

Scientific Computing :: Drop In

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Session: 5

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Activity: R Coding

Functions in R

Basal area of larger trees (BAL , Eq. 1) quantifies the sum of the basal areas of all trees that are larger or equal in basal area compared to that of a given tree i at time t . It is the complement value of the basal area percentile $p_i(t)$ of tree i denoting relative dominance, where $G(t)$ is basal area per hectare of a given forest stand at time t . Basal area of an individual tree is the cross-sectional area of its stem usually measured at 1.3 m above ground level. For convenience basal area is often calculated from stem diameter using the area formula of a circle. Basal area per hectare is a density measure taking both number of trees and their sizes in a certain area into account, see <https://blogg.slu.se/forest-biometrics/2017/05/26/basal-area-in-larger-trees-and-the-growth-compensation-point/>.

$$BAL_i(t) = G(t) \cdot (1 - p_i(t)) \text{ with } p_i(t) = \frac{1}{G(t)} \sum_{\leq g_i(t)} g_i(t) \quad (1)$$

BAL is related to available light, since with increasing basal area of larger trees there is less light available for smaller trees. In a sense BAL is a surrogate for light measurements with the benefit that stem diameters and basal area are easier to measure.

In this session, your task is to write a function calculating the *BAL* and to apply it to the data from a mixed sessile oak – European beech forest stand. Finally plot your *BAL* results over stem diameter (*dbh*).

Download the small data set in file `Mand1.txt` from <https://github.com/apommerening>. The ASCII file has 244 observations relating to the data of research plot Manderscheid in Germany (Rhineland Palatinate). The data are from a managed woodland of sessile oak (*Quercus petraea* MATT.) and European beech (*Fagus sylvatica* L.), where I studied species mingling and other spatial tree diversity indices.