

# Simple Correlated Evolution of Typological Features

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Suppose, for a set of languages, we are given

- A** A database of typological features
- B** A database of genealogical relationships

We suggest the following lightweight method to check to which extent a change in one typological feature  $F1$  triggers a change in another feature  $F2$ :

1. Project values for the typological features to intermediate nodes in the genealogical classification using parsimony reconstruction (Felsenstein 2004)
2. To check whether transitions between the values taken by  $F1$  can be better predicted by knowing the corresponding transitions in  $F2$ , we use the information theoretic implication defined in Hammarström and O'Connor (2013)
3. To the extent that knowing the transitions in  $F2$  helps predicting the transitions in  $F1$  we have evidence for correlated evolution

Applied to 299 languages of the Nijmegen Typological Survey (NTS) dataset and the genealogical relationship of Hammarström et al. (2014), we find that a small number of feature pairs show correlated evolution, and do so even when the evidence from lack of change is disregarded (i.e., they do not show correlated evolution simply because neither of the features ever changed). The feature pairs which exhibit correlated evolution are precisely the ones where one would expect a form-function tradeoff essentially avoiding overloading (“if you use verb final for this, don’t ALSO use verb medial for the same thing”). They are *not* the cases predicted by parsing or cross-categorical symmetry (Hawkins 2014, Song 2012).

The study is similar in spirit to that of Dunn et al. (2011) but with more dense data and differences in method (with both advantages and disadvantages).

## References

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