot2::element_blank(),
    panel.background = ggplot2::element_blank(),
    strip.background = ggplot2::element_rect(fill = "white")
  )

# Check our inventory trees:
trees.circle = data.frame(
  plotID = a$plotID,
  species = a$iLand_name,
  dbh = a$dbh,
  X = a$X,
  Y = a$Y,
  distance = sqrt(a$X * a$X + a$Y * a$Y)
)

g5 <- ggplot2::ggplot(trees.circle, ggplot2::aes(X, Y, color = species)) +
  ggplot2::geom_point(size = trees.circle$dbh / 10) +
  ggplot2::facet_wrap(~ plotID, nrow = 2) +
  ggplot2::xlim(-50, 50) + ggplot2::ylim(-50, 50) +
  ggplot2::theme_bw() + ggplot2::theme(
    panel.grid.major = ggplot2::element_blank(),
    panel.grid.minor = ggplot2::element_blank(),
    panel.background = ggplot2::element_blank(),
    strip.background = ggplot2::element_rect(fill = "white")
  )
```


5 Appendix - Initialize trees for the model based on inventory data

```
# put them all together:
all.trees <- rbind(trees.circle, cutted.tree.list)
```

5.2.5 Give height and plot final layout

```
# add hd ratio to each record and calculate height:
all.trees2 <-
  dplyr::left_join(all.trees, hdratios[, c("iLand_name", "mean.hdratio")],
    by = c("species" = "iLand_name")) |>
  dplyr::mutate(height = dbh * mean.hdratio / 100)

summary(all.trees2$height)
```

| Min. | 1st Qu. | Median | Mean | 3rd Qu. | Max. |
|-------|---------|--------|--------|---------|--------|
| 2.563 | 11.767 | 19.314 | 20.094 | 26.235 | 63.561 |

```
g6 <- ggplot2::ggplot(all.trees, ggplot2::aes(X, Y, color = species)) +
  ggplot2::geom_point(size = all.trees$dbh / 10) +
  ggplot2::facet_wrap(~ plotID, nrow = 2) +
  ggplot2::xlim(-50, 50) + ggplot2::ylim(-50, 50) +
  ggplot2::theme_bw() + ggplot2::theme(
    panel.grid.major = ggplot2::element_blank(),
    panel.grid.minor = ggplot2::element_blank(),
    panel.background = ggplot2::element_blank(),
    strip.background = ggplot2::element_rect(fill = "white")
  )
```

5.2.6 Make files for iLand

Coordinates need to be shifted: 0, 0 is the bottom left corner. So we shift everything back by 50m.

```
# Make the tree list for iLand:
#https://iland-model.org/initialize+trees
#
## this is a sample tree input file
# note that the height is given in meter
# the 2nd tree has no age
# x;y;species;dbh;height;age
```

5 Appendix - Initialize trees for the model based on inventory data

```
# 31.11;8.01;piab;42.2;29.7;120
# 21.11;15.11;piab;52.8;33.5;0
# 11.51;25.11;fasy;55;35;100

plotids <- unique(all.trees2$plotID)
for (i in 1:4) {
  d <- all.trees2 |> dplyr::filter(plotID == plotids[i])

  # order them by dbh
  d <- d[order(d$dbh, decreasing = T), ]

  dat <-
    data.frame(
      x = d$X + 50,
      y = d$Y + 50,
      species = d$species,
      dbh = d$dbh,
      height = d$height,
      age = 0
    )

  out <-
    paste0(here::here("model/iLand_simulations/init/trees/Tree_init_plot_"),
           i,
           ".txt")
  write.table(
    dat,
    out,
    sep = ";",
    col.names = T,
    row.names = F,
    quote = F
  )
}
```