

Gerhard Jäger

*Phylogenetic Typology (joint work with Johannes Wahle)*

In this talk I will describe a novel method to estimate the frequency distribution of typological variables while controlling for statistical non-independence due to shared ancestry. Unlike previous approaches, this technique uses all available data, from language families large and small as well as from isolates, while controlling for different degrees of relatedness on a continuous scale estimated from the data. This approach involves three steps: First, distributions of phylogenies are inferred from lexical data. Second, these phylogenies are used as part of a statistical model to estimate transition rates between parameter states. Finally, the long-term equilibrium of the resulting Markov process is computed. As a case study, I will look at a series of potential word-order correlations across the languages of the world.