Weighing the contribution of substrates and superstrates: another take

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The question of how to account for the similarities between creole languages has been at the heart of the field of creolistics ever since its beginning as a separate branch of linguistics. Early writers such as Adam, Coelho and Schuchardt have paved the way for the current theories concerning the origins of these similarities and their positions are still reflected in today's main schools of thinking.

This paper deals with the issue of the origins of the structural similarities observed in creoles from a new perspective, applying classificatory tools developed for biology to linguistic data.

The set of 97 structural features taken from the sample of 18 creoles presented in the *Comparative Creole Syntax* volume (Holm and Patrick 2007) will serve as the basis for an analysis with the software SplitsTree (Huson and Bryant 2006). A sample of 18 substrate languages will be carefully selected and coded as binary pairs along the lines of Holm and Patrick. Similarly, these morphosyntactic features will be encoded for 6 lexifiers and will be added to the dataset.

The resulting split networks will then be used to assess the validity of the substratist and superstratist positions. If the substratist theory is correct, we expect the creoles to cluster with their respective substrates and, on the contrary, if the superstratist approach is valid, then we expect the creoles to cluster with their respective lexifiers.

References:

Holm, John and Peter L. Patrick. (2007). *Comparative Creole Syntax*. London: Battlebridge.
Huson, Daniel H. and David Bryant. (2006). Application of Phylogenetic Networks in Evolutionary Studies. Molecular Biology and Evolution, 23(2): 254-267.