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### 4.3. FUNCTIONAL BRANCH ANALYSIS TO DERIVE ALLOMETRIC EQUATIONS OF TREES

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By:

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A major part of the carbon and nutrients in terrestrial ecosystems is in the tree component and it is therefore imperative to have appropriate methods for estimating tree biomass. To reduce the need for destructive sampling, biomass can be estimated from an easily measured property such as stem diameter, at specified height, by using an allometric equation. A substantial number of allometric equations have been developed for various climatic zones, forest types and tree species, using a variety of algebraic forms and parameter values. Anybody who wishes to use such equation for a new situation is faced with a difficult choice among the various equations, the result of which may vary over a factor 2 at least when applied to a specific data set. Collecting more empirical equations will hardly reduce this uncertainty for any new situation, unless we can better understand the background of the allometric equations in its link with the shape of trees. The FBA (functional branch analysis) scheme was designed to generate allometric equations on the basis of easily observed properties of branched systems, in order to allow a more informed choice among empirical equations for forest types or even for individual trees in a sampling area (see Figure 4.11).

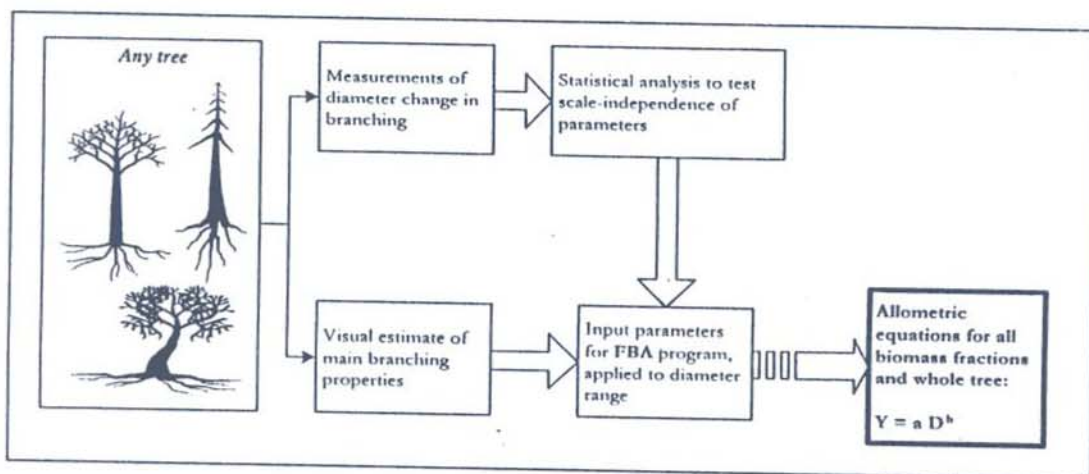


Figure 4.11. FBA estimates tree's biomass using a fractal branching model.

Fractal branching models make use of self-repeating properties in applying simple rules consistently across a range of scales. In trees above- as well as below-ground branching follows a simple logic in that the amount of transport tissue (functional xylem) where two roots come together or where two branches split has to be able to transport the same amount of water before and after the branching point. This consistency leads to a requirement of a near-constant cross-sectional area of xylem, and depending on the stem anatomy, to a proportional relation in the cross-sectional areas of the whole stem.

Any branching point can be described by a parameter for the change in total cross-sectional area ( $\alpha = D^2_{\text{before}} / \sum D^2_{\text{after}}$ ), one for the split of cross-sectional area over the branches ( $q = \max(D^2_{\text{after}}) / \sum D^2_{\text{after}}$ ), one for the number of branches and the angle between the axes before and after branching. The angles are important for a 3D reconstruction of the tree, but not for total biomass. Direct measurement of diameter change at branching points and statistical analysis to test the independence of these parameters from diameter can establish the validity of the fractal model. All tests performed so far on above-ground trees as well as root systems confirm that the principle indeed applies, but with considerable variability in parameter values.

The more extreme cases can be directly recognised by looking at a tree (Figure 4.12), which leads to a considerable simplification of the procedure if an approximation is sufficient.

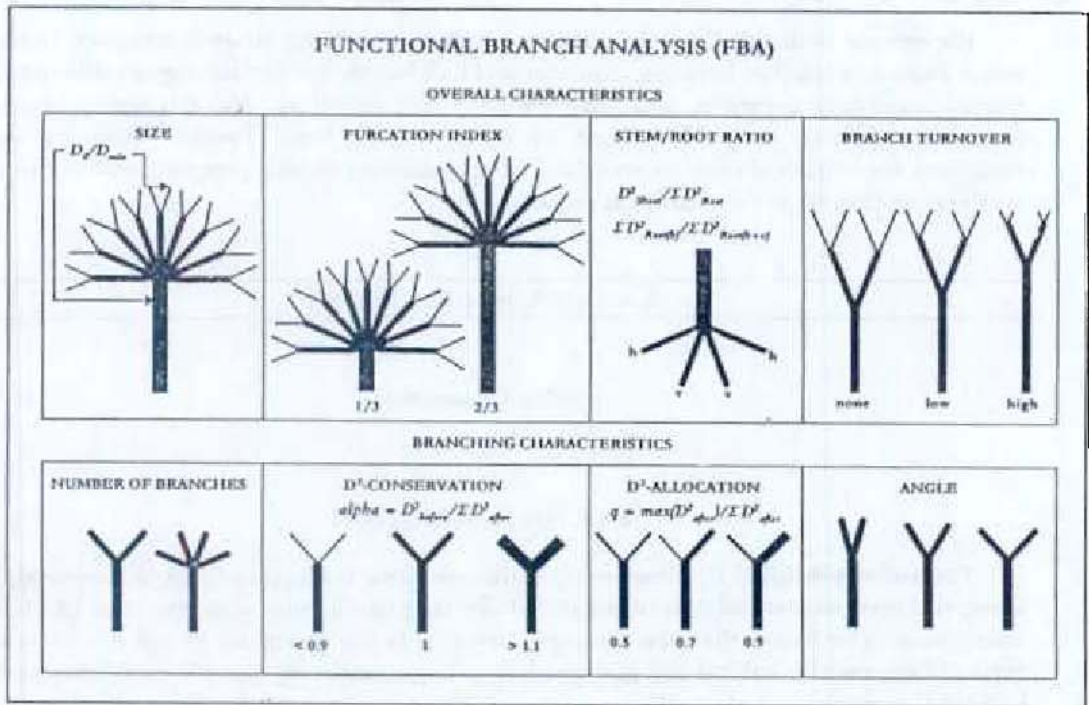


Figure 4.12. The main tree's branching properties used in FBA.

For actual measurement of the branching properties the basic data are collected for 20-50 'links' (sections between two branching points) on a tree, covering the whole diameter range present; Diam1 and Diam2 are measured halfway the link in two mutually perpendicular directions, reflecting the largest and smallest diameter for elliptical cross sections; the 'connected\_to' column refers to the link number before the branching point and is used to sort the data in subsequent analysis. The scheme can be applied above- as well as below-ground, after parts of the root system have been carefully exposed. The last 4 columns are needed when total leaf areas or fine root lengths are to be calculated, or graphical tree reconstructions are to be made:

Link_no	Length cm	Diam1 cm	Diam2 cm	Connected_to:	No. of leaves or fine roots	End link? Y or N	Compass angle	Angle with normal
1	--	--	--	0	--	--	--	--
2	--	--	--	1	--	--	--	--
3	--	--	--	1	--	--	--	--
4	--	--	--	2	--	--	--	--



Experience with the FBA program so far shows that the 'branch turnover' parameter, which links to a relation between diameter and link length has the strongest influence on the overall allometric equation and may explain why equations for relatively young trees (secondary forests) differ for those of more mature trees. Further tests are needed. Programs for statistical analysis and the fractal branching model, programmed as macro's in an Excel workbook are available on request.

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#### 4.4. SOIL MICRO-FLORA

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By:

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##### 4.4.1. INTRODUCTION

The soil is inhabited by a vast array of micro-biota: the soil bacteria, *actinomyces*, fungi, algae, and protozoa are all part of microbial diversity of the most dynamic sites of biological interaction. The forces that play an important role in the dynamics of soil micro-biota and their effects on the habitat are governed to a large extent by the physical, chemical, and biological components of a soil.

The intensification of agriculture in many developing countries is necessary to meet demands for foods due to population pressures. Agricultural lands have been extended by slash-and-burn land clearing, often followed by soil erosion, soil compaction, loss of biodiversity, environmental pollution and flooding.

Microbial diversity is an integral part of the entire biodiversity. It is generally accepted that biodiversity is of paramount importance to sustain agricultural productivity and maintain ecosystem-functioning. However, our knowledge of biodiversity is still limited. It is estimated that only 13% of the earth's microbial populations are identified (Hawksworth, 1991). Table 4.8 shows the number of species in the major group of bacteria, fungi, algae, and virus.