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Proposals for *Nothofagus antarctica* diameter growth estimation: simple vs. global models

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ABSTRACT: Tree growth is one of the main variables needed for forest management planning. The use of simple models containing traditional equations to describe tree growth is common. However, equations that incorporate different factors (e.g. site quality of the stands, crown classes of the trees, silvicultural treatments) may improve their accuracy in a wide range of stand conditions. The aim of this work was to compare the accuracy of tree diameter growth models using (*i*) a family of simple equations adjusted by stand site quality and crown class of trees, and (*ii*) a unique global equation including stand and individual tree variables. Samplings were conducted in 136 natural even-aged *Nothofagus antarctica* (Forster f.) Oersted stands in Southern Patagonia (Argentina) covering age (20–200 years), crown class and site quality gradients. The following diameter growth models were fitted: 16 simple equations using two independent variables (age and one equation for each stand site quality or crown class) based on Richards model, plus a unique global equation using three independent variables (age, stand site quality and crown class). Simple equations showed higher variability in their accuracy, explained between 54% and 92% of the data variation. The global model presented similar accuracy like the better equations of the simple growth models. The unification of the simple growth models into a unique global equation did not greatly improve the accuracy of estimations, but positively influenced the biological response of the model. Another advantage of the global equation is the simple use under a wide range of natural stand conditions. The proposed global model allows to explain the tree growth of *N. antarctica* trees along the natural studied gradients.

Keywords: growth models; site quality; crown class

Tree growth is one of the main variables considered for the forest management planning (García 1988). In the past, it was estimated using fixed values for the whole stand level (Piterbarg 1965). During the last years, models with different complexity have been developed (Vanclay 1994), where different biometric variables of easy mensuration that influence tree growth were included (Pretzsch 2009). As abstractions of reality (Hari 1996), models try to simplify the natural complexity of the forest system (García 1988). Usually, the forest modellers made one model for each stand condition, generating the family of different equations. However, the challenge of tree growth modelling resides in isolating the main variables, and including them in a unique model with an acceptable error of estimation (Martínez Pastur et al. 2008).

Tree growth follows a sigmoid curve responding to environmental trends and fluctuations, however, this long-term pattern remains surprisingly stable (Zeide 1993). Many equations have been proposed to describe this tree growth pattern (e.g. Richards 1959) mainly based on proportionality of growth to tree age, as well as to crown class and stand site quality (Zeide 1993; Vanclay 1994; Martínez Pastur et al. 2008). Simple models

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using traditional equations are commonly used to describe tree growth (e.g. Crecente-Campo et al. 2010; Vanclay 2010), but families of equations that incorporate different factors (e.g. site quality of the stands, crown classes of the trees, silvicultural treatments) improve the accuracy of growth estimation at a landscape level (Martínez Pastur, Fernández 1997; Trasobares et al. 2004; Adame et al. 2008; Subedi, Sharma 2011).

Another option is to modify the traditional equation proposals by the inclusion of more variables, e.g. Ek (1971) was the first who proposed to incorporate the site index with the age to estimate height growth, which was successfully used for several forest timber species during the last decades (Payandeh, Wang 1994; Wang, Payandeh 1994). These models were also successfully applied for native *Nothofagus* forests in Southern Patagonia (Martínez Pastur et al. 1997, 2005, 2008; Lencinas et al. 2002; Ivancich et al. 2011) and were used for different purposes around the world during the last 20 years. The aim of this work was to compare the accuracy of both proposals using (*i*) the family of simple equations adjusted by stand site quality and tree crown classes, and (*ii*) a global unique equation including both stand and individual tree variables. The following questions were asked: (*i*) Is it possible to simplify the diameter growth model estimation using a unique global equation instead of a family of simple equations? (*ii*) Does this simplification greatly influence the accuracy of the estimation? and (*iii*) Does this simplification influence the biological response of the models?

MATERIAL AND METHODS

Data and forest structure characterization. Samplings were conducted in 136 natural even-aged *Nothofagus antarctica* (Forster f.) Oersted stands in Southern Patagonia (Argentina): (1) Santa Cruz (51°13'–51°41'S, 72°15'–72°03'W) and (2) Tierra del Fuego (53°54'–54°28'S, and from 66°44' to 67°42'W). Sampling was designed to cover the natural species gradients of: (*i*) age (20 to 220 years) and (*ii*) site quality of the stands. Site quality (SQ) followed the proposal of Ivancich et al. (2011), who used a site index at the base age of 50 years (SI_{50}): 1 = $SI_{50} > 9.3$ m, 2 = $SI_{50} > 7.2$ and ≤ 9.3 m, 3 = $SI_{50} > 5.1$ and ≤ 7.2 m, 4 = $SI_{50} \leq 5.1$ m, and age measured at a height of 1.30 m (diameter at breast height, DBH). Sampling included only stands with arborescent morphotype trees (Ramírez et al. 1985; Donoso 2006). In each stand, one forest inventory plot was measured by point sampling method using Criterion RD-1000 (Laser Technology, Inc., Centennial, USA) with a variable K coefficient between 3 and 6 (Bitterlich 1984). Sampling areas were selected according to the following requirements: (a) homogeneous and even-aged patches, (b) stocked areas without canopy gaps, (c) areas without presence of recently dead trees, and (d) K coefficient that allows the sampling of 10–15 trees in each plot. All trees were sampled with an increment borer, and their DBH using a diameter tape and total height (TH) using a TruPulse 200 hypsometer (Laser Technology, Inc., Centennial, USA) were measured and they were classified by crown classes (dominant, co-dominant, intermediate and suppressed). Only one core was taken with the borer from each tree, all samples being oriented to the centre of the plot. In each core, tree-rings were counted, measuring 4-year periodic growth during the last 20 years. It was considered that during this period mortality did not occur due to the absence of dead trees in the sampled area. We also estimated density (DEN), basal area (BA), total over bark volume (TOBV) (according to Lencinas et al. 2002), percentage of stand density index (%SDI) (according to Ivancich et al. 2009) and site quality of the stands, using the stand age and the height of 2–3 dominant trees (according to Ivancich et al. 2011).

Data analyses. Data base included 8,059 age-DBH points belonging to 1,635 trees along the sampled site quality, age and crown class gradients (4–5 pseudo-replicates of 4-year period for each tree). Diameter growth models were fitted using this data base: (*i*) a family of 16 simple traditional equations (4 stand site qualities × 4 tree crown classes) based on Richards model (Richards 1959; Rayner 1991; Zeide 1993) with 1 independent variable (age) (Eq. 1), which was successfully used previously for *N. antarctica* by Martínez Pastur and Fernández (1997), and (*ii*) a global unique equation based on Martínez Pastur et al. (2005) with 3 independent variables (age, stand site quality and tree crown class) (Eq. 2). This latter model is a modification of Richards equation based on previous successful proposals (Ek 1971; Payandeh, Wang 1994; Wang, Payandeh 1994).

$$DBH = a(1- n^{(-bt)})^c \tag{1}$$

where:

DBH – diameter at breast height (cm),
a–c – parameters of the equation,
n – base of natural logarithm,
t – age (yr).

$$\mathrm{DBH} = (a(5-\mathrm{CC})^b)(c(6-\mathrm{SQ})^d)(1-n^{(-et)})^{(f(6-\mathrm{SQ})^g)} \qquad (2)$$

where:

DBH – diameter at breast height (cm),

a–g – parameters of the equation,

n – base of natural logarithm,

t – age (yr),

CC – crown class of the trees (1 – dominant, 2 – co-dominant, 3 – intermediate, 4 – supressed),

SQ – site quality of the stands (1 = SI_{50} > 9.3 m, 2 = SI_{50} > 7.2 and ≤ 9.3 m, 3 = SI_{50} > 5.1 and ≤ 7.2 m, 4 = SI_{50} ≤ 5.1 m).

Statistical evaluation of the models. The model was fitted with non-linear regression using the Marquardt algorithm (Fekedulegn et al. 1999; Lei, Zhang 2004; Khamis et al. 2005). Adjusted R-squared (R^2-adj), estimation mean error (EME) (Eq. 3), absolute mean error (AME) (Eq. 4), and residual standard error (RSE) (Eq. 5) were employed to describe the model adjustment. Residual analyses along stand site qualities and DBH frequencies of the trees were conducted using EME and AME (Eq. 3 and 4), and also expressed as a percentage of the predicted DBH (6 and 7).

$$\mathrm{EME} = \Big(\sum_{i=1}^{n} e_i\Big)/n \qquad (3)$$

$$\mathrm{AME} = \Big(\sum_{i=1}^{n} |e_i|\Big)/n \qquad (4)$$

$$\mathrm{RSE} = \sqrt{\Big(\sum_{i=1}^{n} e_i\Big)^2/n} \qquad (5)$$

$$\mathrm{EME}\ (\%) = \Big(\sum_{i=1}^{n} e_i/x_i\Big)/n \qquad (6)$$

$$\mathrm{AME}\ (\%) = \Big(\sum_{i=1}^{n} |e_i/x_i|\Big)/n \qquad (7)$$

where:

n – number of observations,

e_i – residual (observed – predicted values),

x_i – DBH of the trees.

The model also was analyzed according to its biological response along the studied natural gradients, and not only by the statistics. For the biological responses we consider the shape of the curves compared with the other curves in the gradients (e.g. site quality and crown classes) as well as interactions among them.

RESULTS

Forest structure and data characterization

The forest structure changed along site quality gradients and age of the stands (Table 1). In general, while DBH, basal area and total over bark volume increased with age and decreased with stand site quality, density showed the opposite trend. The stand density index tended to increase with age, and then to decrease in the high site quality stands, while it maintained or increased its values in medium and low site quality stands.

Table 1. Forest structure (mean ± standard deviation) of sampling plots classified by stand site quality and age (years)

Site quality	Age	N	DBH (cm)	DEN (thousand·ha^{-1})	BA (m^2·ha^{-1})	TOBV (m^3·ha^{-1})	SDI (%)
1	< 40	4	5.5 ± 1.0	19.5 ± 6.0	44.5 ± 8.0	167.8 ± 39.9	63.2 ± 11.4
	40–80	11	10.9 ± 2.4	7.6 ± 3.6	61.6 ± 10.0	299.5 ± 48.5	87.5 ± 14.2
	80–120	6	25.6 ± 2.8	1.4 ± 0.5	68.1 ± 14.4	455.9 ± 89.5	96.6 ± 20.5
	> 120	12	38.6 ± 9.3	0.6 ± 0.2	62.1 ± 10.2	451.7 ± 80.9	88.2 ± 14.5
2	< 40	11	6.5 ± 2.0	18.0 ± 8.6	51.6 ± 14.5	176.2 ± 61.7	73.3 ± 20.5
	40–80	12	10.0 ± 2.5	7.9 ± 3.9	53.5 ± 12.5	228.4 ± 80.0	75.9 ± 17.7
	80–120	4	31.9 ± 4.3	0.8 ± 0.2	65.0 ± 12.2	411.7 ± 95.0	92.2 ± 17.4
	> 120	6	32.1 ± 10.2	1.1 ± 1.1	62.3 ± 9.0	402.6 ± 62.1	88.5 ± 12.7
3	< 40	14	5.7 ± 1.4	15.3 ± 5.3	36.9 ± 14.8	101.8 ± 51.0	52.4 ± 21.0
	40–80	15	11.5 ± 4.2	5.7 ± 4.0	43.4 ± 14.5	154.5 ± 58.3	61.7 ± 20.6
	80–120	3	28.2 ± 5.4	0.9 ± 0.4	53.7 ± 1.5	285.2 ± 21.9	76.2 ± 2.2
	> 120	10	35.1 ± 4.5	0.8 ± 0.4	71.5 ± 11.2	426.7 ± 47.4	101.5 ± 15.9
4	< 40	3	7.1 ± 3.7	13.8 ± 5.4	49.2 ± 31.9	104.0 ± 66.2	69.8 ± 45.3
	40–80	5	12.6 ± 4.5	4.8 ± 3.4	44.0 ± 7.9	123.7 ± 25.8	62.5 ± 11.2
	80–120	7	18.5 ± 6.4	2.7 ± 1.6	53.1 ± 11.3	192.9 ± 50.1	75.4 ± 16.0
	> 120	13	25.6 ± 7.4	1.3 ± 0.9	53.3 ± 13.4	225.0 ± 72.2	75.6 ± 19.0

1 – SI_{50} > 9.3 m, 2 – SI_{50} > 7.2 and ≤ 9.3 m, 3 – SI_{50} > 5.1 and ≤ 7.2 m, 4 – SI_{50} ≤ 5.1 m, N – number of sampled stands, DBH – diameter at breast height or 1.30 m height, DEN – tree density, BA – basal area, TOBV – total over bark volume, SDI – stand density index

The sampling included between 28 and 42 stands per each site quality (Table 1). However, age-DBH points showed an unequal distribution along the stand site quality gradient (Table 2). This sampling corresponded to the natural tree occurrence in *N. antarctica* forests of Southern Patagonia at a landscape level, where lower and upper site quality classes were less frequent (1,481 for SQ 1 and 1,614 for SQ 4 data pairs) than intermediate classes (2,420 for SQ 3 and 2,544 for SQ 2). Similarly, dominant and co-dominant trees were more represented (2,925 and 2,635 data pairs) than intermediate and supressed trees (1,710 and 789 data pairs). Finally, young trees were more frequent in the data base (2,172 and 2,182 data pairs for the tree age < 30 and 30–60 years) than older trees (1,245 and 712 data pairs for the tree age 120–150 and > 150 years).

Diameter growth models

The Family of simple traditional equations (Eq. 1) fitted for each combination of stand site quality and tree crown classes explained between 54% and 92% of the total data base variation (Table 3). The accuracy was higher in upper site quality classes than in lower site quality ones (e.g. R^2-adj varied between 75% and 92% in SQ 1, and between 54% and 62% in SQ 4). Mean error values for the entire family of simple traditional equations were: EME = 0.09 cm, AME = 4.07 cm and RSE 5.88 cm. Model Eq. 1 presented a small underestimation (observed – predicted values), where EME varied between 0.02 and 0.30 cm, being greater at lower site quality classes. AME and RSE values varied along site quality and crown class gradients (between 1.99 and 7.26 cm, and between 2.55 and 9.13 cm, respectively), being greater in upper crown classes of the trees for each stand site quality.

The global unique equation (Eq. 2) explained 83% of the total data base variation (Table 4), which approximately represented the average within the entire family of simple equations. For example, 10 simple models presented higher and 6 simple models lower R^2-adj (Table 3). Error values of the global equation were comparable with the average values of the family of simple traditional equations: EME = 0.04 cm, AME = 4.11 cm and RSE = 6.00 cm.

Observed vs. predicted values showed a typical data dispersion for forest samples, where small diameters generated less dispersion than larger ones. Both model types presented a similar pattern, where the slope of the mean values for the family of simple traditional equations (Eq. 1) was 0.993 (Fig. 1a), and 0.996 for the global unique equation (Eq. 2) (Fig. 1b).

Table 2. Tree sample distribution classified by stand site qualities and crown classes and age of sampled trees

Site quality	Crown class	Tree age (years)					
		< 30	30–60	60–90	90–120	120–150	> 150
1	DOM	97	210	70	82	120	44
	COD	105	161	78	53	66	64
	INT	55	116	41	71	36	22
	SUP	20	52	9	14	10	18
2	DOM	318	247	81	113	50	126
	COD	334	300	76	163	78	55
	INT	161	124	33	68	39	4
	SUP	56	64	26	19	5	4
3	DOM	300	278	38	33	130	61
	COD	217	239	56	46	115	33
	INT	211	186	39	31	92	63
	SUP	113	78	7	4	29	21
4	DOM	25	32	61	125	179	105
	COD	46	39	65	102	110	34
	INT	62	35	34	49	105	33
	SUP	52	20	23	39	81	25

1 – SI_{50} > 9.3 m, 2 – SI_{50} > 7.2 and ≤ 9.3 m, 3 – SI_{50} > 5.1 and ≤ 7.2 m, 4 – SI_{50} ≤ 5.1 m, DOM – dominant, COD – co-dominant, INT – intermediate, SUP – supressed

Table 3. Coefficients and statistics of diameter growth models (Eq.1) classified by stand site qualities and tree crown classes

Site quality	CC	*a*	*b*	*c*	R^2-adj	EME	AME (cm)	RSE
1	DOM	95.513	0.0056	1.197	83.3	0.11	4.69	6.88
	COD	41.261	0.0178	1.830	84.6	0.08	3.84	5.11
	INT	36.774	0.0204	2.151	74.9	0.11	4.47	5.97
	SUP	31.824	0.0155	1.753	91.8	0.06	1.99	2.55
2	DOM	223.938	0.0018	1.052	88.6	0.08	4.05	6.17
	COD	76.306	0.0069	1.377	85.5	0.11	3.61	5.38
	INT	54.353	0.0079	1.325	78.5	0.05	3.49	5.04
	SUP	46.950	0.0079	1.358	81.9	0.15	2.53	3.35
3	DOM	73.221	0.0068	1.226	85.9	0.03	3.80	5.68
	COD	51.115	0.0131	1.712	86.6	0.09	3.62	5.15
	INT	54.034	0.0094	1.527	86.0	0.04	3.45	5.02
	SUP	100.773	0.0029	1.170	87.7	0.02	2.54	3.79
4	DOM	157.349	0.0017	1.033	53.6	0.02	7.26	9.13
	COD	387.305	0.0006	1.066	61.4	0.19	4.97	6.59
	INT	506.918	0.0003	0.976	62.1	0.30	4.88	6.47
	SUP	848.988	0.0001	0.854	60.3	0.10	3.44	4.80

1 – $SI_{50} > 9.3$ m, 2 – $SI_{50} > 7.2$ and ≤ 9.3 m, 3 – $SI_{50} > 5.1$ and ≤ 7.2 m, 4 – $SI_{50} \leq 5.1$ m, CC – tree crown classes, DOM – dominant, COD – co-dominant, INT – intermediate, SUP – supressed, a–c – parameters of the equation, R^2-adj – adjusted value of the coefficient of determination, EME – estimation mean error, AME – absolute mean error, RSE – residual standard error

Biological response of the models

Diameter growth increased with: (*i*) tree age following a sigmoid shape curve, (*ii*) site quality of the stands, and (*iii*) crown classes of the trees. Generally, the performance of both models included these three key points (Figs 2 and 3). However, the global unique equation (Eq. 2) presented a more desirable biological response than the family of simple equations (Eq. 1), because each curve was proportional to site quality and crown class gradients along tree ages. Simple equations presented a non-proportional response along these gradients, including well-shaped curves (e.g. supressed, intermediate and co-dominant trees of SQ 1), and curves without a clear tendency (e.g. dominant trees of SQ 2 with a more straight line compared with the other crown classes).

It was expected that maximum annual diameter increment (MADI) values were proportional to the site quality of the stands and crown classes of the trees (Table 5). However, the different model types presented dissimilar responses: (*i*) MADI of the global equation (Eq. 2) decreased, as was expected, from high site quality stands and upper crown classes of the trees to lower site quality stands and lower crown classes of the trees; (*ii*) MADI of the family of simple equations (Eq. 1) did not present a clear tendency along the

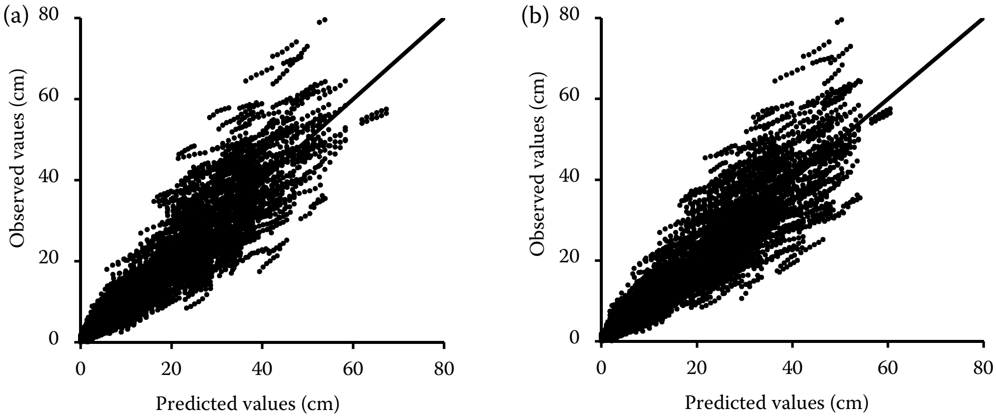

Fig. 1. Observed vs. predicted values for the family of growth models using Eq. 1 (a), and global diameter growth model using Eq. 2 (b)

Table 4. Coefficients and statistics of the global unique growth model (Eq. 2)

Coefficients	Statistics
$a = 0.5802$	R^2-adj = 83.0
$b = 0.3840$	EME = 0.04
$c = 84.1835$	AME = 4.11
$d = 0.1599$	RSE = 6.00
$e = 0.0045$	
$f = 1.3429$	
$g = -0.0111$	

a–g – parameters of the equation, R^2-adj – adjusted value of the coefficient of determination, EME – estimation mean error (cm), AME – absolute mean error (cm), RSE – residual standard error (cm)

studied gradients, where several interactions can be observed (e.g. supressed trees of SQ 4 presented higher increments than intermediate trees of the same site quality stands or supressed trees of SQ 3); and (*iii*) for the entire age period MADI increased with SQ but not varied among crown classes in the unique global equation (Eq. 2), while the family of simple equations (Eq. 1) did not present a clear gradient with SQ and crown classes of the trees, where several interactions were observed.

Residual analyses

Residual analyses were done using the same data base (auto-validation) in order to compare the response of both model proposals along site quality and DBH frequencies (Fig. 4). Both model types presented similar responses: (*i*) when EME were analysed, both models overestimated at low DBH frequencies (< 30 cm) and underestimated at high DBH frequencies (> 30 cm) along all the site quality gradient; (*ii*) EME increased when site quality decreased at high DBH frequencies (> 30 cm); (*iii*) AME (cm) increased with DBH frequency and was slightly higher in the family of simple equations (Eq. 1) than in the global equation (Eq. 2); and (*iv*) in general AME (%) decreased with DBH frequencies and increased with site quality of the stands.

DISCUSSION

Forest structure and data base characterization

The sampling included the entire natural gradient of the *Nothofagus antarctica* in Southern Patagonia (Peri et al. 2010) from stands with high to low SQ, and young secondary to old-growth mature stands. Maximum tree ages reached 200 years, being much lower than other Patagonian *Nothofagus* species. On example, *N. pumilio* and *N. betuloides* trees reached 400–500 years of age (Donoso 2006; Martínez Pastur et al. 2008). The stands with low representation were those belonging to the lower site quality classes, because they were usually growing in extreme environmental conditions (low rainfall or areas exposed to strong winds).

Most of the forest growth studies selected individual trees for sampling (Klepac 1976; Everard, Christie 1995; Kariuki et al. 2006; Derose, Seymour 2009) according to their health and

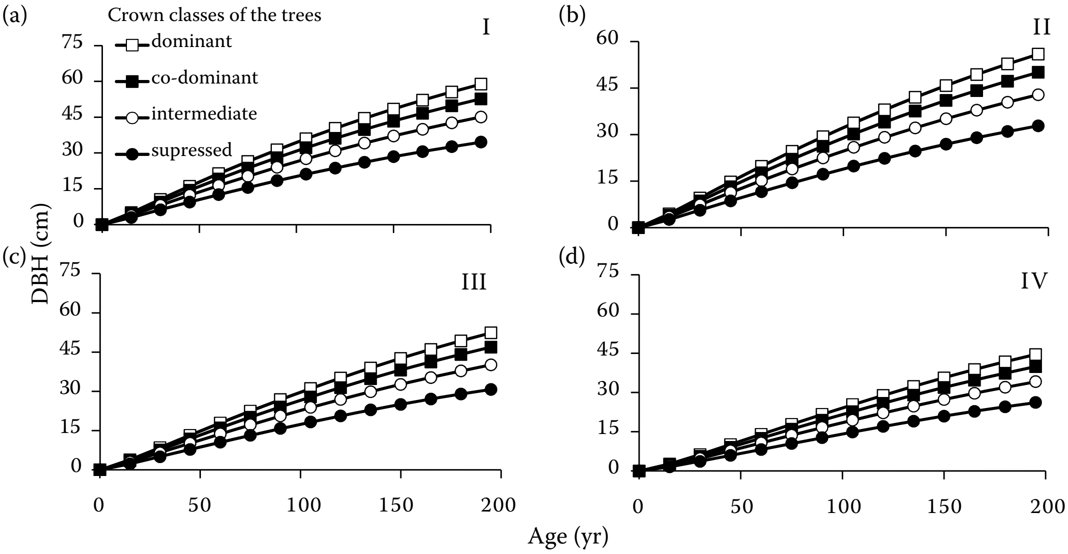

Fig. 2. Diameter simple growth models (Eq. 1) classified by site quality of the stands (I – SI_{50} > 9.3 m, II – SI_{50} > 7.2 and ≤ 9.3 m, III – SI_{50} > 5.1 and ≤ 7.2 m, IV – SI_{50} ≤ 5.1 m) and crown classes of the trees

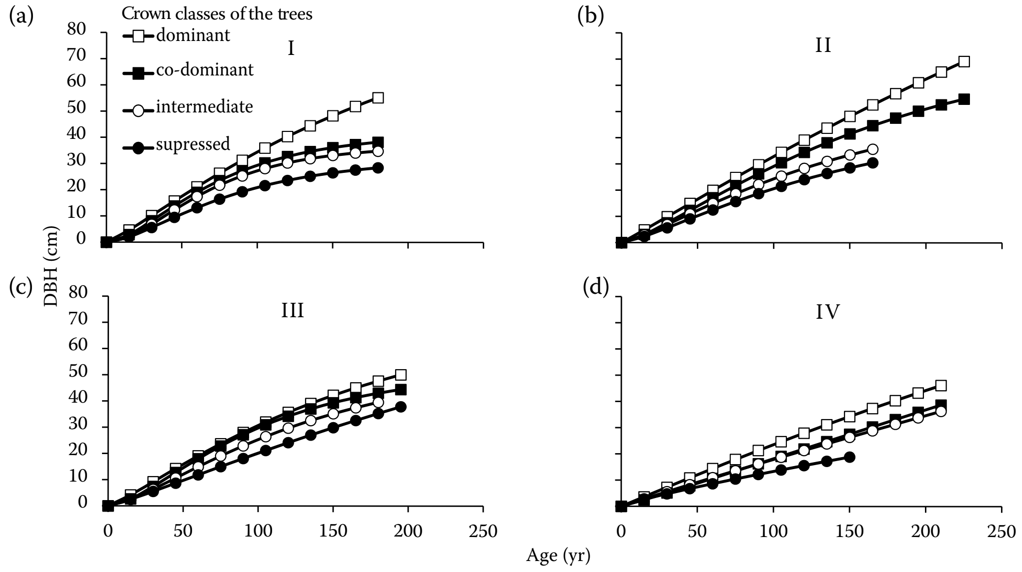

Fig. 3. Global diameter growth model (Eq. 2) classified by site quality of the stands (I – SI_{50} > 9.3 m, II – SI_{50} > 7.2 and ≤ 9.3 m, III – SI_{50} > 5.1 and ≤ 7.2 m, IV – SI_{50} ≤ 5.1 m) and crown classes of the trees

individual tree characteristics. In this work, we employed a less frequent method, where all trees of the entire plot were included in the sampling (Martínez Pastur et al. 2008; Subedi, Sharma 2011), which allowed to fit precise models with greater biological response.

Another non-common characteristic of the employed sampling design is the considered growth period included in the analyses (the last 20 years). This design presents fewer auto-replications (4–5 auto-replicates per tree) than using the entire age gradient for each tree, decreasing autocorrelation errors. A serial correlation was expected when auto-replications were used, violating the assumption of independent error terms in most statistical methods (Cochran 1977; Koak 1997). In this work, the number of age-DBH points was larger compared with the number of re-measurements of each tree. Therefore, the assumption of non-serial correlation should be reasonable in this situation (Vanclay 1991, 1995; Zhao et al. 2004). On the other hand, plots were widely spaced at

Table 5. Maximum annual diameter increment (cm·yr^{-1}) and observed age period (yr) (in brackets) for stand site qualities and tree crown classes for the studied diameter growth models

Model		Site quality	DOM	COD	INT	SUP
Eq. 1	$DBH = a(1- n^{(-bt)})^c$	1	0.37 (32–33)	0.38 (34–35)	0.37 (38–39)	0.26 (36–37)
		2	0.34 (28–29)	0.32 (46–47)	0.27 (35–36)	0.23 (38–39)
		3	0.34 (29–30)	0.36 (41–42)	0.29 (45–46)	0.21 (53–54)
		4	0.24 (18–19)	0.19 (56–57)	0.20 (0–1)	0.26 (0–1)
Eq. 2	$DBH = (a(5-CC)^b)(c(6-SQ)^d)(1-n^{(-et)})^{(f(6-SQ)^g)}$	1	0.37 (25–26)	0.33 (25–26)	0.28 (25–26)	0.22 (25–26)
		2	0.34 (31–32)	0.31 (31–32)	0.26 (31–32)	0.20 (31–32)
		3	0.32 (38–39)	0.28 (38–39)	0.24 (38–39)	0.19 (38–39)
		4	0.26 (55–56)	0.23 (55–56)	0.20 (55–56)	0.15 (55–56)

family of simple growth models (Eq.1) and global diameter unique growth model using (Eq. 2); 1 – SI_{50} > 9.3 m, 2 – SI_{50} > 7.2 and ≤ 9.3 m, 3 – SI_{50} > 5.1 and ≤ 7.2 m, IV – SI_{50} ≤ 5.1 m, DOM – dominant, COD – co-dominant, INT – intermediate, SUP – supressed

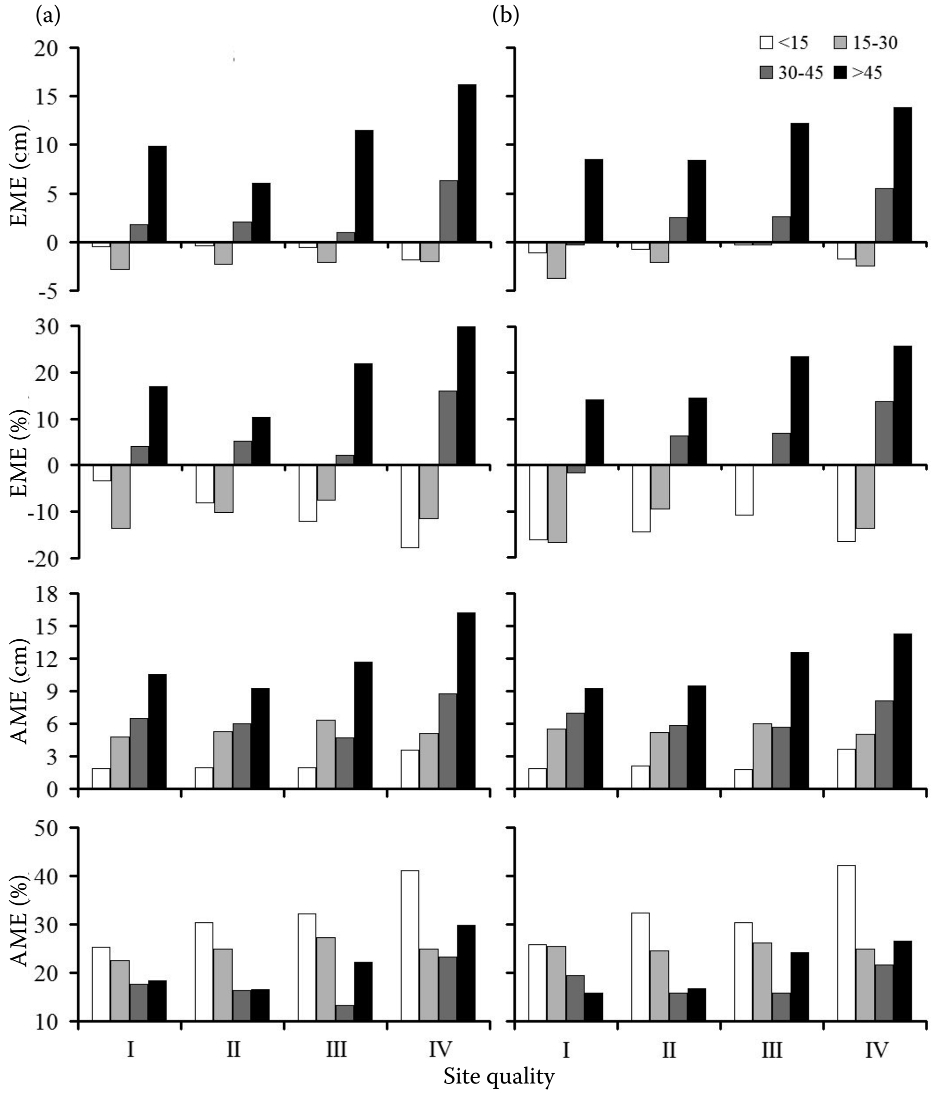

Fig. 4. Auto-validation analyses for the family of growth models using Eq.1 (a) and global diameter growth model using Eq.2 (b), classified by stand site quality (I – $SI_{50} > 9.3$ m, II – $SI_{50} > 7.2$ and ≤ 9.3 m, III – $SI_{50} > 5.1$ and ≤ 7.2 m, IV – $SI_{50} \leq 5.1$ m) and tree age (yr). EME – estimation mean error (cm and %) and AME – absolute mean error (cm and %)

a landscape level and the plot correlation should therefore be small. Thus, we assume that the spatial correlation did not significantly occur in the adjusted models (Zhao et al. 2004).

Family of simple traditional equations or global unique models?

During the last years, growth models with a high number of independent variables were proposed in the forest science (Lessard et al. 2001; Weiskittel et al. 2007), considering factors related to stand and tree levels (e.g. site quality of the stands or tree crown class of the trees). One successful example was the evolution of the proposals for height growth models used for site quality estimation. Most of these proposals were based on Richards (1959), where the age of the trees defines height, but each stand type needs one equation for dominant trees. Ek (1971) proposed a modified equation where independent variables included age and site index, which simplified the use of this kind of equations. This last proposal defined a model which can be used in a wide range of stand conditions. After that, other authors (Payandeh, Wang 1994; Wang, Payandeh 1994) proposed modifications to increase the accuracy of these estimations. This last methodology was successfully applied in Southern Patagonian forests, e.g. in *N. antarctica* (Ivancich et al. 2011) and *N. pumilio* (Martínez Pastur et al. 1997). Also, global models based on these proposals were applied in volume models for *N. antarctica* (Lencinas et al. 2002), and tree diameter (Martínez Pastur et al. 2005) and volume stand growth (Martínez Pastur et al. 2008) for *N. pumilio* forests. The major advantage in the use of global unique equation is the simplicity of the use under a wide range of stand conditions. According to these results, it was possible to simplify the diameter growth model estimation using a unique global equation instead a family of simple equations.

The influence of simplification over the accuracy of models

The accuracy of models in forestry is related to the forest structure variability, being higher in natural forests without silvicultural management (Zeide 1978). In our study, the adjustments were comparable to those found in the literature, e.g. Subedi and Sharma (2011), who presented diametric models for *Picea mariana* and *Pinus banksiana*, obtained R^2 between 69% and 76%, and Lhotka and Loewenstein (2011) proposed global models for several *Quercus* species with R^2 between 40% and 57%. Our family of simple growth models (Eq. 1) showed higher variability in their R^2-adj, explained between 54% and 92% in each model. The global growth model (Eq. 2) included more variables and presented similar accuracy to the better equations of the simple growth models family. According to our results, the unification of a family of simple growth models into a unique global equation did not have a greater influence on the accuracy of the estimation.

Biological response of the models

The Richards model is a widely-used and flexible sigmoid function for growth modelling which has been extensively used in several forest species around the world (Zeide 1993). However, this flexibility increases the risk to reduce the biological response of the adjusted models (e.g. with the Richards models it is possible to obtain from a sigmoid curve to a straight line). The family of simple growth models introduced several inconsistencies among the models and across the studied gradients (e.g. site quality of the stands and crown class of the trees). The global model was fitted with the entire data base, avoiding these inconsistencies and increasing the biological response of the model. Another inconsistency was observed in the MADI determination and age occurrence, where MADI must have occurred before in better growing conditions (Klepac 1976), as was described for the *Nothofagus* species before (Peri, Martínez Pastur 1996; Martínez Pastur, Fernández 1997; Ivancich et al. 2011). The global unique model presented better performance in the Madi estimation than the family of simple traditional growth models. According to our results, the use of a global equation positively influenced the biological response compared to the use of a family of simple traditional growth models.

CONCLUSIONS

Global growth unique models constitute a simple tool to support decision taking in forest management compared to the application of a family of simple equations. The use of global unique growth models: (*i*) simplifies the calculation of tree growth, (*ii*) does not greatly influence the accuracy of the global estimation, and (*iii*) positively influences the biological response of the models. The proposal of global unique models with greater complexity and higher number of independent variables allows researchers to better explain tree growth in general environmental conditions, but maintaining the rationality within the entire data base.

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