

## S1: AMAPsim model calibration

The AmapSim model relies on the concept of axis of development to simulate the evolution (i.e. the transition between PAs) of an axis along its lifespan [1]. The model considers 4 PAs and in some cases the transitions from  $PA_i$  to  $PA_{i+1}$  are allowed (axis drift, [2]). In our simulations PA1 is defined as the first PA that occurs in the tree development (i.e. the trunk) while PA4 is the ultimate PA a tree can produce. As our objective was to simulate trees from 5 to 15 years old and we did not observe any evidence of transitions between PAs on the trunk (related to the base effect or drift, [2]) for this period of time, we parameterized the axis of development so that the tree trunk is only composed of AS of PA1. In the simulation, PA2 transforms into PA3 after 8 years. PA1, PA2 and PA3 are allowed to grow indefinitely while PA4 dies and falls after 5 years. A visual representation of the axis of development is shown in Figure S1a.

In AmapSim, the branching relation uses Markov chains to define the state, i.e. branched or non-branched, of each internode within an AS. Markov chains are calibrated from our data based on the average number of lateral axes and the average number of internodes observed in the ASs of each PA. The primary probability, that defines whether an axe is branched or not is set for each PA to the observed proportion of branched AS of the corresponding PA. The secondary probability, that sets the probability of a branched internode to remain branched, is calculated as:

$$p_i = \ln(2n_i) / \ln(l_i)$$

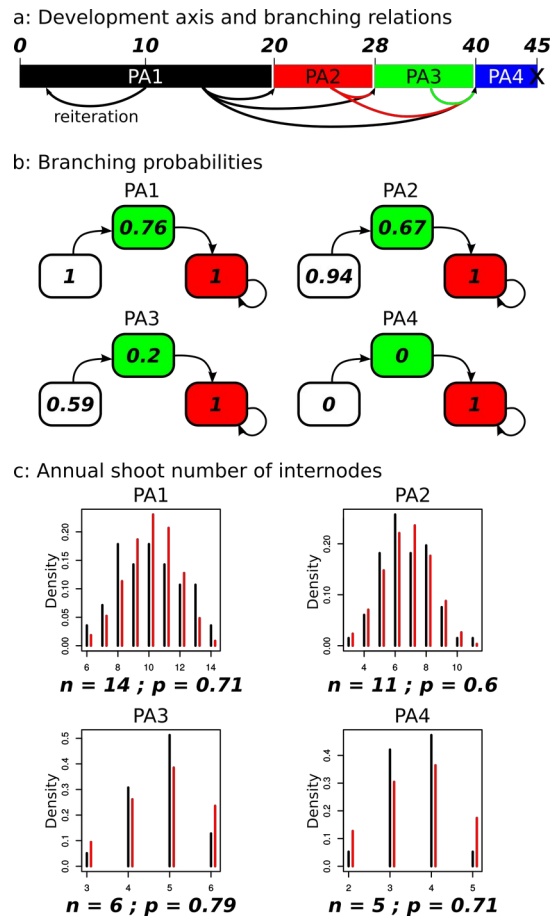
where  $n$  is the average number of internode and  $l$  is the average number of lateral axis in  $PA_i$ . Note that  $2n$  is used since in opposite phyllotaxy each internode can bear two axes. Finally, the non-branched state was considered as an absorbing state and no further branching was allowed after it was reached. The Markov chains parameters are shown in Figure S1b.

The branching relations are set so that an AS of  $PA_i$  could bear only AS of  $PA_{>i}$ . The only exception to this rule concerns reiterations of the trunk that occur after ten growing seasons which is modeled with a systematic reiteration wave occurring with a probability of 1 at year ten. This reflects field observations of a systematic occurrence of reiterations at the same time and height within all the trees of the experiment. When reiteration occurs, an AS of PA1 with full potential of development (starting at year 3 of the axis of development) is initiated. Finally, it is important to note that during the tree development, the first two AS of the trunk are not allowed to branch in order to create a non-branched trunk at the tree base.

The parameters that describe the AS are estimated for each PA from the field measurements of 117 axes taken at the internode level, see section "*Sampled trees and architectural measurements*". A

binomial law, which is used in AmapSim to generate random AS, is fitted to the frequency distribution of the number of internodes observed in the AS of each PA. The retrieved parameters as well as the observed and theoretical distribution are shown in Figure S1c. The binomial is fitted using the *fidistrplus* R package [3] using the maximum observed number of internode as a fixed parameter for the number of trials while the probability of success of each Bernoulli test is estimated from the distributions (see Figure 5c for comparison between the observed and fitted distributions).

The average internode length is then calculated for each PA. The estimated length is  $8.12(\pm 6.88)$  cm,  $4.04(\pm 4.15)$  cm,  $1.66(\pm 1.85)$  cm and  $0.40(\pm 0.41)$  cm (for PA1, PA2, PA3, and PA4, respectively). The initial internode diameter is set to 0.5 cm in all PAs.



**Figure S1.** Parameters used to simulate red ash growth using the AmapSim model. Axis of development and branching relations (a) showing the four physiological ages with different colours. The branching relations are represented by the arrows below the axis of development. The important years of transitions from a PA to another are indicated above the axis. Markov chains used to run random branching patterns (b) uses three states: the initial probability that sets if the annual shoot of the previous year enters into the branched state or not (white box), the probability of remaining in the branched state (green box) and the probability of remaining in the unbranched state (red box). Binomial laws used to simulate random AS for each PA (c) are fitted to the distribution of the observed number of internodes. The plots show the observed (black) and fitted (red) density for each PA. The binomial law parameters are shown in bold below the graphs.

## References

1. Barczi, J.-F.; Rey, H.; Caraglio, Y.; de Reffye, P.; Barthelemy, D.; Dong, Q.X.; Fourcaud, T. AmapSim: A Structural Whole-Plant Simulator Based on Botanical Knowledge and Designed to Host External Functional Models. *Ann. Bot.* **2007**, *101*, 1125–1138.
2. Barthélémy, D.; Caraglio, Y. Plant Architecture: A Dynamic, Multilevel and Comprehensive Approach to Plant Form, Structure and Ontogeny. *Ann. Bot.* **2007**, *99*, 375–407.
3. Delignette-Muller, M.L.; Dutang, C.; Pouillot, R.; Denis, J.B.; Siberchicot, A. Fitdistrplus: Help to Fit of a Parametric Distribution to Non-Censored or Censored Data. <https://CRAN.R-project.org/package=fitdistrplus> (accessed on 14 January 2021).