COMPARATIVE ANALYSIS OF WOOD ANATOMICAL DATA USING GEE MODELS.

<u>R. Aguirre-Hernández</u>¹, M. Olson², J. Rosell-García²

¹Faculty of Medicine, UNAM, Mexico ²Institute of Biology, UNAM, Mexico

Email: rebeca-aguirre@jmvertiz.posgrado.unam.mx

Comparative methods are used in biology to study the association between a trait and environmental variables or between different traits of related species. It has been recognized that species did not evolved independently over time. Thus, the correlation between species, depicted by the phylogeny, must be taken into account when analyzing the relationship between characters. Comparative data have been analyzed using generalized weighted least squares models. For response variables not having a normal distribution, generalized estimating equations were recently proposed by Paradis and Claude. In both types of models, special correlation matrices must be considered that reflect the mode of evolutionary change (Brownian motion, Martins and Hansen, etc.). Special subroutines have also been written to fit these models. In the mid eighties, Carlquist and Hoekman collected a large ecological wood anatomical data set on the flora of southern California. The authors performed a simple statistical analysis assuming independence between plants. We reanalyzed the data set with the aim of studying the relationship between the presence and absence of water conductive cells (the response variable) and vessel anatomical characteristics (the explanatory variables). We fitted two regression models. The first is a logistic regression model that assumes independence between plant species. The other is a generalized estimating equation that takes into account the phylogenetic relationships. The idea is to highlight any differences found between the two models with regard to the relationship between the response variable and the explanatory variables.