

BRANCHED STRUCTURES: THE OCCURRENCE, MORPHOLOGY
AND FUNCTION OF TREE-LIKE SYSTEMS

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Abstract

A tree in the botanical sense is a branching system designed to provide the greatest sunlight exposure of the leaves and to provide transport systems for water and nutrients between the soil and the leaves. The form of the tree and its roots is determined by genetic and environmental factors. The vascular system in plants has its counterpart in animals. The arterial systems in humans have specialized substructures which help, among other things, to control temperature and to promote reproduction. Malfunctioning of the arterial system is the principal cause of death among humans. The bronchial system (a tree with 30 generations of bifurcations) is uniquely designed for the transport and exchange of gases. The most complex forest of trees is the neural system of the cerebral cortex of man. The development and elaboration of the neural system, especially the details of branching of the dendrites and the distribution of spines, is governed by factors which have their analogies in botany.

The largest tree system on earth is the Amazon River basin. Theories of rivers, particularly as regards flow pattern, optimization, drainage and hierarchy have their analogies in living systems. The smallest tree system is a simple hydrocarbon. A. Cayley a century ago enumerated the isomers of octane. General methods have been worked out for more elaborate molecules. Branched molecules have different chemical reactivities and physical properties from linear molecules. This is of importance in combustion engineering (the anti-knock problem) and in the metabolism of stored carbohydrates (the diabetes problem). Stylized (Christmas tree) branching occurs in the RNA transcription required for protein synthesis and in the dendritic growth of crystals.

Tree-like systems can be conceptual as with the genealogical tree or with the phylogenetic tree. The former is only rarely a tree. The phylogenetic tree, in its modern form (e.g., the evolution of amino acid sequence in the phylogeny of hemoglobins), is the weighted binary decision-making tree of the computer programmer.

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