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*A Statistical Analysis of Allometric Size Distributions in Clonal and Non-Clonal Forests*

It has been shown that the branching network of the tallest tree, and the trunk distributions in an entire forest scale identically. This project studied whether clonal forests (such as those of the genus *Populus*) or non-clonal forests (such as those of the genera *Pinus* and *Pseudotsuga*) had trunk distributions closest to the expected inverse square law exponent of -2. Several broad locations were selected to examine, and within those locations, several areas were chosen, in the form of fifteen by fifteen meter groves. Within these groves, the diameter at breast height (dbh) of each of the trees of a single species was taken, ignoring trees less than breast height. This was repeated with another nearby grove of the opposite genus (clonal vs. non-clonal), and many times within each of the broad areas. The results were then converted into frequency distributions, binned to size classes of 1cm. The sample groves of each genus were synthesized together to form a representative population, and when analyzed based on an ordinary least squares power regression, *Populus* resulted in a scaling exponent of -2.007, *Pinus* and *Pseudotsuga* with a result of -1.649. Based on these results, clonal forests are more effective at distributing resources than non-clonal forests, because the scaling exponent of the *Populus* forests was closer to the expected value of -2, showing that the forests perform better structurally as a scaled version of the largest tree.