Appendix 3

Detailed information on the methods used for investigating the relationship between the variability in ΔB and stand variables

1. Site index (SI) estimation for each NFI plot

For each plot SI was determined based on the method presented in Brandl *et al.* (2018): First, top height h_{top} (defined as the height corresponding to the root mean square diameter d_{top} of the top 100 diameters of a tree species on a site) was determined. Second, SI was determined by scaling the position of $h_{top}(i)$ between a lower and upper boundary height at age i with the ratio of the span between lower and upper boundary height at age 100 and the span between lower and upper boundary height at age i (Fig. A3.1):

$$\widehat{SI} = h_{top\,l(100)} + \left(h_{top\,(i)} - h_{top\,l(i)}\right) \cdot \frac{h_{top\,u(100)} - h_{top\,l(100)}}{h_{top\,u(i)} - h_{top\,l(i)}}$$

with $h_{top\ l}$ and $h_{top\ u}$ as the lower and upper boundary height at the respective age.

Lower and upper boundary lines had been adopted from Brandl *et al.* (2018) and are described by the Chapman-Richards functions (Richards, 1959):

$$h_{top\,(i)} = A * \left(1 - e^{-k * age_i}\right)^p$$

with A = 42.014, k = 0.029 and p = 1.048 for the upper boundary line and with A = 26.159, k = 0.045 and p = 2.346 for the lower boundary line.

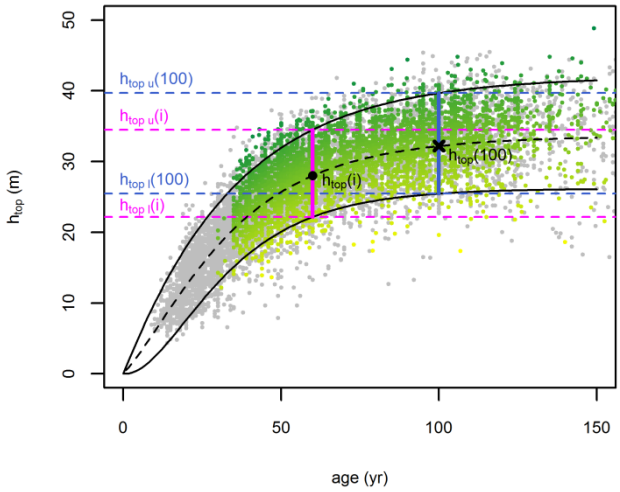

Figure A3.1. Illustration of translating the top height $h_{top}(i)$ of a NFI plot of age i to the corresponding height $h_{top}(100)$ at the reference age of 100 years i.e. the SI; green points mark heights and ages of NFI plots used in the study; grey points correspond to the data used for the determination of the boundary lines (solid black curves); the black dot marks an example stand at age 60 with a top height of 28 m. The black cross marks its translation to h_{top} at age 100, resulting in a SI of about 32 m.

2. Generalized additive model (GAM): ΔB in dependence on SI and stand age

A GAM was fitted explaining ΔB in dependence on SI and stand age using the package mgcv (Wood, 2011) in R 3.3.2 (R Core Team, 2016) (Table A3.1; Fig. A3.2):

$$\Delta B = \exp(f(SI) + f(age) + \varepsilon)$$

The residuals of this model can be interpreted as the variation in ΔB not explained by SI and age.

Table A3.1. Detailed model summary for the GAM

	Estimate	**Standard error**	**T statistics**	**p value**
Intercept	9.0736	0.0054	1680	$< 2 \times 10^{-16}$
	edf	**df residuals**	**F statistics**	**p value**
f(SI)	4.150	5.171	131.5	$< 2 \times 10^{-16}$
f(stand age)	6.533	7.671	332.9	$< 2 \times 10^{-16}$
Adjusted R^2		0.474		

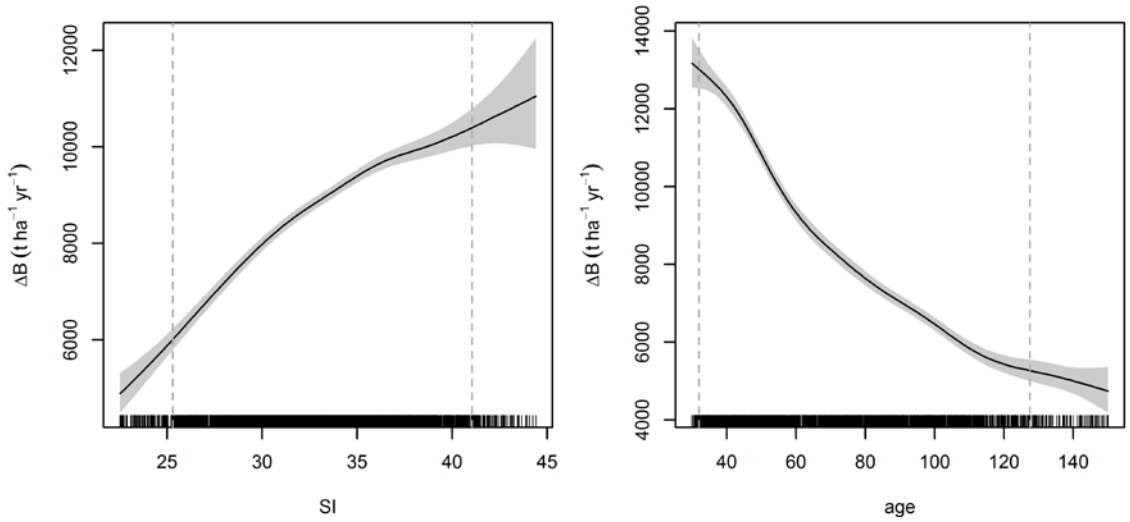

Figure A3.2. Effects of SI and stand age respectively on ΔB when the other variable is set to its mean. Grey areas comprise 95% pointwise prognosis intervals; a rug plot shows the distribution of the covariate; the vertical dashed lines mark the 2.5 and 97.5% quantiles of the covariate's distribution.

3. Quantile regression for rescaling single tree height and dbh

In order to be able to compare trees of varying ages height and dbh had to be rescaled: A 95%-quantile regression was fitted to the respective variable (height or dbh) as a fourth order polynomial of age (Table A3.2; Fig. A3.3).

$$variable = \alpha + \beta_1 age + \beta_2 age^2 + \beta_3 age^3 + \beta_4 age^4$$

The result can be interpreted as the maximum height or dbh that can be reached at a certain age. In order not to give outliers too much influence a 95%-quantile regression was used instead of simply drawing an envelope curve.

In the next step, each tree's height or dbh respectively was divided by the predicted 95%-quantile of height or dbh respectively at the tree's age. The resulting value is independent of age and can be interpreted as the percentage of the maximum height or dbh a tree can reach.

Table A3.2. Estimates of coefficients and statistical characteristics of the quantile regressions on height and dbh

	coefficient	Estimate	Standard error	T Statistics	p value
height	α	7.50790	1.83909	4.08240	0.00004
	β_1	0.83118	0.10557	7.87308	0.00000
	β_2	-0.00939	0.00213	-4.41139	0.00001
	β_3	0.00005	0.00002	3.04934	0.00230
	β_4	0.00000	0.00000	-2.32715	0.01996
dbh	α	-17.64376	7.33892	-2.40414	0.01622
	β_1	2.55928	0.42098	6.07933	0.00000
	β_2	-0.03399	0.00852	-3.98666	0.00007
	β_3	0.00022	0.00007	3.01045	0.00261
	β_4	0.00000	0.00000	-2.33020	0.01980

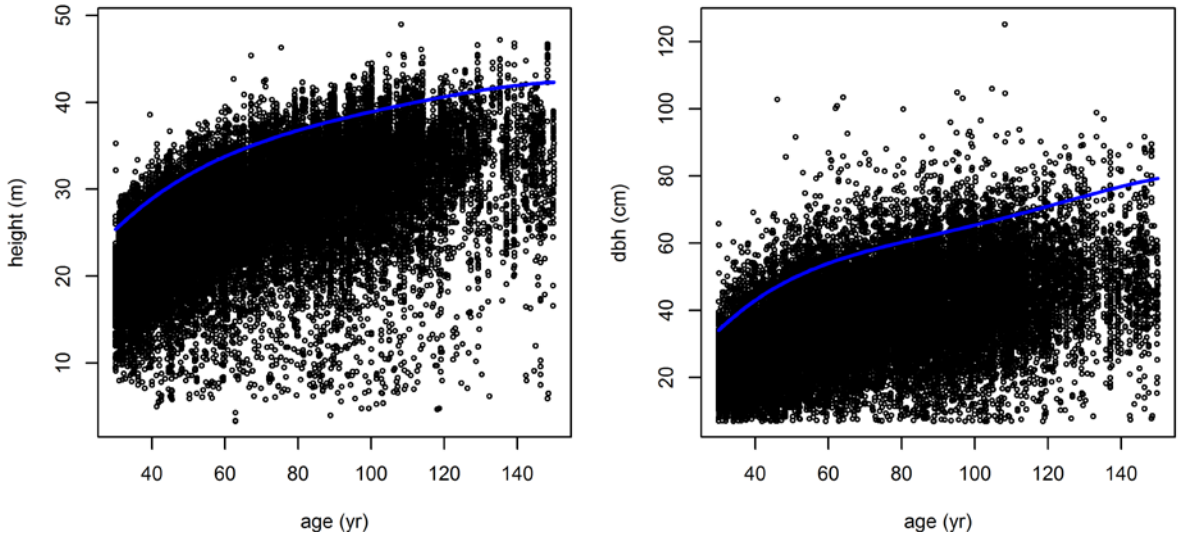

Figure A3.3. Height or dbh respectively plotted against age of single trees on NFI plots used in the study. The blue line marks the fit of the quantile regression.

References

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