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How to efficiently estimate biomass of woody roots: Identifying and minimising the sources of error

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Accurate estimation of below-ground biomass (BGB) of terrestrial ecosystems is critical to understanding ecosystem function, and informing models of carbon and nitrogen cycles in the rhizosphere. However, due to the difficulty of measurement, BGB is often estimated using simplistic default values based limited empirical data. To improve this, we used a dataset of 2,000 measurements of individual tree and shrub BGB, together with BGB data from whole-plot excavations in 11 contrasting stands from across a range of woody ecosystems, to derive evidence-based approaches for accurate prediction of BGB at both individual, and more importantly, whole stand scales. A reasonable accuracy of prediction of BGB of individual trees or shrubs (MAPE, mean absolute prediction error, being 21–55%) was found when allometric equations based on stem diameter were generalised at the level of plant functional type (e.g. shrub, multi-stemmed tree, hardwood tree, softwood tree, etc.), with consideration of other factors (e.g. species, climate, age or management) resulting in negligible further improvement in accuracy. When tested against the whole-plot excavation data, the application of such generic equations to estimate stand-scale BGB resulted in a mean absolute prediction error of only 6.5%. Hence, results indicated that a collaborative effort on collation of large datasets (N > ca. 150) from the various key plant functional types at continental or sub-continental-scale can provide generic allometric equations of BGB that can then be widely applied within that domain. Given the source of error in stand-level BGB prediction obtained by application of such generic equations is small relative to potentially large sources of error in stand-based biomass estimates attributable to sampling errors, results also suggest limited resources for field measurements should be directed at maximising the number of individuals measured for stem diameter within the stand rather than excavation of BGB to develop new site- or species-specific allometric equations. However, validation may be required when an existing equation is applied to a species not yet represented in the datasets used to construct that equation. We found that to ensure a statistically valid outcome a sample size of N > ca. 70–100 is required. An equivalence test may then be applied to determine if the minimum detectable negligible difference between the existing model and the new independent data is less than a given threshold deemed to be acceptable. If so, the new dataset may then be combined with existing data to refine the generic model. If not, then the sample size is still sufficient to develop a new model suitable for application to the specific species sampled. Such a collaborative approach will result in a continuous process of improved confidence in BGB estimates.