

Appendix S1 – Relative performance of six commonly-used growth models used to predict the growth performance of 5524 individual trees from 50 neotropical species.

We report in the following table the number of times each growth model (number of parameters including the error term in bracket) was ranked first using the 3 commonly used model selection criteria.

	Canham (4)	Gompertz (3)	Korf (4)	Logistic (3)	Power (3)	Weibull (4)
Adjusted R ²	27	7	0	0	3	12
AIC	19	14	0	10	6	0
BIC	12	18	0	13	6	0

From these results, we retained the Canham’s growth model, considering that the AIC was more appropriate than the BIC in order to give the same penalty for each species in spite of their number of individual trees.

Canham’s growth model

$$\log(AGR_i + 1) = \theta_{c1} \times \exp \left[-\frac{1}{2} \left(\frac{\log(DBH_i/\theta_{c2})}{\theta_{c3}} \right)^2 \right] + \varepsilon_i$$

Gompertz’s growth model

$$\log(AGR_i + 1) = \theta_{g1} \times DBH_i \times \log \left(\frac{\theta_{g2}}{DBH_i} \right) + \varepsilon_i$$

Korf's growth model

$$\log(AGR_i + 1) = \theta_{k1} \times DBH_i \times \left(\log\left(\frac{\theta_{k2}}{DBH_i}\right) \right)^{(1+\theta_{k3})} + \varepsilon_i$$

Logistic's growth model

$$\log(AGR_i + 1) = \theta_{l1} \times DBH_i \times \left(1 - \frac{DBH_i}{\theta_{l2}}\right) + \varepsilon_i$$

Power growth model

$$\log(AGR_i + 1) = \theta_{p1} \times DBH_i^{\theta_{p2}} + \varepsilon_i$$

Weibull's growth model

$$\log(AGR_i + 1) = \theta_{w1} \times \left(1 - \frac{DBH_i}{\theta_{w2}}\right) \times \left[\log\left(\frac{\theta_{w2}}{\theta_{w2} - DBH_i}\right) \right]^{1-\theta_{w3}} + \varepsilon_i$$

With $\varepsilon_i \sim N(0; \sigma^2)$ and θ_{ij} , the j^{th} parameter of the growth model i .

Appendix S2 – List of the 50 neotropical tree species used for growth modeling: values of the parameters of the Species-Model and values of the functional traits used selected for inclusion in the Trait-Model.

<i>Species</i>	Gmax	Dopt	K	DBHmax	Height	Wood Density	δ13C
<i>Abarema jupunba</i>	4.53	317.60	0.66	468.00	45.00	0.66	-30.15
<i>Bocoa prouacensis</i>	0.58	407.37	1.71	408.00	37.00	1.22	-31.50
<i>Brosimum rubescens</i>	1.66	294.75	0.76	428.40	40.00	1.01	-31.36
<i>Carapa procera</i>	1.82	227.82	0.73	405.05	35.00	0.70	-31.04
<i>Caryocar glabrum</i>	1.75	375.00	1.09	660.20	48.00	0.79	-29.49
<i>Chaetocarpus schomburgkianus</i>	0.94	157.37	1.39	396.90	33.00	1.13	-33.42
<i>Chaunochiton kappleri</i>	2.03	308.95	0.67	525.80	24.00	0.90	-32.68
<i>Chrysophyllum prieurii</i>	1.75	260.89	0.83	456.95	33.00	1.10	-30.51
<i>Chrysophyllum sanguinolentum</i>	1.46	332.10	0.94	472.20	36.00	0.74	-30.38
<i>Couepia bracteosa</i>	1.92	283.38	0.70	393.20	28.00	0.94	-32.12
<i>Couepia guianensis</i>	2.33	361.62	0.85	379.50	30.00	0.94	-33.01
<i>Couratari multiflora</i>	1.19	286.95	0.62	383.75	36.00	0.63	-30.21
<i>Dendrobangia boliviana</i>	2.22	263.86	0.92	451.00	38.00	0.80	-31.46
<i>Dicorynia guianensis</i>	2.63	332.52	0.87	630.20	50.00	0.79	-29.34
<i>Drypetes variabilis</i>	1.03	338.58	1.15	501.00	34.00	0.93	-30.69
<i>Eperua falcata</i>	1.43	318.57	1.10	614.00	34.00	0.86	-29.74
<i>Eperua grandiflora</i>	3.49	309.62	0.94	636.90	42.00	0.92	-30.35
<i>Eschweilera coriacea</i>	1.42	262.87	0.93	399.65	37.00	0.99	-32.45
<i>Eschweilera sagotiana</i>	0.82	362.41	1.34	470.00	44.00	1.05	-32.31
<i>Goupia glabra</i>	2.75	289.78	0.85	622.20	37.00	0.84	-30.99
<i>Hevea guianensis</i>	1.02	394.61	1.40	418.50	56.00	0.78	-31.33
<i>Humirastrum subcrenatum</i>	4.02	488.60	1.06	700.00	30.00	0.92	-32.03
<i>Jacaranda copaia</i>	2.72	247.10	0.74	336.10	28.00	0.46	-31.30
<i>Licania alba</i>	1.08	212.19	0.85	382.00	31.00	1.06	-32.55
<i>Licania laxiflora</i>	1.85	231.31	0.55	362.20	48.00	0.81	-31.84
<i>Licania licaniiflora</i>	2.49	294.51	0.75	522.00	35.00	0.79	-32.72
<i>Licania membranacea</i>	2.26	257.26	0.73	413.40	42.00	1.08	-33.21
<i>Licania micrantha</i>	1.76	370.96	0.89	428.80	25.00	1.05	-33.90
<i>Licania ovalifolia</i>	1.62	333.31	1.05	522.00	35.00	1.13	-31.33

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<i>Manilkara bidentata</i>	2.69	471.91	1.19	543.75	38.00	1.10	-32.17
<i>Micropholis egensis</i>	1.46	445.22	1.31	548.00	32.00	0.77	-32.08
<i>Moronobea coccinea</i>	2.41	511.99	1.45	631.00	36.00	0.90	-31.98
<i>Mouriri crassifolia</i>	1.99	297.66	0.88	367.35	27.00	1.10	-31.81
<i>Parinari campestris</i>	3.98	295.29	0.64	635.95	33.00	0.89	-30.70
<i>Parinari montana</i>	3.48	381.77	0.60	585.50	30.00	0.89	-31.77
<i>Platonia insignis</i>	1.87	504.53	1.29	727.00	30.00	0.85	-28.54
<i>Pouteria ambelaniifolia</i>	1.60	286.12	1.24	364.95	31.00	1.03	-32.73
<i>Pouteria eugeniifolia</i>	1.56	444.63	1.26	592.00	43.00	1.01	-31.38
<i>Pouteria guianensis</i>	1.04	240.55	0.74	369.60	34.00	1.03	-32.87
<i>Pradosia cochlearia</i>	1.75	323.53	0.89	509.80	40.00	0.96	-31.07
<i>Qualea rosea</i>	3.21	364.34	0.88	739.50	42.00	0.71	-31.68
<i>Recordoxylon speciosum</i>	2.32	371.27	1.24	559.10	35.00	1.00	-31.35
<i>Sacoglottis guianensis</i>	3.12	337.97	1.16	492.40	27.00	1.01	-31.31
<i>Sextonia rubra</i>	2.96	596.22	0.87	792.20	50.00	0.65	-30.88
<i>Sterculia pruriens</i>	3.27	475.58	1.06	569.30	40.00	0.64	-31.43
<i>Swartzia panacoco</i>	1.08	168.71	1.51	422.80	32.00	1.11	-29.02
<i>Symphonia globulifera</i>	5.51	318.19	0.81	558.20	26.00	0.72	-31.14
<i>Symphonia spl</i>	3.27	252.95	0.83	489.20	26.00	0.72	-31.14
<i>Virola michelii</i>	2.45	245.81	0.55	386.10	38.00	0.59	-32.85
<i>Vouacapoua americana</i>	1.56	195.19	0.79	498.75	42.00	0.92	-31.84

Appendix S3 –Detailed MCMC algorithms used to calibrate the growth models

1. Calibrating the Species-Model

For all individuals $i=1, \dots, n$ from the species s , we considered the following growth model:

$$\log(AGR_i + 1) = Max_s \times \exp\left(-0.5 \times \left(\log\left(\frac{DBH_i}{Dopt_s}\right)/K_s\right)^2\right) + \varepsilon_i$$

where AGR_i is the observed growth, DBH_i the diameter at breast height, ε_i the error term which was assumed to follow a centered normal distribution with variance σ_s^2 and $Gmax_s$, $Dopt_s$, K_s the unknown parameters associated to the species s . For convenience, we worked with the precision of the error $\lambda_s = 1/\sigma_s^2$ instead of the variance in the inference procedure. The likelihood is then defined by

$$L(AGR_{1:n}, DBH_{1:n}; Max_s, Dopt_s, K_s, \lambda_s) = \frac{\lambda_s^n}{(2\pi)^{\frac{n}{2}}} \exp\left\{-\frac{\lambda_s}{2} \sum_{i=1}^n (\log(AGR_i + 1) - Max_s \times g(DBH_i, Dopt_s, K_s))^2\right\}$$

with $g(DBH_i, Dopt_s, K_s) = \exp\left(-0.5 \times \left(\log\left(\frac{DBH_i}{Dopt_s}\right)/K_s\right)^2\right)$. To alleviate notation we note $L(Data; Max_s, Dopt_s, K_s, \lambda)$ instead of $L(AGR_{1:n}, DBH_{1:n}; Gmax_s, Dopt_s, K_s, \lambda)$. The parameters were estimated through the Bayesian framework using a Monte Carlo Markov Chain algorithm (MCMC). In the Bayesian framework, the parameter inference consists in updating the prior knowledge on the parameters $\theta = (Max_s, Dopt_s, K_s, \lambda_s)$, the prior distribution on the parameter π_θ^0 , thanks to the data which leads to the posterior distribution of the parameter π_θ^p . According to the Bayes formula we know that the posterior distribution is proportional to the likelihood multiplied by the prior distribution:

$$\pi_\theta^p(\theta|Data) \propto L(Data; Max_s, Dopt_s, K_s, \lambda_s) \times \pi_\theta^0(\theta)$$

For $Max_s, Dopt_s, K_s$ we used uninformative priors:

- For Max_s : $\pi_g^0 = N(\mu_0 = 1, \lambda_0 = 10^4)$
- For $Dopt_s$: $\pi_D^0 = N(1, 10^4)$

- For K_s : $\pi_K^0 = N(1, 10^4)$
- For λ_s : $\pi_\lambda^0 = Ga(\alpha_0 = 1, \beta_0 = 0.1)$

The MCMC algorithm provides a numerical estimate of the posterior distribution of the unknown parameter, π_θ^p , which consists in a sequence of values (a MCMC chain) sampled from the posterior distribution. We used the below Metropolis-Hastings within Gibbs algorithm to build the chains for the unknown parameters. This is a type of MCMC algorithm that consists in updating sequentially the chain of each parameter:

step 0: initialization of the chains $\text{Max}_s^{(0)} = g_0$, $\text{Dopt}_s^{(0)} = d_0$, $K_s^{(0)} = k_0$ and $\lambda_s^{(0)} = l_0$

For $k = (1 \text{ to } \text{Niter}) \{$

Step 1 updating $\text{Max}_s^{(k)}$:

$$\text{Max}_s^{(k)} \sim N \left(\frac{\lambda_s^{(k-1)} \sum_i g \left(\text{DBH}_i, \text{Dopt}_s^{(k-1)}, K_s^{(k-1)} \right) \log(\text{AGR}_i + 1) + \lambda_0 \mu_0}{\lambda_s^{(k-1)} \sum_i g \left(\text{DBH}_i, \text{Dopt}_s^{(k-1)}, K_s^{(k-1)} \right)^2 + \lambda_0}, \lambda_s^{(k-1)} \sum_i g \left(\text{DBH}_i, \text{Dopt}_s^{(k-1)}, K_s^{(k-1)} \right)^2 + \lambda_0 \right)$$

Step 2 updating $\text{Dopt}_s^{(k)}$:

$$d \sim N \left(\text{Dopt}_s^{(k-1)}, 1 \right) \text{ and } u \sim U[0, 1]$$

$$\text{Dopt}_s^{(k)} = \begin{cases} \text{Dopt}_s^{(k-1)}, & u > r \\ d, & u \leq r \end{cases}$$

$$\text{with } r = \frac{L(\text{Data}; \text{Max}_s^{(k)}, d, K_s^{(k-1)}, \lambda_s^{(k-1)}) \times \pi_D^0(d)}{L(\text{Data}; \text{Max}_s^{(k)}, \text{Dopt}_s^{(k-1)}, K_s^{(k-1)}, \lambda_s^{(k-1)}) \times \pi_D^0(\text{Dopt}_s^{(k-1)})}$$

Step 3 updating $K_s^{(k)}$:

$$k \sim N \left(K_s^{(k-1)}, 0.1^2 \right) \text{ and } u \sim U[0, 1]$$

$$K_s^{(k)} = \begin{cases} K_s^{(k-1)}, & u > r \\ k, & u \leq r \end{cases}$$

$$\text{with } r = \frac{L(Data; \text{Max}_s^{(k)}, \text{Dopt}_s^{(k)}, k, \lambda_s^{(k-1)}) \times \pi_K^0(k)}{L(Data; \text{Max}_s^{(k)}, \text{Dopt}_s^{(k)}, K_s^{(k-1)}, \lambda_s^{(k-1)}) \times \pi_K^0(K_s^{(k-1)})}$$

Step 4 updating $\lambda_s^{(k)}$:

$$\lambda_s^{(k)} \sim \text{Ga} \left(\alpha_0 + \frac{n}{2}, \beta_0 + \frac{1}{2} \sum_i \left(\log(AGR_i + 1) - \text{Max}_s^{(k)} \times g(DBH_i, \text{Dopt}_s^{(k)}, K_s^{(k)}) \right)^2 \right)$$

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The chains $\text{Max}_s^{(k)}$ and $\lambda_s^{(k)}$ are built according to a Gibbs scheme, the new values are sampled according their marginal posterior distribution. The chains $\text{Dopt}_s^{(k)}$ and $K_s^{(k)}$ are built according to a Metropolis scheme, the possible new values are proposed according to a random walk and may be accepted or not.

2. Calibrating the DBH-Model

We used the same methodological framework as for the species- model. We simply joined all the species data to estimate the four parameters σ^2 and Max, Dopt, K as if there was only one species.

3. Calibrating the Trait-Model

We generalized the case of the Species-Model assuming that the three parameters Max, Dopt, K can be expressed as linear functions of trait values for all individuals $i=1, \dots, n$: $Gmax_i = g_0 + g_1 \times TG_i^1 + \dots + g_p \times TG_i^p$, $Dopt_i = d_0 + d_1 \times TD_i^1 + \dots + d_q \times TD_i^q$ and $K_i = k_0 + k_1 \times TK_i^1 + \dots + k_r \times TK_i^r$.

That leads to the following Trait-Model:

$$\log(AGR_i + 1) = (g_0 + g_1 \times TG_i^1 + \dots + g_p \times TG_i^p) \times h(DBH_i, d_{0:q}, k_{0:r}) + \varepsilon_i$$

with

$$h(DBH_i, d_{0:q}, k_{0:r}) = \exp\left(-0.5 \times \left(\frac{\log\left(\frac{DBH_i}{d_0 + d_1 \times TD_i^1 + \dots + d_q \times TD_i^q}\right)}{k_0 + k_1 \times TK_i^1 + \dots + k_r \times TK_i^r}\right)^2\right)$$

with ε_i the error term assumed to follow a centered normal distribution with precision λ . The likelihood is then defined by:

$$L(\text{Data}; g_{0:p}, d_{0:q}, k_{0:r}, \lambda) = \frac{\lambda^n}{(2\pi)^{\frac{n}{2}}} \exp\left\{-\frac{\lambda}{2} \sum_{i=1}^n \left(\log(AGR_i + 1) - (g_0 + g_1 \times TG_i^1 + \dots + g_p \times TG_i^p) \times h(DBH_i, d_{0:q}, k_{0:r})\right)^2\right\}$$

As for the Species-Model, the parameters $\theta = (g_{0:p}, d_{0:q}, k_{0:r}, \lambda)$, were estimated through the Bayesian framework using a Monte Carlo Markov Chain algorithm (MCMC). For inference we used no informative priors:

- For $(g_0, g_1, g_2, \dots, g_p)$: a multivariate normal distribution $\pi_g^0 = N_{p+1}(\mu_0 = (1, 0, \dots, 0), \lambda_0 * I_{p+1})$ with $\lambda_0 = 10^4$ and I_{p+1} the identity matrix of dimension $p+1$.
- For $(d_0, d_1, d_2, \dots, d_q)$: $\pi_d^0 = N_{q+1}((1, 0, \dots, 0), \lambda_0 * I_{q+1})$
- For $(k_0, k_1, k_2, \dots, k_r)$: $\pi_k^0 = N_{r+1}((1, 0, \dots, 0), \lambda_0 * I_{r+1})$
- For λ : $\pi_\lambda^0 = Ga(\alpha_0 = 1, \beta_0 = 0.1)$

We used a Metropolis-Hastings within Gibbs algorithm, similar to the Species-Model case, to build the MCMC chains. The chains of the parameters $d_0, d_1, d_2, \dots, d_q$ and $k_0, k_1, k_2, \dots, k_r$ are build using the Metropolis framework (cf. step2 and step3), we simply substitute the likelihood and the prior in the step 2. The chain of the parameter λ is build according to a Gibbs scheme (cf. step 4), its new marginal posterior distribution is given by:

Step 4' updating $\lambda^{(k)}$:

$$\lambda^{(k)} \sim \text{Ga} \left(\alpha_0 + \frac{n}{2}, \beta_0 + \frac{1}{2} \sum_i \left(\log(AGR_i + 1) - (g_0^{(k)} + g_1^{(k)} \times TG_i^1 + \dots + g_p^{(k)} \times TG_i^p) \times h(DBH_i, d_{0:q}^{(k)}, k_{0:r}^{(k)}) \right)^2 \right)$$

The chains of the parameters $(g_0, g_1, g_2, \dots, g_p)$ are build according to a Gibbs scheme (cf. step 1), its new marginal posterior distribution is given by:

Step 1' updating $(g_0, g_1, g_2, \dots, g_p)^{(k)}$:

$$(g_{0:p})^{(k)} \sim N_{p+1} (L^{-1} \times (\Lambda_0 \times \mu_0 + \Lambda^{(k)} X'Y), L)$$

With the precision matrix $L = \Lambda^{(k)} X'X + \lambda_0 I_{p+1}$, the matrix

$$X = \begin{pmatrix} g_0^{(k)} \times h(DBH_1, d_{0:q}^{(k)}, k_{0:r}^{(k)}) & g_1^{(k)} \times TG_1^1 \times h(DBH_1, d_{0:q}^{(k)}, k_{0:r}^{(k)}) & \dots & g_p^{(k)} \times TG_1^p \times h(DBH_1, d_{0:q}^{(k)}, k_{0:r}^{(k)}) \\ \vdots & \vdots & \vdots & \vdots \\ g_0^{(k)} \times h(DBH_n, d_{0:q}^{(k)}, k_{0:r}^{(k)}) & g_1^{(k)} \times TG_n^1 \times h(DBH_n, d_{0:q}^{(k)}, k_{0:r}^{(k)}) & \dots & g_p^{(k)} \times TG_n^p \times h(DBH_n, d_{0:q}^{(k)}, k_{0:r}^{(k)}) \end{pmatrix}$$

and the vector

$$Y = \begin{pmatrix} \log(AGR_1 + 1) \\ \vdots \\ \log(AGR_n + 1)_n \end{pmatrix}$$

Appendix S4. Modeled adult growth trajectories of 50 neotropical tree species.

Observed absolute growth rates (AGR mm/yr) plotted against the observed diameters at breast height (DBH). The curves indicate the kernel regression estimates (grey curves), predictions of the Species-Model (dashed dark curves), the DBH-Model (pointed dark curves) and the Trait-Model (red plain curves with 90% credibility intervals).









