

# Summary

## Introduction

Functional Ecology → Functional Traits

From Hutchinson definition of niche (Hutchinson, 1957), Violle and Jiang (2009) extended the definition to a multi-dimensional volume, called the "functional space" ; it is an n-dimensional space defined by measures on n traits. In such a space an individual is defined by all the values of its traits, each one on a distinct axis; a species niche would then be the average of trait values of all individuals of the species. In three dimensions, the species niche would be the volume encompassing all its individuals; the center of gravity of the cloud would be the species average trait values, defining niche position, while the shape of the general "cloud" would define niche breadth, as suggested by Violle and Jiang (2009).

The concept of functional niche helps understand community ecology and assemblage. In this view, two species would coexist if their functional volumes would not intersect. The high number of dimensions, i.e. traits, of the functional "hyper-volume" as called by [citation needed] makes it difficult to apprehend: the volume may have "holes" where some trait combinations are impossible. An individual is located by its own trait values or relatively to its species average. The distance from species average translates the intra-specific variability in the species.

Species functional niche reflects their ecological strategies. For plants, four traits have been identified to underline distinct strategies: the classical Leaf Area - Height - Seed mass triangle, suggested by [citation needed].

Diameter Growth & Tropical Forests → French Guiana Context

We assume that species niche do not evolve dramatically over time, otherwise we would expect species to change their traits continuously. As there is no such thing as "darwinian demon" that would be perfectly fit to its environment [citation needed]. Resource and energy trade-offs limit the capacity of species to evolve [citation needed].

Several growth models created, used → estimate growth using measured traits

In tree growth model, intra-specific variability is rarely considered, i.e. all individuals of the same species share the average species trait value.

However, there is trait variability, intra-specific variability. What importance does it have? To what extent is it important to consider it?

Being different from mean species trait → importance?

## Materials and Methods

### Data Provenance

#### Growth Data

The first data set is an inventory of all trees over 10cm in Diameter at Breast Height (DBH), i.e. measured at 1.3m high, in nine 1-ha plots in French Guiana (see map [missing figure]). In each plot, trees diameter were measured every two or five years depending on the plot.

We selected a common measured period between 2001 and 2013 comprising a total of 3549 trees; we estimated annual growth rate (AGR) in diameter by fitting a linear regression of DBH over years. The slope of the regression gave us an "average" AGR for each followed tree on the comprised

Trait Name	Units	Role
Trunk bark thickness	mm	Defence, Stem economics spectrum
Xylem density (wood density)	$\text{g.cm}^{-3}$	Stem economics
Specific Leaf Area (SLA)	$\text{cm}^2.\text{g}^{-1}$	Leaf economics
Laminar total chlorophyll	$\mu\text{m}.\text{mm}^{-2}$	Leaf economics
Laminar toughness	N	Leaf economics

**Table 1:** Selected functional traits.

## Trait Data

The second data set comes was a collection of five functional traits (see [Table 1](#)) extracted from a bigger database ([Baraloto et al., 2010a,b](#)) on the same trees. Traits were not followed through time and measured only once. Selected traits are related to leaf and wood economics spectrum.

## Growth model

To predict the growth of tree from a single trait we used a linear mixed-model with the general formula:

$$\log(\text{AGR}_{i,s,p} + 1) = \theta_0 + \gamma_{0,s} + \gamma_p + (\theta_1 + \gamma_{1,s}) \times \text{DBH} + (\theta_2 + \gamma_{2,s}) \times \log(\text{DBH}) + \delta + \epsilon_i, \quad (1)$$

with  $\epsilon_i \sim \mathcal{N}(0, \theta_3)$  the individual residual, where  $\text{AGR}_{i,s,p}$  is the AGR of tree  $i$  of species  $s$  in plot  $p$ ;  $\theta_0 \dots \theta_3$  are parameters to be estimated;  $\gamma_{0,s} \dots \gamma_{2,s}$  and  $\gamma_p$  follow a centered Gaussian distribution with unknown variances  $\sigma_{0,s}^2 \dots \sigma_{2,s}^2$  and  $\sigma_p^2$ ;  $\text{Tr}_s$  is the average trait value for species  $s$ .

To understand how the distance to species average value affected the predicted growth, we used different  $\delta$  values:  $\theta_4 \times \text{Tr}_s$  the species average value, with a parameter  $\theta_4$ ;  $\theta_4 \times \text{Tr}_s + \theta_5 \times (\text{Tr}_i - \text{Tr}_s)$  the distance of individual trait value  $\text{Tr}_i$  to species average, with the species term  $\text{Tr}_s$ ; or  $\theta_4 \times \text{Tr}_s + \theta'_5 \times |\text{Tr}_i - \text{Tr}_s|$  the absolute distance to species average trait, with the species term  $\text{Tr}_s$ ; or  $\theta'_4 \times \text{Tr}_i$  the individual trait value.

Our models tested the difference of prediction between using only the species average trait value to predict growth and the same term plus an individual distance term (real or absolute) vs. the individual trait value.

## Data analysis

All data analyses were made using [R Core Team \(2015\)](#), plots were made with [Wickham \(2009\)](#). We fit mixed-models with "lme4" R package ([Bates et al., 2014](#)) and computed adapted R-squared for mixed-models ([Nakagawa and Schielzeth, 2013](#)) implemented in "MuMIn" R package ([Bartón, 2015](#)).

## Results

## Discussion

## Authors Contributions and Acknowledgments

## References

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