

# Biomass estimation as a function of vertical forest structure and forest height. Potential and limitations for Radar Remote Sensing.

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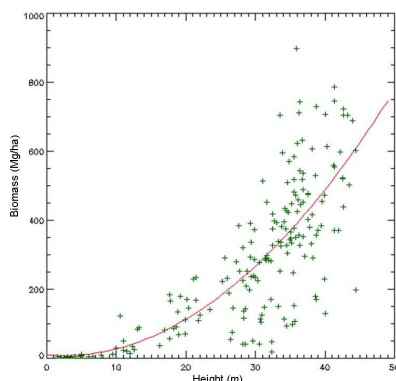
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## Abstract

One common method to estimate biomass is measuring forest height and applying allometric equations to get forest biomass. Conditions like changing forest density or changing forest structure bias the allometric relations or biomass estimation fails completely. Remote sensing systems like SAR or LIDAR allow to measure vertical structure of forests. In this paper it is investigated whether vertical structure is sensitive to biomass. For this purpose vertical biomass profiles were calculated using forest inventory data. Fourier and Legendre decomposition were tested and finally, vertical structure was quantified by decomposing the biomass profiles by means of Legendre polynomials. This is a case study based on inventory data from the Traunstein test site, a temperate mixed forest, located in the southeast of Germany.

## 1. Introduction

Forest biomass stock and spatial distribution is still an unknown parameter for many forest regions of the world. Today's information is largely based on ground measurements on a plot basis without remote regions coverage. At the same time, magnitude, location and causes of several terrestrial carbon sinks are not well quantified [1]. Thus, a method capable of quantifying biomass by means of Remote Sensing could help to reduce these uncertainties and contribute to a better understanding of the carbon cycle.



**Figure 1. Height-Biomass relation on forest level.**

In this paper, a new approach for biomass estimation based on the vertical forest structure is proposed. This approach, can be implemented by remote sensing sys-

tems, like multibaseline SAR or LIDAR, being able to resolve the vertical structure of forests.

The investigations are based on inventory data from the Traunstein test site, a highly structured temperate mixed forest situated in the south east of Germany. On the test site 231 ground plots (0.05 ha) on a 100m by 100m grid were measured. Main tree species are Norway spruce (*Picea abies*), beech (*Fagus sylvatica*) and silver fir (*Abies alba*). The maximum biomass per plot is 800 Mg/ha with a forest maximum measured height of 45 m. Average tree Biomass level is around 350 Mg/ha.

### 1.1 Biomass a function of Height

In [9] a biomass estimation using the allometric relationship between biomass and forest height from ground inventories has been proposed:

$$B = 1.66 H^{1.58} \quad \text{Eq.1}$$

where  $B$  is the biomass and  $H$  forest top height.

This approach performs best for fully stocked single species even-aged forest systems, while changes in density and structure due to management, disturbances, or species composition introduce significant deviations. Figure 1 shows the height to biomass relation for Traunstein test site, where biomass saturation achieves high values (~800 Mg/ha, for 0.05 ha plots). However, in this scenario the changing conditions of the forest in terms of density, tree species composition and management system limit the accuracy using Equation 1 to estimate biomass from height measured

by remote sensing techniques like Pol-InSAR [1]0- [7]. Forest structure heterogeneity increases the variance in the height to biomass allometry so that the relationship between height and biomass becomes inaccurate for complex forest systems, as in the case of Traunstein test site.

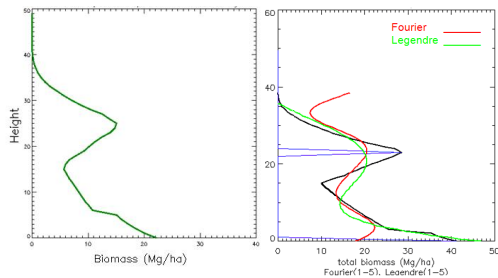
To improve biomass estimation accuracy in heterogeneous forest systems, additional forest parameters need to be measured. While density or species composition are rather difficult to be estimated by SAR, Multibaseline (Pol-In) SAR techniques are able to resolve forest vertical structure [2][3]0[5][8][10] [11][12]. It can be hypothesized that vertical forest structure is a suitable predictor for forest biomass from itself but also as it is related to density and spatial species composition.

In this context, the main objective of the present study is to investigate whether vertical forest structure, at a plot level, is linked to total biomass and to develop a methodology for estimation above-ground biomass from forest structure parameters.

## 2. Biomass Profiles

### 2.1 Physical interpretation.

Forest structure depends on competition amongst trees and their static characteristics. Competition is based on the availability of three types of resources: nutrients, light and water. Thus, the capacity of the trees to assess them, defines their form and height, leading to a characteristic spatial distribution within the forest. Accordingly, an important factor that impacts the structural evolution of a forest is the limited availability of resources determining the amount of biomass that an ecosystem can produce.



**Figure 2. Biomass profiles. Left: sample vertical biomass profile; right: Reconstruction of biomass profiles with 5 Legendre components (green) and Fourier coefficients (red).**

Forest structure changes in time due to mainly forest growth and dieback but also by human impact (logging and harvesting) and other calamities (fire, storm damages or insect diseases...). Hence, a stand with a constant top height changes as the different components of the system (trees) change and occupy the available space, depending on the ongoing processes or disturbances. The theory of allometry is based on the relations between living organisms to derive bio-

mass from single variables, like ground measured height [9].

### 2.2 Biomass Profiles.

Above-ground biomass of a single tree can be divided into two main components: crown and stem. As the exact biomass content of a stand is a parameter that requires intensive measurements, allometric relations are used to define the biomass of stems and crowns. Allometric equations are species dependent and are chosen to fit best to the growing conditions found in the test site [13][14]. Defining the form of stem and crown as well as amount of biomass per compartment for every tree, a vertical biomass distribution in 1m steps is given.

A vertical biomass profile is obtained by summing up the biomass of all trees within a measurement plot (0.05ha) in 1m steps along height (see Figure 2-left).

Profiles can be characterized by decomposing them into a set of basis functions. Two sets of functions have been applied: Fourier and Legendre series.

Fourier series: a biomass profile function  $B(z)$  is expressed by a set of sines and cosines functions:

$$B(z) = \frac{a_0}{2} - \sum_{n=1}^{\infty} a_n \cos(nz) + \sum_{n=1}^{\infty} b_n \sin(nz) \quad \text{Eq.2}$$

where:

$$\begin{aligned} a_0 &= \int_{-\pi}^{\pi} B(z) dz \\ a_n &= \int_{-\pi}^{\pi} B(z) \cos(nz) dz \\ b_n &= \int_{-\pi}^{\pi} B(z) \sin(nz) dz \end{aligned} \quad \text{Eq.3}$$

The profile is assumed to be represented within one period  $[-\pi, \pi]$ . The Legendre series  $B(z)$  described as [2][10][11]:

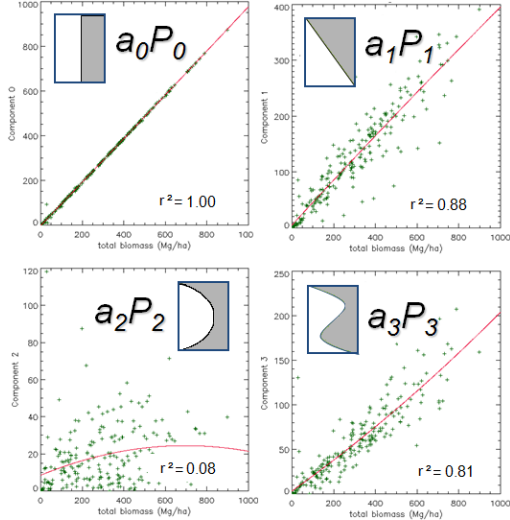
$$\begin{aligned} B(z) &= \sum_n a_n P_n(z); \quad \text{where :} \\ a_n &= \frac{2n+1}{2} \int_{-1}^1 B(z) P_n(z) dz \end{aligned} \quad \text{Eq.4}$$

where  $a_n$  is the Legendre coefficient and equation 5 shows the Legendre polynomial up to the fourth order as a function of height:  $P_k(z)$  where k stands for the order (0 to 4).

$$\begin{aligned} P_0(z) &= 1 \\ P_1(z) &= z \\ P_2(z) &= \frac{1}{2}(3z^2 - 1) \\ P_3(z) &= \frac{1}{2}(5z^2 - 3z) \\ P_4(z) &= \frac{1}{8}(35z^2 - 30z + 3) \end{aligned} \quad \text{Eq.5}$$

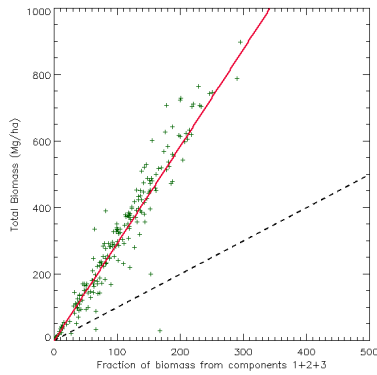
The ability of both methods to reconstruct vertical biomass profiles is compared in Figure 2-right. Legendre polynomials tend to reconstruct the original

profile with fewer components and adopt better the main features of the profile (especially in the bottom a top of the curve). Fourier reconstruction tends to underestimate biomass in the lower parts of the profile and overestimate in the upper because it is forced to keep the same value at the beginning and the end of the period. Thus Legendre polynomials are chosen for a further analysis.



**Figure 3. Correlation of the biomass represented by individual Legendre Components (0, 1, 2 and 3) versus total biomass..**

The first Legendre component  $P_0(z)$  describes a box with the same integral as the vertical biomass profile.  $P_1(z)$  to  $P_3(z)$  describe vertical structure as the proportion of the total biomass accounted by each polynomial (see Figure 3). For the rest of the polynomials any correlation with the total biomass was found.



**Figure 5. Biomass represented by Legendre Coefficient 1 to 3; Correlation coefficient  $r^2=0.92$ .**

### 3. Validation

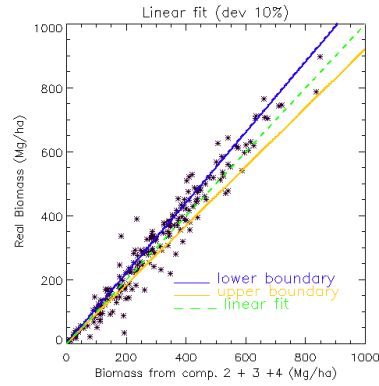
$P_1(z)$  to  $P_3(z)$  cover the structural parameter sensitivity to total biomass. They were used to investigate

the structure to biomass relationship. In Figure biomass covered by Legendre polynomial  $P_1(z)$  to  $P_3(z)$  is plotted against total biomass describing a linear relationship, which can be described by:

$$B = 2.88 \sum_{i=0}^H \sum_{j=1}^3 a_j \cdot P_j \quad \text{Eq.6}$$

$B$  is the biomass in Mg/ha,  $H$  the height of the profile in m;  $a$  the Legendre coefficient,  $i$  the samples along height (intervals of 1m),  $P$  the Legendre polynomial and  $j$  the order of the Legendre polynomial.

The correlation coefficient is with an  $r^2$  0.92 very high proofing a strong relation amongst the two parameters.



**Figure 4. Measured (real) biomass vs. estimated biomass; Performance analysis for 10% standard deviation for each component with lower (yellow) and upper (blue) boundary of the fitted line.**

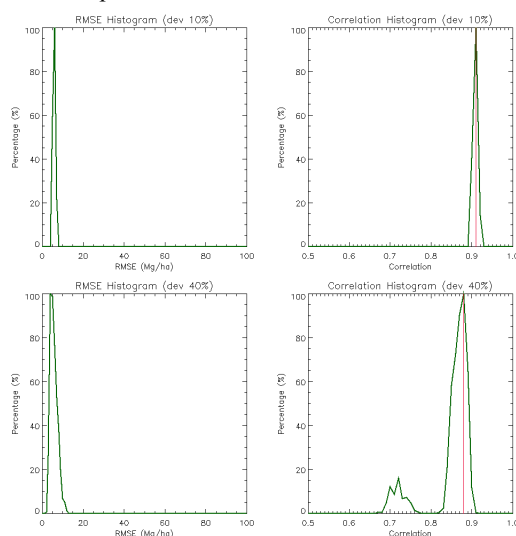
To test the robustness of Equation 3 a performance analysis by means of a Monte Carlo simulation was performed. For this purpose, deviations of 10%, 20%, 30% and 40% from the real values (assuming a Gaussian distribution) were added on the Legendre coefficients  $a_1$  to  $a_3$  and on forest height. Results from error analysis are summarized in Table 1.

**Table 1. Results of performance analysis (Monte Carlo simulations).**

Deviation	RMSE (Mg/ha)			$r^2$		
	Min	Max	Mean	Min	Max	Mean
10%	4	6	5	0.89	0.93	0.91
20%	3	10	6	0.87	0.94	0.90
30%	2	11	6	0.85	0.92	0.89
40%	1	13	7	0.68	0.81	0.88

Figure 4 shows results of the Monte Carlo simulation for the 10% error. The blue and yellow lines show the fitted lines for the maximum deviations. Changes in the Correlation coefficient and in the root mean square error (RMSE) are shown in Figure 6. For the 10% error case (Figure 6 top) the RMSE moves

around 5Mg/ha with  $r^2$  around 0.91(see Table 1). For a 40% error (Figure 6 bottom-left) the RMSE increases until 7 Mg/ha with a low variance. The correlation coefficient decreases to 0.88 with high variance and showing a second relative maximum in 0.73 (Figure 6 bottom-right). Monte Carlo simulations show that biomass reconstruction is stable at least for deviations up to 30%.



**Figure 6. Histograms of performance analysis with 10 % error in the upper line and 40% in the lower; left: Root Mean Square Error (RMSE); right: Correlation Coefficient**

## 4. Conclusions.

The results of this study indicate a strong relation between vertical structure of forests and above-ground biomass. Compared to a simple height to biomass relation the correlation is significantly improved, from a correlation coefficient  $r^2$  0.52 to  $r^2$  0.92.

Legendre polynomials are performing well when used to describe vertical forest structure. Biomass is primary related to low frequency Legendre components. There is also a strong indication that the polynomials up to the third order are sufficient to describe vertical forest structure for biomass estimations. The investigation was done on inventory data from a single test site. Validity of this approach needs to be tested on a larger range of forest conditions.

It was shown that the approach is quite stable, even errors of 30% led to acceptable results.

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