Title: Structural stability across methods, language families and geographic areas
Category: Oral presentation
Theme: Quantitative Linguistic Typology

Typological features vary in terms of their stability (Wichmann & Holman, 2009; Dediu, 2011), as do meanings in the basic vocabulary (Pagel *et al*., 2007) and biological genes (Woese et al., 1990). This talk will address the patterning of these differences in stability <u>across language families, methods of estimation, and geographical areas</u>, using advanced quantitative methods.

First, the talk will show that despite the large number of conceptualizations and ways of estimating structural stability, there is a <u>general agreement across very different quantitative methods</u> in what features tend to be stable and which not (Dediu & Cysouw, *in press*). This empirical result is very important and suggests that despite the inherent complexities involved in defining structural stability, there is exists a cross-method latent characteristic that ranks features on a stability scale.

Then the focus will move on a particular such method which uses <u>modern Bayesian phylogenetics</u> (Dediu, 2011; Dediu & Levinson, 2012) to estimate the stability of the structural features in WALS across as many language families as possible. To guard against methodological and data coding biases, I used two different software implementations (the off-the-shelf `MrBayes 3` widely used in evolutionary biology, and the custom-written `BayesLang`), two different coding of the WALS data (the original polymorphic and a binary coding) and three genealogical classifications of languages (WALS, the Ethnologue, and Hammarström's 2010 "orthodox" families). This quantitative method found that (i) there are <u>cross-family (universal) tendencies</u> for some structural features to be more stable than others, but that (ii) there are <u>important inter-family differences</u> in their ranking of features' stabilities, and, surprisingly, (iii) that there is also <u>large-scale among-families patterning</u> of structral stability.

The first level (i) reinforces the idea that features are differently affected by the factors driving language change across families and areas in that some <u>features tend to be universally more stable</u>. The second level (ii) simply shows that <u>language family-specific factors</u> have an important role to play. The intermediate level (iii) seems to point to <u>deep genealogical and areal relationships between families</u>, such as the similarity between language families within the Americas, and between those spanning the Americas and North-East Eurasia, possibly reaching to a time-depth of at least 12,000 years ago.

Taken together, these findings suggest that s<u>tructral stability can be measured across methods</u>, and that it is <u>patterned at three levels</u>: universal tendencies, large-scale among family, and between individual families.

References
Dediu, D. (2011). A Bayesian phylogenetic approach to estimating the stability of linguistic features and the genetic biasing of tone. *Proceedings of the Royal Society B* **278**:474-479.
Dediu, D., & Cysouw, M. A. (*in press*). Some structural aspects of language are more stable than others: A comparison of seven methods. *PLoS One*.
Dediu, D., & Levinson, S. C. (2012). Abstract profiles of structural stability point to universal tendencies, family-specific factors, and ancient connections between languages. *PLoS One*, **7**:e45198.
Hammarström, Harald. (2010) A full-scale test of the language farming dispersal hypothesis. *Diachronica* **27**:197-213.
Pagel, M., Atkinson, Q. D., & Meade, A. (2007). Frequency of word-use predicts rates of lexical evolution throughout Indo-European history. *Nature*, **449**:717–721.
Wichmann, S. & Holman, E. (2009). Assessing temporal stability for linguistic typological features *LINCOM Europa:Munchen*, http://email.eva.mpg.de/ wichmann/WichmannHolmanIniSubmit.pdf.
Woese, C.R., Kandler, O. & Wheelis, M.L. (1990). Towards a natural system of organisms: proposal for the domains Archaea, Bacteria, and Eucarya. *PNAS* **87**:4576-4579.