



Towards a common methodology to simulate tree mortality based on ring-width data

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Individual mortality is a key process of population and community dynamics, especially for long-lived species such as trees. As the rates of vegetation background mortality and of massive diebacks accelerated during the last decades and would continue in the future due to rising temperature and increasing drought, there is a growing demand of early warning signals that announce that the likelihood of death is very high. If physiological indicators have a high potential to predict tree mortality, their development requires an intensive tree monitoring which cannot be currently done on a representative sample of a population and on several species. An easier approach is to use radial growth data such as tree ring-widths measurements. During the last decades, an increasing number of studies aimed to derive these growth-mortality functions. However, as they followed different approaches concerning the choice of the sampling strategy (number of dead and living trees), of the type of growth explanatory variables (growth level, growth trend variables...), and of the length of the time-window (number of rings before death) used to calculate them, it makes difficult to compare results among studies and a subsequent biological interpretation.

We detailed a new methodology for assessing reliable tree-ring based growth-mortality relationships using binomial logistic regression models. As examples we used published tree-ring datasets from *Abies alba* growing in 13 different sites, and from *Nothofagus dombeyi* and *Quercus petraea* located in one single site. Our first approach, based on constant samplings, aims to (1) assess the dependency of growth-mortality relationships on the statistical sampling scheme used; (2) determine the best length of the time-window used to calculate each growth variable; and (3) reveal the presence of intra-specific shifts in growth-mortality relationships. We also followed a Bayesian approach to build the best multi-variable logistic model considering the collinearity between the different growth variables.

We observed that the structure of such mortality models strongly depends on the size and properties of the sampling (number of dead and living observations; proportion of young vs. old trees) as growth-mortality relationships may vary through tree's life cycle and with the main factor that trigger mortality. The sampling scheme especially affects the determination of the length of the time-window that maximizes the discrimination ability of each growth variable (from one to fifty rings).

The present study highlights the need to sample a significant number (>20 per class) of both dead and living trees in different age classes and growing in different sites, and to use a consistent methodology that accounts for all types of biases to determine reliable species-specific growth-mortality relationships. In our opinion, this would be an important step to move forward a better understanding of the mortality process among tree species and a better representation of mortality in ecosystem process-based models.