

Multi-scale Analysis of Forest Management Scenarios: Testing Indicators Forest Management Scenarios Overview

Clementine de Montgolfier

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Note on simulation protocol and convention chosen

I created 1 command file for each patch Inside I have one line for each itinerary

With Briex naming convention : each line get a unique identifier simply simulation_# from 1 to number of itineraries ran.

To add repetitions (see forceeps_replicates analyses) there are multiple possibilities :

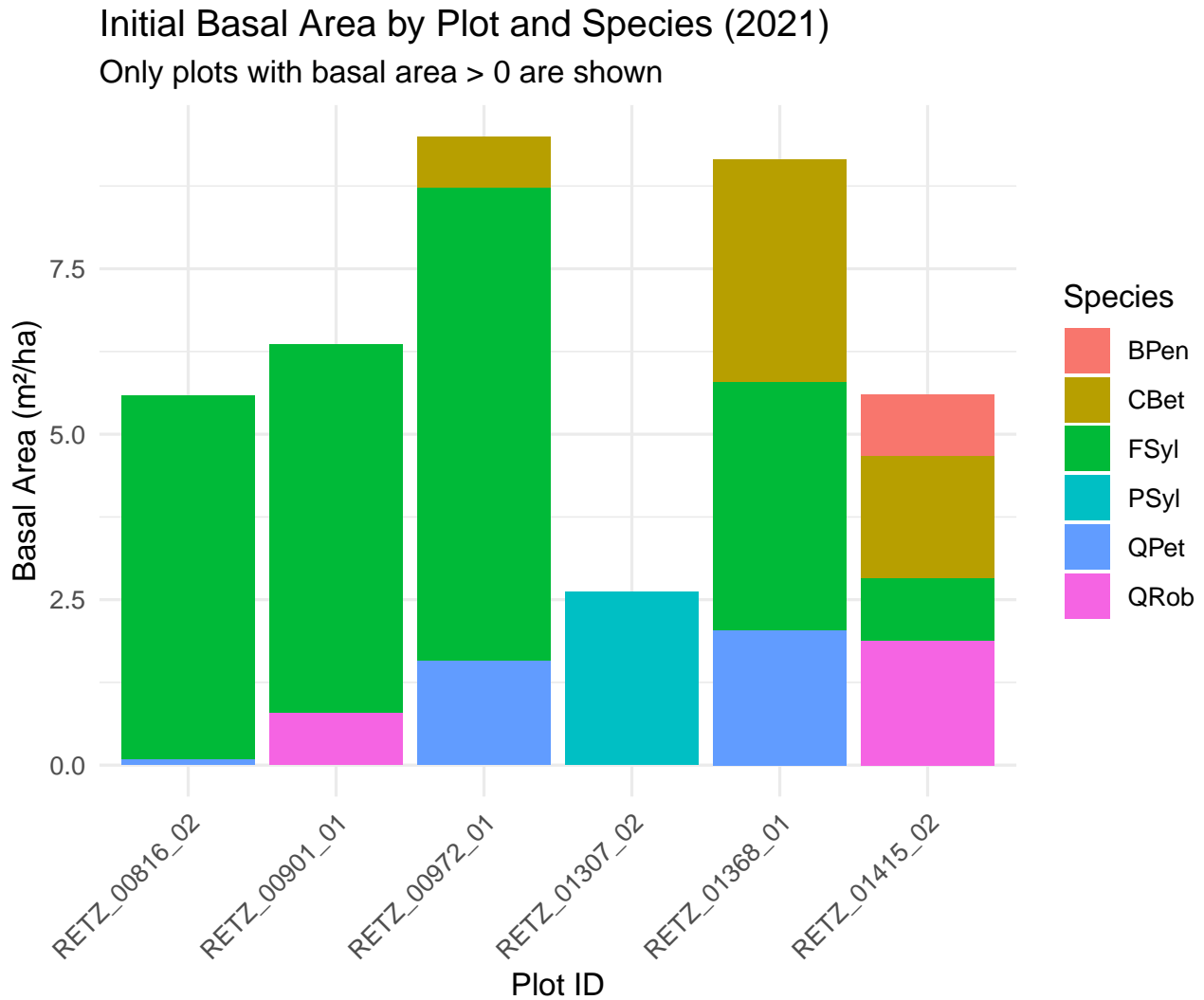
- use different seed in the command file and then regroup simulations together. For example simulation 1-10 for the first itinerary, 11-20 for the second. . . (either by keeping very good track of what is done (and a lot of loops when importing data) or by having a table that gives the correspondances between simulation number and characteristics of the simulation.)

- change naming convention in forceeps (by modifying briex scripts to get our own)

☐ Implement a system to repeat simulations

Initial Stand Conditions

Surface (ha)	Stand Type	Silviculture Species	Dominant Species 1	Dominant Species 2	Structure & Soil Cover	Basal Area (m ² /ha)	Mean DBH (cm)	Median Age (years)
2.50	FHETE	HET	HET		F	0.0	7.5	12.0
0.94	FHET1	HET	HET		F	17.5	12.5	12.0
10.23	FHETG	HET	HET	CHP	F	21.0	57.5	144.5
4.59	FHETG	HET	HET	CHS	F	31.0	57.5	144.5
3.38	FHETS	HET	HET	CHS	F	0.0	3.5	12.0
1.73	FCHPE	CHP	CHP		F	0.0	7.5	12.0
3.10	FCHSE	CHS	CHS		F	0.0	7.5	12.0
1.28	FDOUG	DOU	DOU		F	29.0	52.5	59.5
7.91	FHETM	HET	HET	CHA	F	31.0	37.5	114.5
2.23	FCHPG	CHP	CHP	CHA	F	17.5	62.5	125.0



The table below summarizes the diversity of the selected plots in terms of stand type and dominant species. This highlights the current selection's limited heterogeneity, suggesting the need to include a broader range of patches and avoid relying solely on random selection to ensure a more representative sample. (See 1.32 in `Generate.R`)

- ☐ Change `Generate.R` to include more diverse plot selection criteria.

Also in subsequent analyses I considered each plot as equal but for applicable results :

- ☐ Need to add a weight to account for plot size

Itinerary exploration

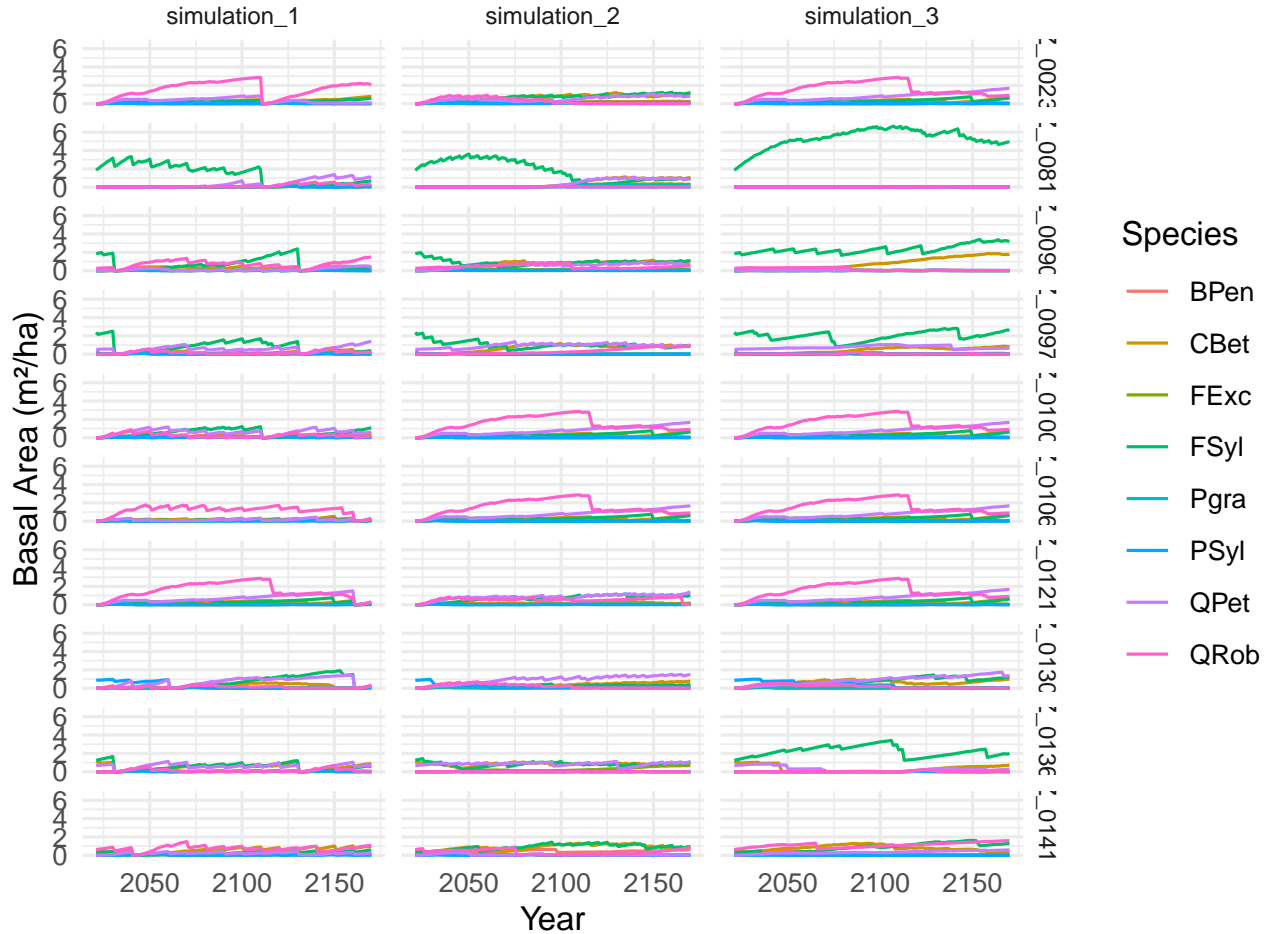
The study evaluates three distinct silvicultural strategies:

- **Clear-cut management** (*simulation1*)
 - Management cutting every 10 years removing 30% of volume (cutting type 0.5)
 - While maintaining initial species composition
 - Final clear-cut at maturity age of the dominant species
- **Continuous cover forestry** (*simulation2*)
 - Partial cutting every 5 years removing 10% of volume (cutting type 0.5)
 - Targeting equal (25%) composition of the four (or less if not found) main species

- **Note:** Harvesting only occurs when exploitability thresholds are met
- **Natural evolution** (*simulation3*)
 - No management intervention
 - Natural forest dynamics without human interference

Forest Productivity by Plot and Species

Basal area evolution over time across management scenarios



Note: The decline in basal area observed in simulation 3 (natural evolution) likely results from natural mortality, as the management strategy is set to no intervention (150_3_0.5_0%_FSyl-80).

Plot-Level Indicators Calculation and Visualization

Over the 80-year simulation period, we calculate the following indicators:

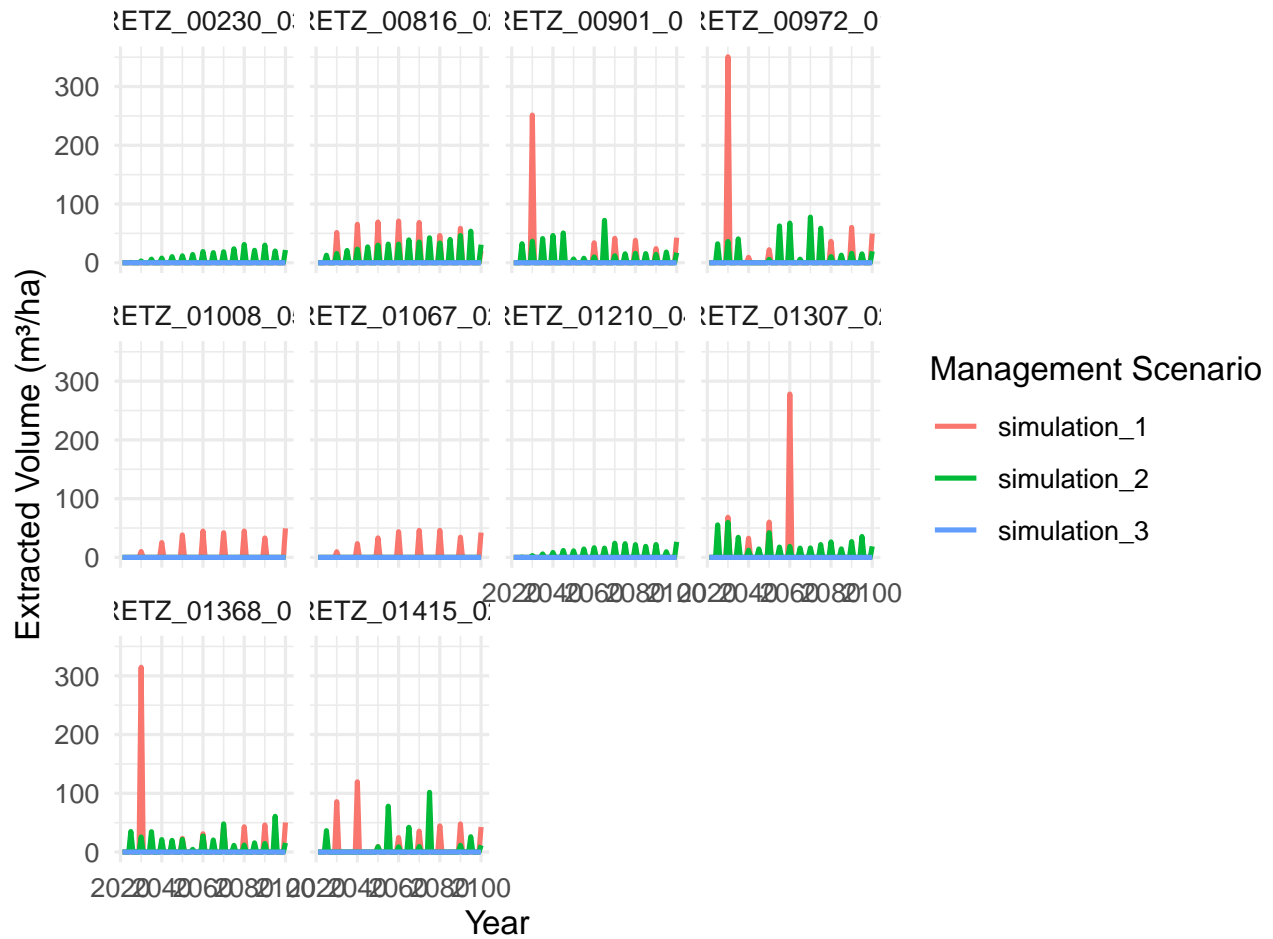
- **Hill diversity indices** (richness, Shannon, Simpson, Hill 0, Hill 1, Hill 2)
- **Harvested volume** by scenario
- **Standing biomass** total and by species

☐ Work is needed to analyse structural diversity (either find a better forCEEPS output file or analyse the complete output file)

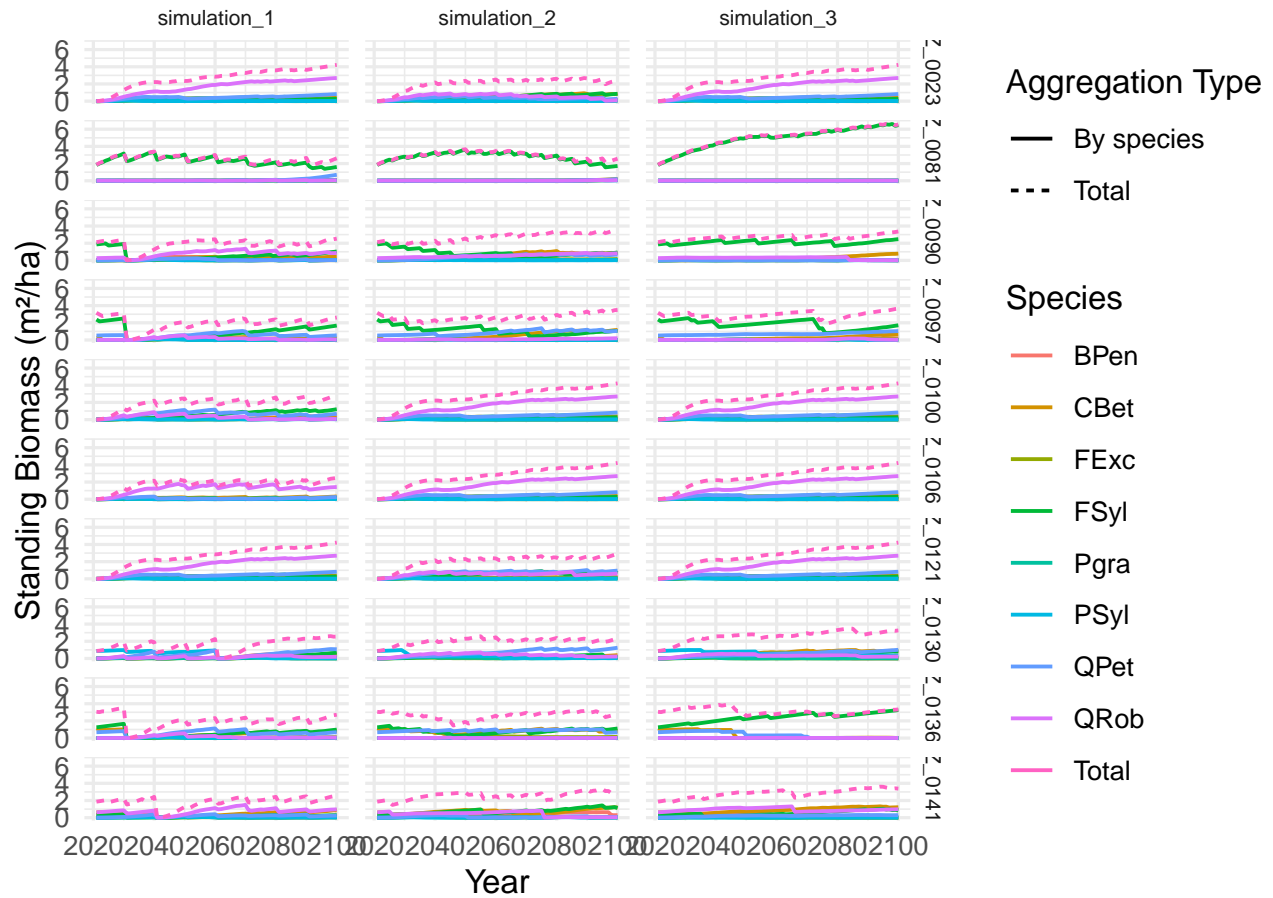
```
final_table <- biomasse_all %>% left_join(div, by = c("plot_id", "date", "scenario")) %>%
left_join(mean_scene1, by = c("plot_id", "date", "scenario")) ""
```

Harvested Wood Volume by Plot

Note: Absence of regular harvesting may indicate exploitability thresholds



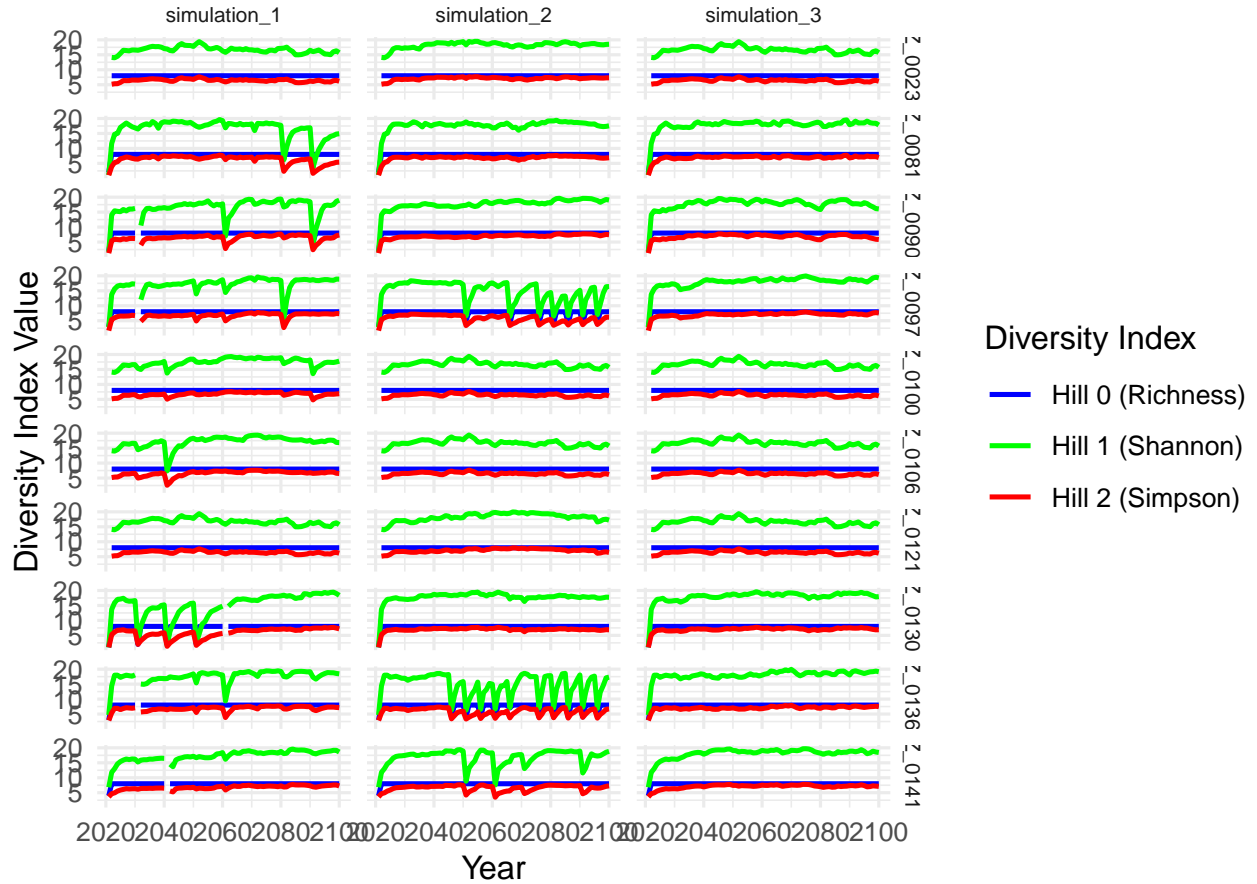
Standing Biomass by Plot, Species, and Total Evolution of basal area over time



Solid lines show individual species, dashed lines show total biomass

Diversity Indices Evolution

Hill numbers representing different aspects of diversity



Hill 0 = Species richness, Hill 1 = Shannon diversity, Hill 2 = Simpson diversity

Global Indicators

Definition of Local vs Global Diversity

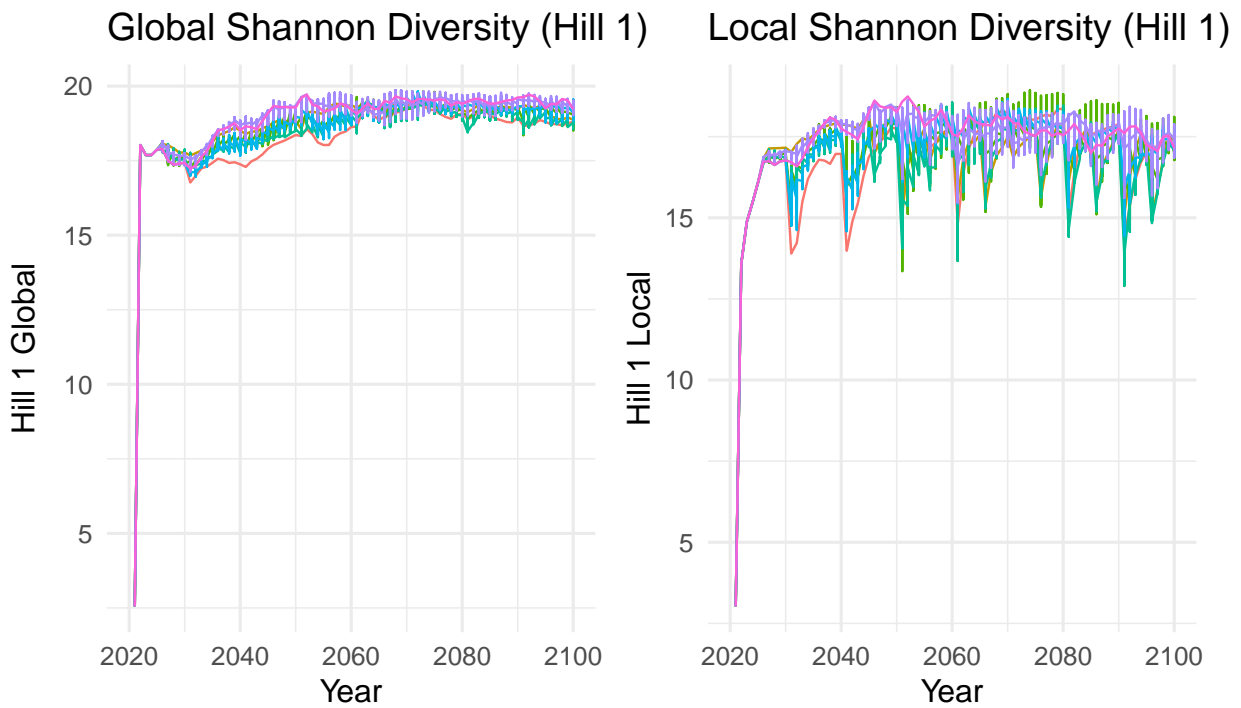
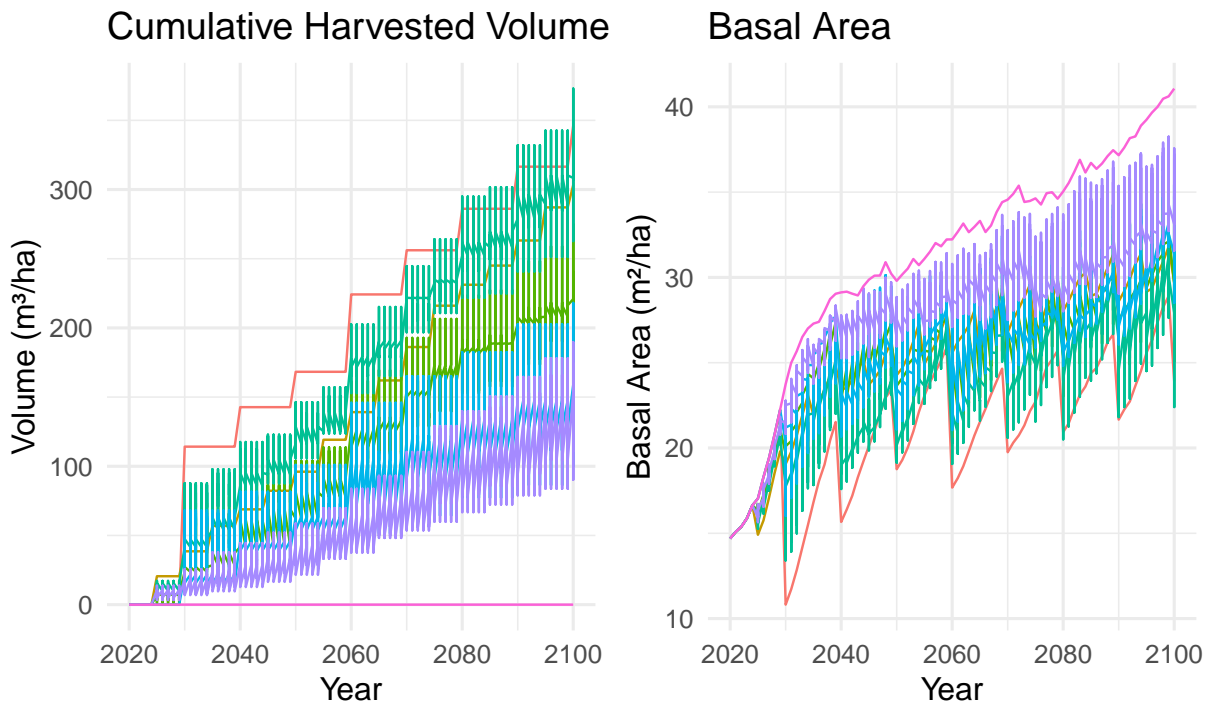
Before presenting the global indicators, it's important to clarify the difference between local and global diversity measures:

- **Local diversity (Hill local):** Average diversity calculated within each individual plot, then averaged across all plots in a scenario. This represents the typical diversity found in a single forest stand.
- **Global diversity (Hill global):** Diversity calculated by pooling all species abundances across all plots in a scenario before computing the diversity index. This represents the overall landscape-level diversity.

The relationship between local and global diversity provides insights into beta diversity (turnover between plots). When global diversity is higher than local diversity, it indicates high species turnover between plots.

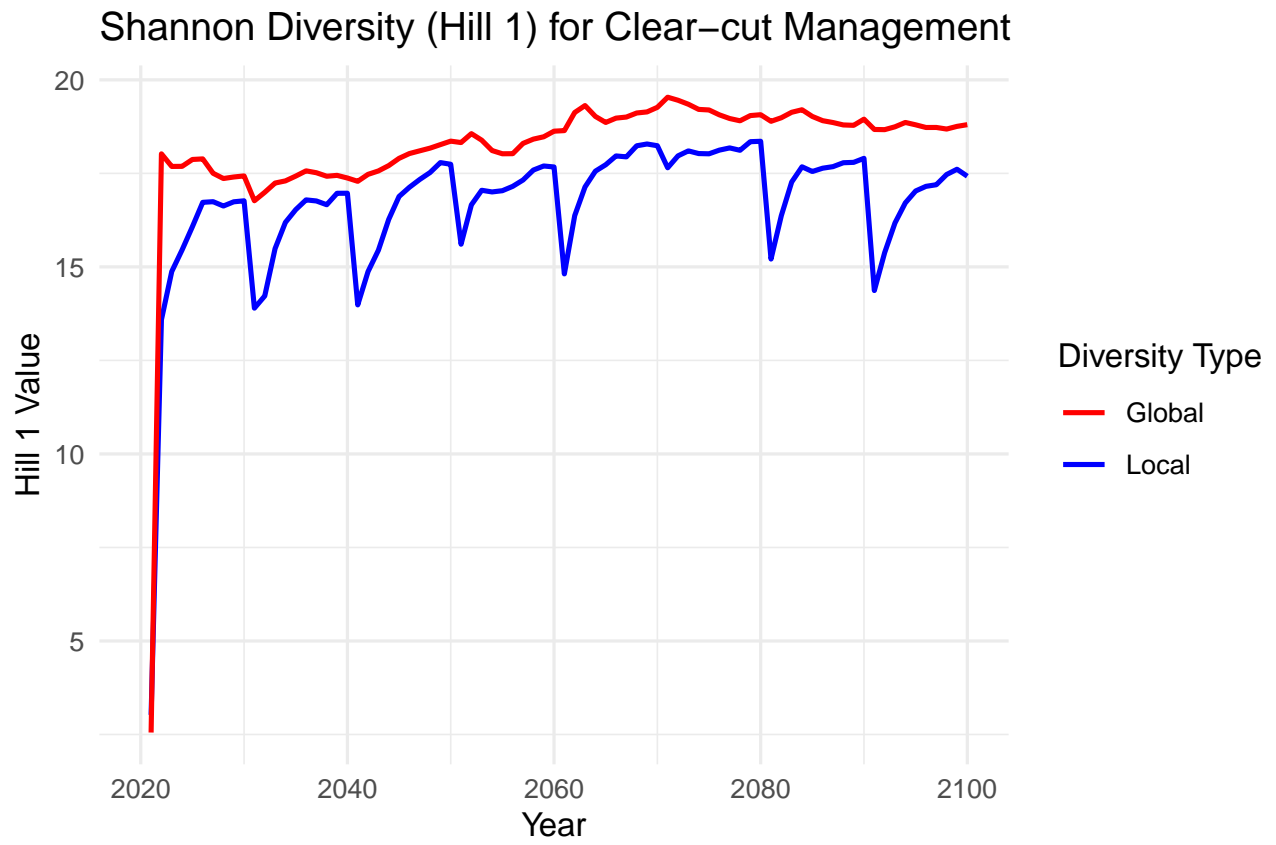
To create scenarios I combined different itineraries together.

To be able to conclude on different proportions effect and to take into account that the dynamic of one scenario can depend on which plot were chosen I repeated each scenarios 10 times. Example: for half clearcut, half no management, I randomly selected half of the plots for each itinerary and repeated this process 10 times to capture variability in the results.

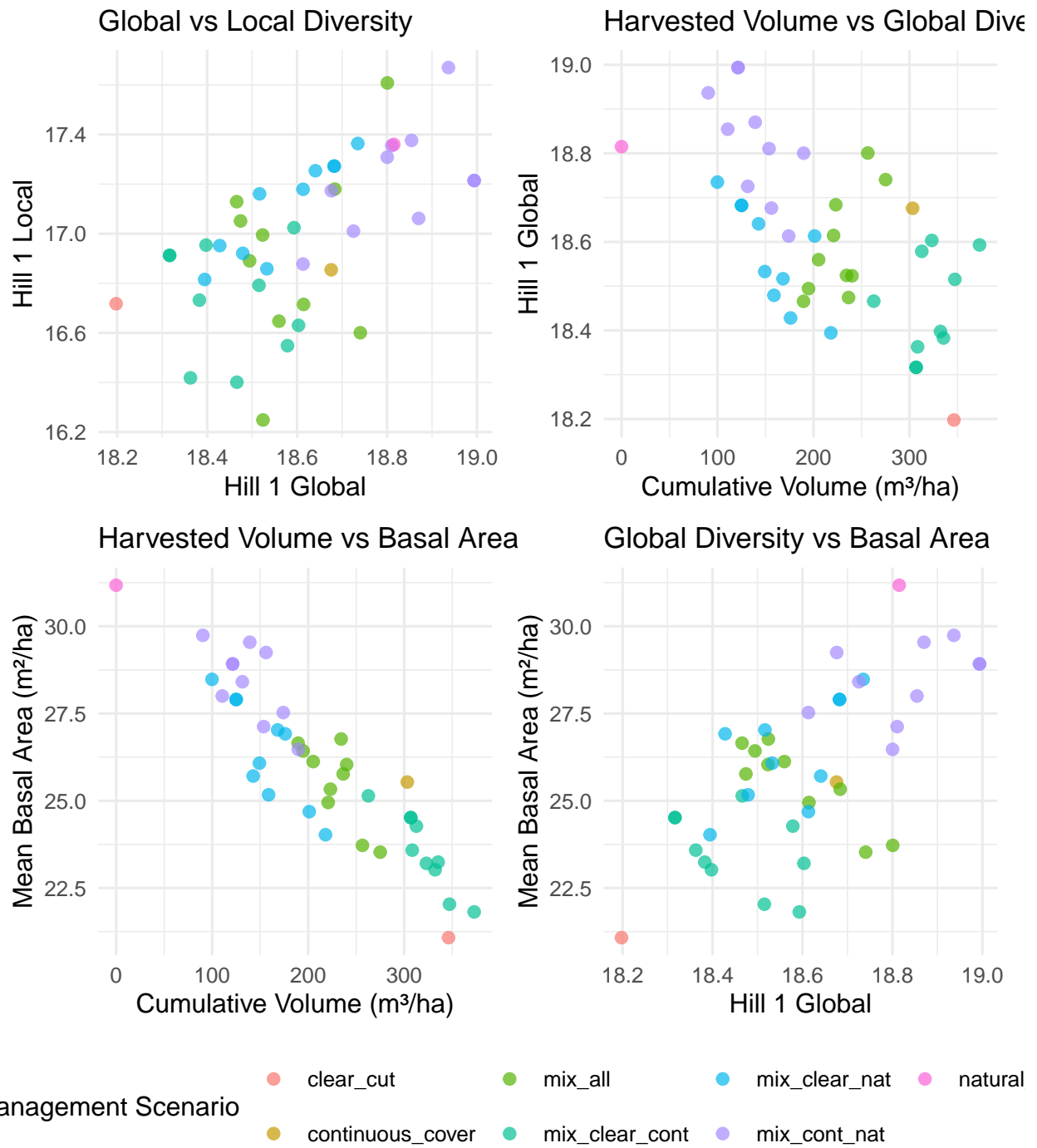


Management Scenario

clear_cut	mix_all	mix_clear_nat	natural
continuous_cover	mix_clear_cont	mix_cont_nat	



Relationships Between Global Indicators



Future Work

- ☐ **Select more diverse and representative plots** to better capture forest heterogeneity
- ☐ **Add additional indicators** (structure, canopy cover, recruitment, dead biomass)
- ☐ **Implement calculations with complete dataset** (code to be written and memory-optimized) as this may be necessary for structural diversity indices (needs consideration, but potentially no other)

output will contain the necessary data)

- **Integrate FORCEEPS replications** to calculate means and assess how this fits into the workflow