

THE COMPLEXITY HYPOTHESIS AS AN UNDERLYING EXPLANATION OF VARIABLE RATES OF DIFFUSION

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Following Thomason and Kaufmann (1988) there has been growing acceptance that there are no fixed constraints on which linguistic features can potentially be transferred between languages (Aikhenvald 2006). This does not mean that all features are equally likely to be transferred however, and a number of “Borrowability hierarchies” have been proposed (Curnow 2001, Haspelmath & Tadmor 2009). This paper applies the *Complexity Hypothesis* of evolutionary biology to give a Darwinian explanation of these hierarchies. The *Linguistic Complexity Hypothesis* is shown to account for several previously identified factors affecting borrowability patterns, linking these factors together and explaining their relevance.

In biology genetic borrowing between species follows similar patterns to those observed in linguistics, certain types of gene are more likely to diffuse than others. The “complexity hypothesis” offers a simple and elegant evolutionary explanation for this (Jain et al. 1999). This paper argues that the complexity hypothesis can be generalized to a Universal Darwinian principle (Blackmore 1999) equally applicable to linguistics as to biology. It is not the original biological theorem that is applied, rather a suitably modified linguistic version.

Applying this modified version to linguistic diffusion accounts for the suggested borrowability hierarchies. Interestingly it can also be seen as explaining a number of the factors previously identified as affecting these hierarchies, such as structural complexity and morphosyntactic transparency. Several subtler patterns of borrowing are also predicted by the complexity hypothesis. These are empirically testable and provide a potential way of verifying or refuting the applicability of the complexity hypothesis to linguistics.

References.

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