Reproducing the Emerge parametrisation by C. Deleuze

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Introduction

The original model can be found in Deleuze et al. (2014). In their scripts, they used the following code:

```
Modele_mai2 = nlme(formTotNew ~ a + b*hdn + d*hsurd, data = Grdata.PV,
    start = c(a = 0.4, 0, b = 1.5, 0, d = 0.0005, 0),
    fixed = list(a + b + d ~ feuil.res), random = a + d ~ 1|nomessence2)
```

The model `Modele_mai2` computes the form factor $\mathcal{F}$ for an individual of height h and circumference at breast height c, of species j and functional group i (conifer or broadleaf) as:

$$
\begin{aligned}
\mathcal{F} &\sim \boldsymbol{\mathcal{N}}(\mu, \sigma) \\
\mu_{i,j} &= a_{i,j} + b_i \frac{\sqrt{c}}{h} + d_{i,j} \frac{h}{c} \\
a_{i,j} &\sim \boldsymbol{\mathcal{N}}(\alpha_i, \sigma_\alpha) \\
d_{i,j} &\sim \boldsymbol{\mathcal{N}}(\delta_i, \sigma_\delta),
\end{aligned}
\tag{1}
$$

where α_i and δ_i are the 'group intercepts' (common values within conifers and broadleaves). Therefore, it seems to be a GLMM, and I am not sure `nlme` is relevant here. In the next sections, I will try to reproduce their study with a Bayesian model, although I am not sure I succeeded to recreate their dataset completly. A previous analysis was done in the file `00_notes.qmd` with simulated data in order to verify my Bayesian model.

I rewrite the equation (**??**) with new variable names and without the indices i and j, in order to correspond to the bayesian model (written in Stan, see Section):

$$\begin{aligned}
\mathcal{F} &\sim \boldsymbol{\mathcal{N}}(\mu, \sigma) \\
\mu &= \beta_0 + b_1 \frac{\sqrt{c}}{h} + \beta_2 \frac{h}{c} \\
\beta_0 &\sim \boldsymbol{\mathcal{N}}(b_0, \sigma_0) \\
\beta_2 &\sim \boldsymbol{\mathcal{N}}(b_2, \sigma_2),
\end{aligned} \tag{2}$$

Prepare the data

Packages and helpers

First, I load the necessary packages:

```r
#### Clear space and load packages
rm(list = ls())
graphics.off()

options(max.print = 500)

library(data.table)
library(MetBrewer)
library(cmdstanr)
    register_knitr_engine(override = TRUE)
library(stringi)
library(nlme)
library(gt)

setHook(packageEvent("grDevices", "onLoad"),
function(...) grDevices::X11.options(type='cairo'))
options(device='x11')
```

Stan engine

By default, Quarto uses the knitr's built-in stan engine `rstan`. To override it so that all stan chunks are processed with `CmdStanR`, I need to specify:

```r
register_knitr_engine(override = TRUE)
```

Then, I define useful functions:

```r
#### Tool functions
## Tools
source("./toolFunctions.R")

## Function to compute tree volume according to model
vol_fct = function(params_vec, predictor_mat, corrected_cyl_vol)
    return((predictor_mat %*% params_vec) * corrected_cyl_vol)
```

Tree data

The data are stored on the remote server `smb://del1509n015/` in the folder `2024_faircarbon/data_orig/`. On Linux, it is first necessary to mount locally the folder, so that R can access the files:

1. Switch to super user where you replace `JohnField-Admin` (really nice Irish composer) by your admin name (typically, your IGN id followed by `-Admin`):

```
su JohnField-Admin
```

Your **admin** password will be asked

2. Create a directory where you will mount the remote folder. By default I like to put it in `/mnt/local_share`. You need to be super user to write in `/mnt/`:

```
sudo mkdir /mnt/local_share
```

This step should be done only once.

3. Mount the remote folder `smb://del1509n015/2024_faircarbon/`, where you replace `your_name` by your **usual** IGN id (NOT the admin one):

```
sudo mount -t cifs -o username=your_name,domain=ign,uid=your_name //del1509n015/2024_faircar
```

Maybe two passwords will be asked, first your **admin** password to execute the `sudo`, and then your **usual** password. If you just did step 2, then the prompt will not ask again for your password.

4. Check that it worked, especially the reading and writting rigths:

```
ls -l /mnt/local_share/
```

The content of the remote folder should appear. You can close your admin session by using `ctrl + d` or `Cmd + d`

Now that the raw data are accessible to R, it is time to prepare them:

```
#### Prepare data
## Loading
os = Sys.info()[['sysname']]
mnt_point = "/mnt/local_share/"
if (os == "Linux" || os == "Darwin")
{
    if (!dir.exists(mnt_point))
        stop(paste0("The mounting point <", mnt_point, "> does not exist"))
} else if (os == "Windows") {
    stop("TO DO!!! No idea how that works on Windows!")
} else {
    stop(paste("Unknown Operating System:", os))
}

path_data = paste0(mnt_point, "/data_orig/")
if (!dir.exists(path_data))
    stop(paste0("Folder <", path_data, "> does not exist! Are you sure you mounted the good f

if (list.files(path = path_data) != "EMERGE.RData")
    stop("There should be only the file <EMERGE.RData> in the data_orig folder")

load(paste0(path_data, "EMERGE.RData"))
setDT(inra_arbres)

## Keep only column of interest and rename them
inra_arbres[, tot_vol := v_tronc_verif + v_fourche_verif + v_fourche2_verif + v_br_verif + v_
inra_arbres = unique(inra_arbres[, .(nom_fichier, essence, c130, h_tot, tot_vol, genre)])
inra_arbres = na.omit(inra_arbres)

setnames(inra_arbres, new = c("unique_id", "speciesName_sci", "circumference_cm", "height", "

inra_arbres[, fct_type := "broadleaf"] # Functional type, either broadleaf or conifer
inra_arbres[genus %in% c("Abies", "Cedrus", "Larix", "Picea", "Pinus", "Pseudotsuga", "Thuya"
    fct_type := "conifer"]
```

```r
inra_arbres[, unique_id := as.character(unique_id)]
inra_arbres[, speciesName_sci := as.character(speciesName_sci)]
inra_arbres[, genus := as.character(genus)]

inra_arbres[, nb_indiv := .N, by = speciesName_sci]
# inra_arbres = inra_arbres[nb_indiv > 20]

## Compute (total) volume in m³, circumference in m, hardiness, and slenderness
inra_arbres[, volume_m3 := tot_vol/1e3]
inra_arbres[, circumference_m := circumference_cm/100]
inra_arbres[, hdn := sqrt(circumference_m)/height]
inra_arbres[, slenderness := height/circumference_m]

## In the original model, there are the variables formTot, and formTotNew. I need to rebuild
inra_arbres[, formTot := 4*pi*volume_m3/(height*circumference_m^2)]
inra_arbres[, formTotNew := formTot * (1 - 1.3/height)^2]
inra_arbres[, feuil.res := as.factor(fct_type)]

## Indices
# Find start and end indices for each species
setkey(inra_arbres, fct_type, speciesName_sci, unique_id)
ind_species = inra_arbres[, .(start = .I[1], end = .I[.N]), by = .(speciesName_sci)]
ind_species[, n_indiv := end - start + 1, by = speciesName_sci]

if (ind_species[, sum(n_indiv)] != inra_arbres[, .N])
    stop("The number of individuals in ind_species does not correspond to the number of indi

ind_species = merge.data.table(ind_species, unique(inra_arbres[, .(speciesName_sci, fct_type
ind_species[, colour := if(fct_type == "broadleaf") "#FFAF37" else "#007BA5", by = speciesNa
setorder(ind_species, start)

n_sp = ind_species[, .N, by = fct_type]
setkey(n_sp, fct_type)

## Stan data
stanData = list(
    N = inra_arbres[, .N],
    S = ind_species[, .N],
    n_sp_conif = n_sp["conifer", N],
    n_sp_broad = n_sp["broadleaf", N],
    ind_start_broad = ind_species[fct_type == "broadleaf", start],
    ind_start_conif = ind_species[fct_type == "conifer", start],
    ind_end_broad = ind_species[fct_type == "broadleaf", end],
    ind_end_conif = ind_species[fct_type == "conifer", end],
    height = inra_arbres[, height],
    circumference_m = inra_arbres[, circumference_cm/100],
    volume_m3 = inra_arbres[, volume_m3]
)
```

The data are now ready! Here is the composition:

The correlation between the hardiness and the slenderness is -0.51, which is expected and I guess problematic…

Data for posterior checks

After running a Bayesian model, it is important to do a 'predict' on new data to check that the model can generate sensible volume. For this, I use the volume-measured trees dataset from 2010, which I format in the following code snippet.

```r
## Add species to the profiles
setDT(emerge_2010_profils)
setDT(emerge_2010_arbres)

emerge_2010_arbres = unique(emerge_2010_arbres[, .(tree, species, c130)])
emerge_2010_profils = emerge_2010_arbres[emerge_2010_profils, on = "tree"]

## Compute dbh top/bottom of each log
emerge_2010_profils[, dbh_bottom_m := circ_bas_cm/(100*pi)]
emerge_2010_profils[, dbh_top_m := circ_haut_cm/(100*pi)]

## Reorganising
emerge_2010_profils[, species := as.character(species)]
setorder(emerge_2010_profils, tree, niveau_bas_m)
emerge_2010_profils[, id := NULL]
emerge_2010_profils[, c130 := c130/100]
setnames(x = emerge_2010_profils, old = c("niveau_bas_m", "niveau_haut_m", "c130"), c("h_bot
emerge_2010_profils = emerge_2010_profils[, .(tree, species, dbh_bottom_m, dbh_top_m, h_bott

## Compute log and cumulated volumes
emerge_2010_profils[, height := max(h_top), by = tree]
emerge_2010_profils[, volume_m3 := pi/12*max(dbh_bottom_m)^2*height, by = tree]
emerge_2010_profils[, vol_log := pi/12*dbh_bottom_m^2*(height - h_bottom) - pi/12*dbh_top_m^
```

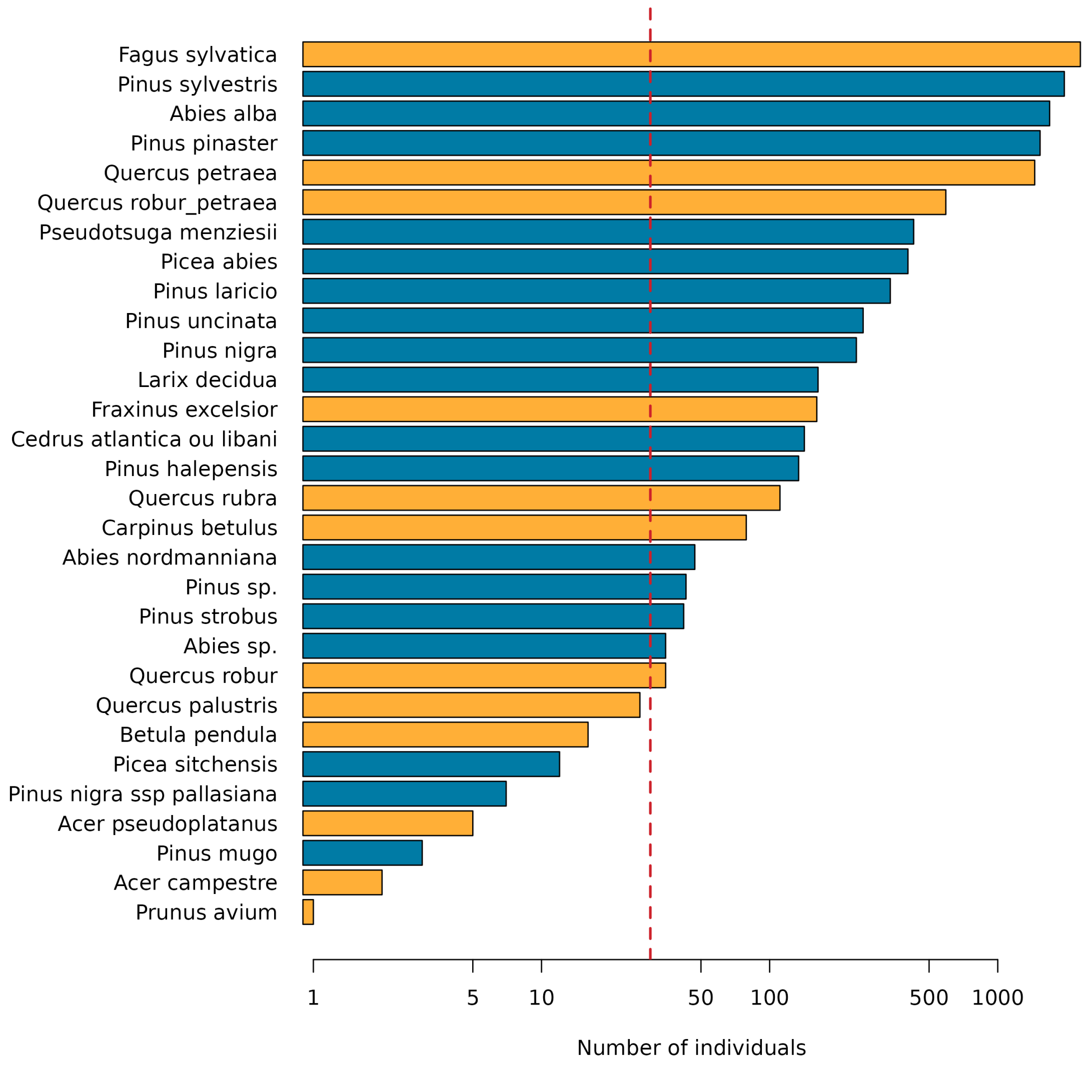


Figure 1: Number of individuals per species, with conifers in blue and broadleaves in orange. Watch out, it is a $\log_{10}$ scale

```
emerge_2010_profils[, cumulated_vol := cumsum(vol_log), by = tree]
emerge_2010_profils[, cumulated_percent_vol := cumulated_vol/volume_m3, by = tree]

## Keep only variables of interest
data_check = unique(emerge_2010_profils[, .(tree, species, volume_m3, height, circumference_m

## Change vernacular species names to scientific
species_dt = data.table(species = c("Frêne", "Chêne vert", "Tilia cordata", "Chêne sessile",
        "Robinier", "Pin Alep", "Chêne pubescent", "Aulne", "Bouleau"),
    speciesName_sci = c("Fraxinus excelsior", "Quercus ilex", "Tilia cordata", "Quercus petra
        "Robinia pseudoacacia", "Pinus halepensis", "Quercus pubescens", "Alnus glutinosa",
    fct_type = c(rep("broadleaf", 6), "conifer", rep("broadleaf", 3)))

data_check = merge.data.table(data_check, species_dt, by = "species")
data_check[, species := NULL]
data_check[speciesName_sci == "Quercus petraea", speciesName_sci := "Quercus robur_petraea"]
setkey(data_check, speciesName_sci)

data_check = data_check[speciesName_sci %in% species_nb[, speciesName_sci]]

data_check[, hdn := sqrt(circumference_m)/height]
data_check[, slenderness := height/circumference_m]
data_check[, corrected_cyl_vol := height*circumference_m^2/(4*pi*(1 - 1.3/height)^2)]

data_check[, feuil.res := as.factor(fct_type)]
```

Here is the composition of the data for the posterior predictive checks:

Model using `CmdStanR`

I use the following model, which has been tested with simulated data in `00_notes.qmd`:

```
data {
    // Dimensions and indices
    int N; // Number of individuals
    int S; // Number of species
    int<lower = 0, upper = S> n_sp_broad; // number of broadleaf species
    int<lower = S - n_sp_broad, upper = S - n_sp_broad> n_sp_conif; // number of conifer spe
    array[n_sp_broad] int ind_start_broad; // Broadleaf species index start
    array[n_sp_conif] int ind_start_conif; // Conifer species index start
    array[n_sp_broad] int ind_end_broad; // Broadleaf species index end
```

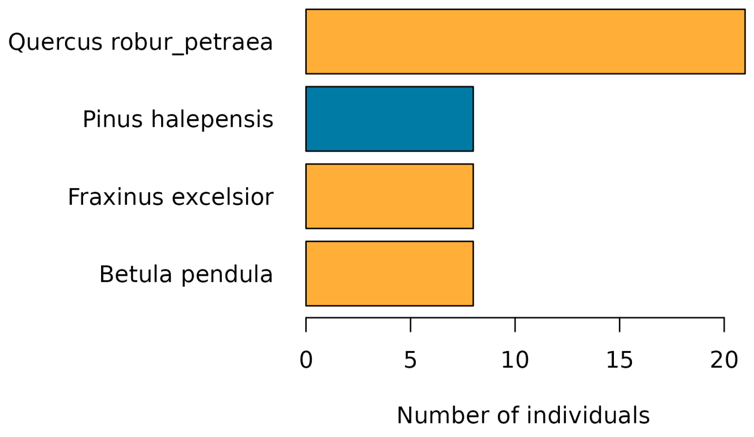


Figure 2: Number of individuals per species for the posterior checks data, with conifers in blue and broadleaves in orange

```
    array[n_sp_conif] int ind_end_conif; // Conifer species index end

    // Predictors
    vector<lower = 0> [N] height;
    vector<lower = 0> [N] circumference_m;

    // Response variable
    vector [N] volume_m3;
}

transformed data {
    vector [N] hdn = sqrt(circumference_m) ./ height;
    vector [N] slenderness = height ./ circumference_m;
    vector [N] corrected_cyl_vol = height .* circumference_m^2 ./ (4*pi()*(1 - 1.3/height)^2
}

parameters {
    // Fixed effects (population parameters) for broadleaf and conifer
    vector[2] b0;
    vector[2] b1;
    vector[2] b2;

    // Random effects (group parameters)
    // vector[S] eta0;
    // vector[S] eta2;
    vector[S] beta0;
    vector[S] beta2;

    // Variances
    real<lower = 0> sigma; // sd residuals
    real<lower = 0> sigma_beta0; // sd random effect beta0
    real<lower = 0> sigma_beta2; // sd random effect beta2
}

// transformed parameters {
//  vector[S] beta0;
//  vector[S] beta2;

//  beta0[1:n_sp_broad] = b0[1] + eta0[1:n_sp_broad]*sigma_beta0;
//  beta0[(n_sp_broad + 1):S] = b0[2] + eta0[(n_sp_broad + 1):S]*sigma_beta0;

//  beta2[1:n_sp_broad] = b2[1] + eta2[1:n_sp_broad]*sigma_beta2;
//  beta2[(n_sp_broad + 1):S] = b2[2] + eta2[(n_sp_broad + 1):S]*sigma_beta2;
// }

model {
    // Priors
    // --- Population parameters
    target += normal_lpdf(b0 | 0, 1);
    target += normal_lpdf(b1 | 2, 1);
    target += normal_lpdf(b2 | 0, 0.2);

    // --- Residual variance and population variance
    target += inv_gamma_lpdf(sigma | 2, 1); // Uses shape and scale (which is the rate from
    target += inv_gamma_lpdf(sigma_beta0 | 3, 0.5);
    target += inv_gamma_lpdf(sigma_beta2 | 3, 0.5);

    // Hierarchy
    target += normal_lpdf(beta0[1:n_sp_broad] | b0[1], sigma_beta0);
    target += normal_lpdf(beta2[1:n_sp_broad] | b2[1], sigma_beta2);
    target += normal_lpdf(beta0[(n_sp_broad + 1):S] | b0[2], sigma_beta0);
    target += normal_lpdf(beta2[(n_sp_broad + 1):S] | b2[2], sigma_beta2);
    // target += normal_lpdf(eta0 | 0, 1);
    // target += normal_lpdf(eta2 | 0, 1);

    // Likelihood broadleaves, i = species
    for (i in 1:n_sp_broad)
    {
        target += normal_lpdf(volume_m3[ind_start_broad[i]:ind_end_broad[i]] |
            (beta0[i] +
            b1[1]*hdn[ind_start_broad[i]:ind_end_broad[i]] +
            beta2[i]*slenderness[ind_start_broad[i]:ind_end_broad[i]]) .*
            corrected_cyl_vol[ind_start_broad[i]:ind_end_broad[i]],
            sigma);
    }

    // Likelihood conifers, i = species
    for (i in 1:n_sp_conif)
    {
        target += normal_lpdf(volume_m3[ind_start_conif[i]:ind_end_conif[i]] |
            (beta0[n_sp_broad + i] +
            b1[2]*hdn[ind_start_conif[i]:ind_end_conif[i]] +
            beta2[n_sp_broad + i]*slenderness[ind_start_conif[i]:ind_end_conif[i]]) .*
            corrected_cyl_vol[ind_start_conif[i]:ind_end_conif[i]],
            sigma);
    }
}
```

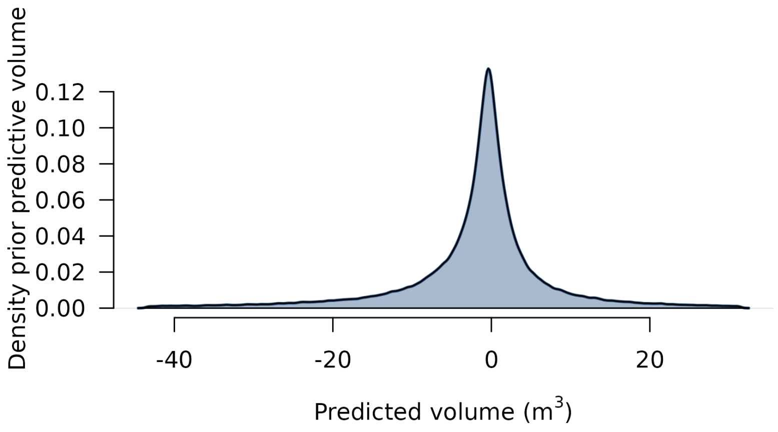
The commented parts correspond to a non-centred parametrisation, which did not work in my case. I now do the standard procedure for a Bayesian analysis:

1. Computational model checks using fake data simulation (done in `00_notes.qmd`) and the prior predictive distribution (done in Section)
2. Run the model (in Section)
3. Posterior predictive checks (in Section)

Prior predictive checks

The aim here is to verify that the priors are ‘sensible’, *i.e.,* that this prior predictive distribution for the data has at least some mass around extreme but plausible datasets. However, there should be no mass on completely implausible data sets. Indeed, it is too often recommended to use a prior with a wide tail, as it seems uninformative and then ‘let the data speak’. If the data are informative enough, this approach is fine. However, if not (and it is the case for us as some species are censored once or twice), then the prior has more influences. So better not put most of the prior probability mass out of line.

```r
n_sim = 20
gen_data = vector(mode = "list", length = 20)
S = ind_species[, .N]
volume = numeric(length = inra_arbres[, .N])

corrected_cyl_vol = inra_arbres[, height]*inra_arbres[, circumference_m^2]/(4*pi*(1 - 1.3/in

for (sim in seq_len(n_sim))
{
    # Simulate the variances
    sigma = 1/rgamma(n = 1, shape = 2, rate = 1);
    sigma_beta0 = 1/rgamma(n = 1, shape = 3, rate = 0.5);
    sigma_beta2 = 1/rgamma(n = 1, shape = 3, rate = 0.5);

    # Simulate the common group intercepts and hdn/slenderness slopes
    b0 = rnorm(n = 2, mean = 0, sd = 1);
    b1 = rnorm(n = 2, mean = 2, sd = 1);
    b2 = rnorm(n = 2, mean = 0, sd = 0.2);

    # Simulate group-specific intercepts and slenderness slopes
    n_sp_broad = stanData[["n_sp_broad"]]
    n_sp_conif = stanData[["n_sp_conif"]]
    beta0 = numeric(length = S)
    beta2 = numeric(length = S)
    beta0[1:n_sp_broad] = rnorm(n = n_sp_broad, mean = b0[1], sd = sigma_beta0);
    beta0[(n_sp_broad + 1):S] = rnorm(n = n_sp_conif, mean = b0[2], sd = sigma_beta0);
    beta2[1:n_sp_broad] = rnorm(n = n_sp_broad, mean = b2[1], sd = sigma_beta2);
    beta2[(n_sp_broad + 1):S] = rnorm(n = n_sp_conif, mean = b2[2], sd = sigma_beta2);

    # Simulate individual volume data
    # --- Broadleaves
    for (s in 1:n_sp_broad)
    {
        ind_start = ind_species[s, start]
        ind_end = ind_species[s, end]
        n_indiv = ind_species[s, n_indiv]

        volume[ind_start:ind_end] = rnorm(n = n_indiv, mean = (beta0[s] +
            b1[1]*inra_arbres[ind_start:ind_end, hdn] +
            beta2[s]*inra_arbres[ind_start:ind_end, slenderness]) * corrected_cyl_vol[ind_sta
            sd = sigma);
    }
    # --- Conifers
    for (s in (n_sp_broad + 1):S)
    {
        ind_start = ind_species[s, start]
        ind_end = ind_species[s, end]
        n_indiv = ind_species[s, n_indiv]

        volume[ind_start:ind_end] = rnorm(n = n_indiv, mean = (beta0[s] +
            b1[2]*inra_arbres[ind_start:ind_end, hdn] +
            beta2[s]*inra_arbres[ind_start:ind_end, slenderness]) * corrected_cyl_vol[ind_sta
            sd = sigma);
    }

    gen_data[[sim]] = data.table(volume = volume)
}

gen_data = rbindlist(l = gen_data, idcol = "simulation")
bounds = quantile(x = gen_data[, volume], probs = c(0.025, 0.975))
dens_gen = density(gen_data[(bounds["2.5%"] < volume) & (volume < bounds["97.5%"]), volume])

plot(dens_gen, axes = FALSE, xlab = expression("Predicted volume (m"^3*")"), ylab = "Density
    main = "", lwd = 2, col = "#295384")
polygon(dens_gen, col = "#29538466")
axis(side = 1)
axis(side = 2, las = 1)
```



Here, for sure I put some mass on irrealistic data sets, but it is not too bad!

Run the model

```r
n_chains = 4
# woodstock_seed = 1969 - 08 - 18
iter_warmup = 750
iter_sampling = 1250

## Fit
if (!file.exists("fit_deleuze.rds"))
{
    fit = stan_deleuze$sample(data = stanData, chains = n_chains, parallel_chains = ifelse(n
        seed = NULL, refresh = 200, max_treedepth = 12, save_warmup = TRUE,
        iter_sampling = iter_sampling, iter_warmup = iter_warmup, adapt_delta = 0.95)
    fit$save_output_files(dir = "./", basename = paste0("fit_deleuze"), random = FALSE)
    saveRDS(fit, "./fit_deleuze.rds")
} else {
    fit = readRDS("./fit_deleuze.rds")
}

# mcmc_rhat(bayesplot::rhat(fit))
# mcmc_neff(bayesplot::neff_ratio(fit))
# mcmc_nuts_divergence(bayesplot::nuts_params(fit), lp = log_posterior(fit))

# mcmc_scatter(x = fit$draws(c("b2[1]", "b1[1]")), alpha = 1, np = nuts_params(fit))
# mcmc_hex(x = fit$draws(c("b0[1]", "b1[1]")))

# mcmc_pairs(x = fit$draws(c("b0", "b1", "b2", "sigma")), np = nuts_params(fit))
```

Posterior predictive checks

In this section, I do a posterior predictive check, that is to say: can the fitted model predict sensible new volumes? For this, I use the `generated quantities` block of Stan language.

```stan
// This standalone script generates volume for a given species

data {
    // Dimensions and indices for parameters
    int S; // Number of species
    // New data for generating posterior
    int N_new; // Number of new individuals
    int<lower = 1, upper = S> species_id; // Index of the species
    int<lower = 1, upper = 2> fct_type; // Functional type, 1 = broadleaf, 2 = conifer

    // Predictors
    vector [N_new] hdn_new;
    vector [N_new] slenderness_new;
    vector [N_new] corrected_cyl_vol_new;
}

parameters {
    // Fixed effects (population parameters) for broadleaf and conifer
    vector[2] b0;
    vector[2] b1;
    vector[2] b2;

    // Random effects (group parameters)
    vector[S] beta0;
    vector[S] beta2;

    // Variances
    real<lower = 0> sigma; // sd residuals
    real<lower = 0> sigma_beta0; // sd random effect beta0
    real<lower = 0> sigma_beta2; // sd random effect beta2
}

generated quantities {
    vector[N_new] avg = (beta0[species_id] + b1[fct_type]*hdn_new + beta2[species_id]*slende
        corrected_cyl_vol_new;
    array[N_new] real volume_new = normal_rng(avg, sigma);
}
```

I predict new volumes based on the dataset collected in 2010, here for the species 'Quercus robur_petraea'.

```
selected_sp = "Quercus robur_petraea" # Maybe in inra_arbres it is a hybrid, i.e. should be r
species_id = ind_species[speciesName_sci == selected_sp, which = TRUE]
fct_type = ifelse(ind_species[speciesName_sci == selected_sp, fct_type] == "broadleaf", 1, 2)

stanData_new = list(
    S = S,
    N_new = data_check[selected_sp, .N],
    species_id = species_id,
    fct_type = fct_type,
    hdn_new = data_check[selected_sp, hdn],
    slenderness_new = data_check[selected_sp, slenderness],
    corrected_cyl_vol_new = data_check[selected_sp, corrected_cyl_vol]
)

posteriorVol = genQ$generate_quantities(fitted_params = fit$draws(inc_warmup = FALSE), data =

avg_vol = apply(X = posteriorVol$draws("volume_new"), MARGIN = 3, FUN = mean)
quant_vol = apply(X = posteriorVol$draws("volume_new"), MARGIN = 3, FUN = quantile, probs = c

params = c(paste0("beta0[", species_id, "]"), paste0("b1[", fct_type, "]"), paste0("beta2[",
bayes_p = round(getParams(model_cmdstan = fit, params_names = params, type = "mean"), 4)
```

This ends the bayesian section. In the next two sections, I reproduce the study of Deleuze et al. (2014) with `nlme` (used in the original studt) and `lme4`.

Model using `nlme`

This is the model and package used in Deleuze et al. (2014):

```
Modele_mai2 = nlme(formTotNew ~ a + b*hdn + d*slenderness, data = inra_arbres,
    start = c(a = 0.4, 0, b = 1.5, 0, d = 0.0005, 0),
    fixed = list(a + b + d ~ feuil.res), random = a + d ~ 1|speciesName_sci)
```

Rebuild the parameters for *Fagus sylvatica*:

```
## Rebuild species-specific params from nlme
fixed_effects_nlme = fixed.effects(Modele_mai2)
random_effects_nlme = ranef(Modele_mai2)[selected_sp, ]

if (nrow(random_effects_nlme) != 1)
    stop("Dimensions mismatch")

b0_nlme = fixed_effects_nlme["a.(Intercept)"] + random_effects_nlme[1, "a.(Intercept)"] +
    if (fct_type == 2) fixed_effects_nlme["a.feuil.resconifer"] else 0

b1_nlme = fixed_effects_nlme["b.(Intercept)"] + if (fct_type == 2) fixed_effects_nlme["b.feu
```

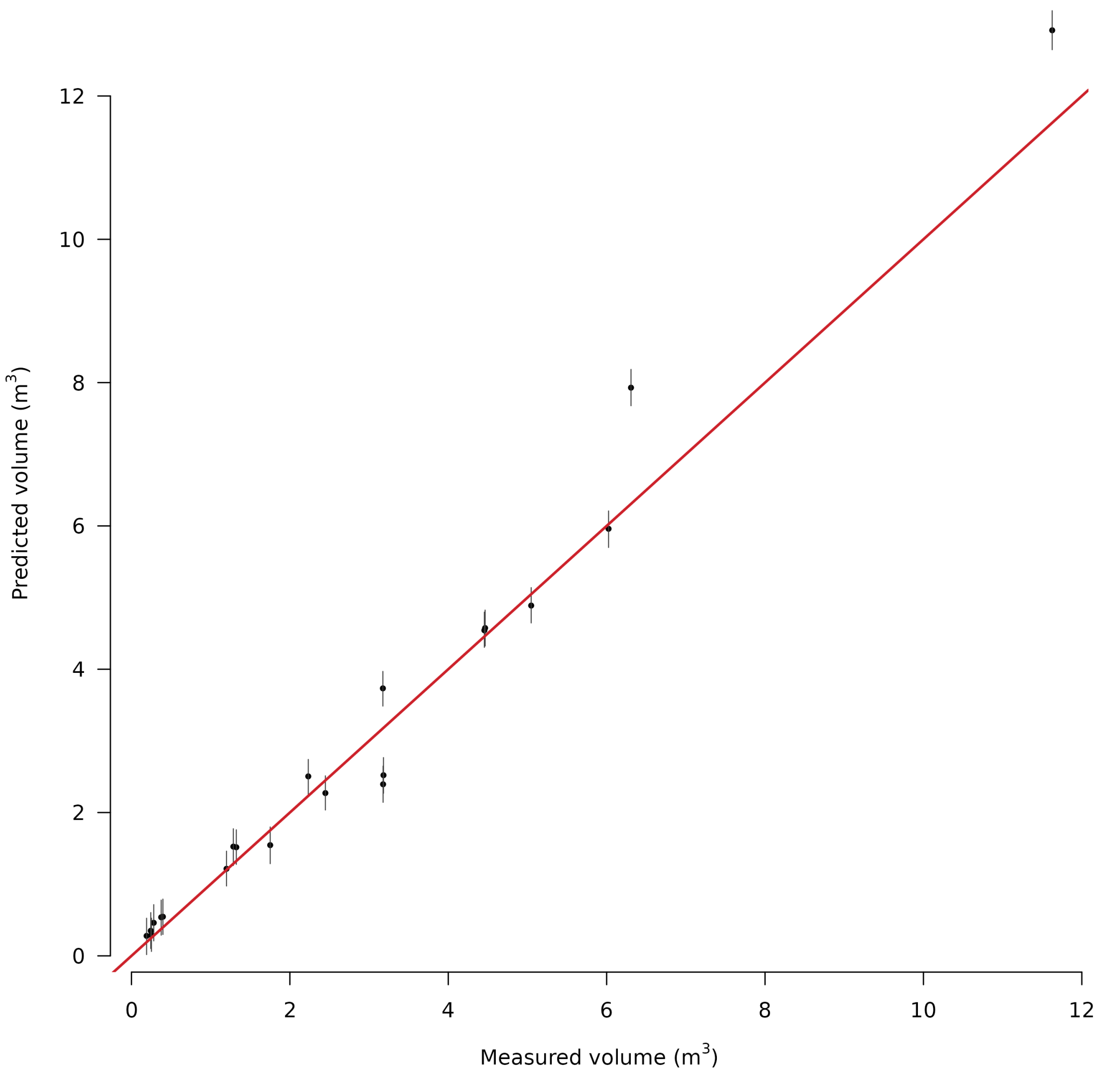


Figure 3: Predicted vs observed volume for Quercus petrae. The vertical bars are the 90% intervals

```
b2_nlme = fixed_effects_nlme["d.(Intercept)"] + random_effects_nlme[1, "d.(Intercept)"] +
    if (fct_type == 2) fixed_effects_nlme["d.feuil.resconifer"] else 0

nlme_p = round(c(beta0 = unname(b0_nlme), b1 = unname(b1_nlme), beta2 = unname(b2_nlme)), 4)

pred_nlme = predict(Modele_mai2, newdata = data_check[selected_sp])*data_check[selected_sp, 
```

Model using `lme4`

This is the equivalent model with the package `lme4`:

```
test_lme4 = lme4::lmer(formTotNew ~ feuil.res * (hdn + slenderness) + (1 + slenderness | spe
```

```
Warning: Some predictor variables are on very different scales: consider
rescaling
```

```
Warning in checkConv(attr(opt, "derivs"), opt$par, ctrl = control$checkConv, :
Model failed to converge with max|grad| = 0.599522 (tol = 0.002, component 1)
```

```
fixed_effects_lme4 = lme4::fixef(test_lme4)
random_effects_lme4 = lme4::ranef(test_lme4)$speciesName_sci[selected_sp, c("(Intercept)", "

if (nrow(random_effects_lme4) != 1)
    stop("Dimensions mismatch")

b0_lme4 = fixed_effects_lme4["(Intercept)"] + random_effects_lme4[1, "(Intercept)"] +
    if (fct_type == 2) fixed_effects_lme4["feuil.resconifer"] else 0

b1_lme4 = fixed_effects_lme4["hdn"] + if (fct_type == 2) fixed_effects_lme4["feuil.resconife

b2_lme4 = fixed_effects_lme4["slenderness"] + random_effects_lme4[1, "slenderness"] +
    if (fct_type == 2) fixed_effects_lme4["feuil.resconifer:slenderness"] else 0

lme4_p = round(c(beta0 = unname(b0_lme4), b1 = unname(b1_lme4), beta2 = unname(b2_lme4)), 4)

pred_lme4 = predict(test_lme4, newdata = data_check[selected_sp])*data_check[selected_sp, co
```

Comparison of the predictions

I plot on this figure the predictions for `Quercus robur_petraea` (is it a hybrid?) for both the baysian and the `nlme` model. As can be seen, they are quite similar:

However, the parameter values (displayed in Table 1 for `Quercus robur_petraea`, but the conclusion is the same for all species) are quite different, which proves that the parameter set is not unique. Therefore, I would not recommend this model:

Table 1: Parameter values for both models

Parameter	nlme	Bayesian
β_0	0.5795	0.3669
b_1	0.5471	3.6992
β_2	-0.0025	8×10^{-4}

Residuals

And here are the residuals computed as the mean of the bayesian simulation minus the observed:

Deleuze, Christine, François Morneau, Jean-Pierre Renaud, Yannick Vivien, Michaël Rivoire, Philippe Santenoise, Fleur Longuetaud, Frédéric Mothe, Jean-Christophe Hervé, and Patrick Vallet. 2014. "Estimer le volume total d'un arbre, quelles que soient l'essence, la taille, la sylviculture, la station." *Rendez-Vous Techniques de l'ONF* 44: 22–32.

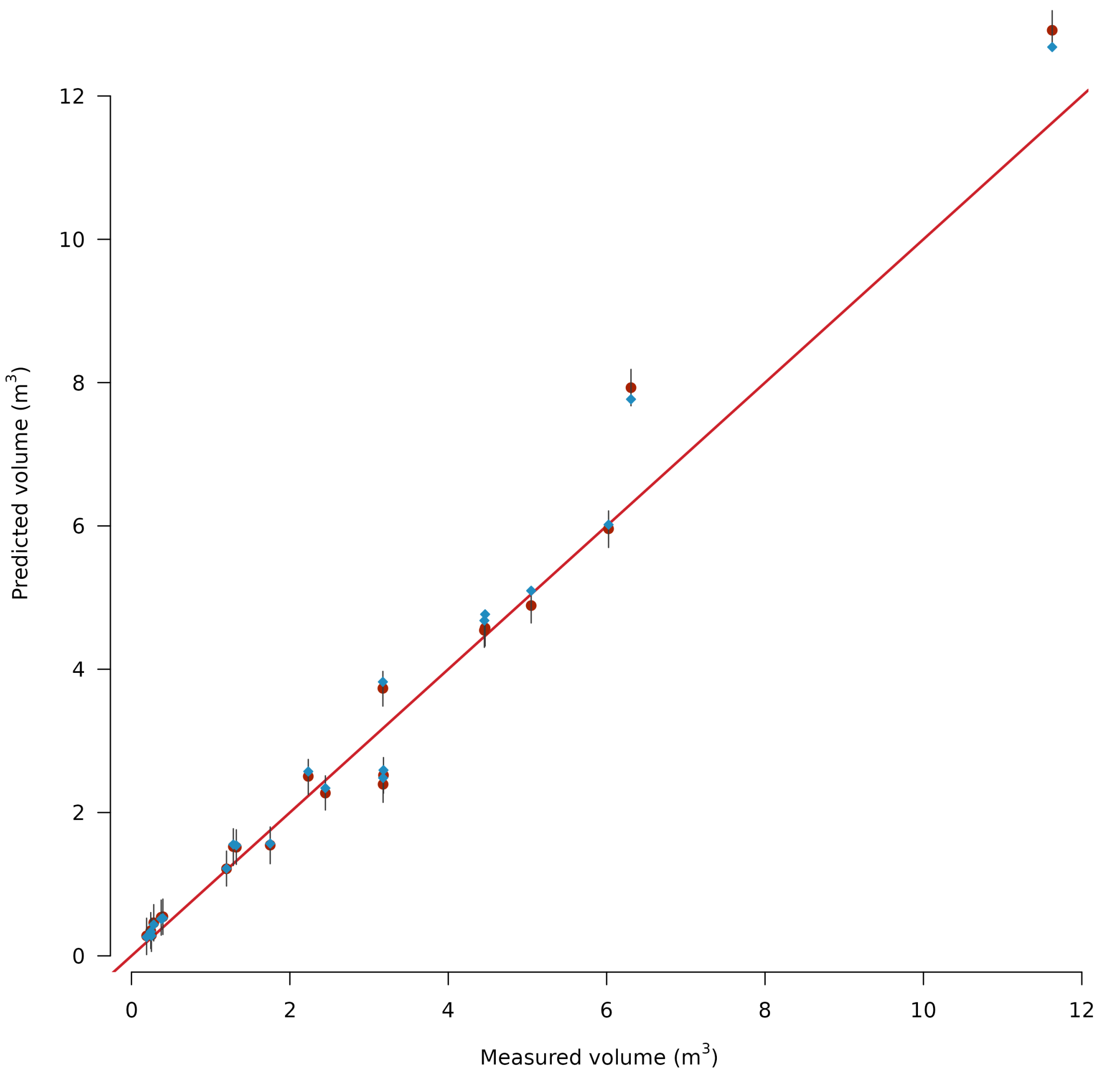


Figure 4: Predicted vs observed volume for Quercus robur_petraea (in red, bayesian model, and in blue, nlme). The vertical bars are the 90% intervals