Disentangling contact and inheritance in lexical semantics

We invite scholars working on areal or phylogenetic dimensions of lexical semantics to submit abstracts of up to 300 words for a proposed workshop at SLE 2025. Please send abstracts to John Mansfield john.mansfield@uzh.ch and Paul Widmer paul.widmer@uzh.ch, by **Tuesday 19 November**. We will include selected abstracts in our workshop proposal, which will be evaluated by the SLE committee. If successful, final abstracts will be due in January.

SLE 2025 will be held in Bordeaux, France, from 26-29 August.
https://societaslinguistica.eu/sle2025/first-call-for-papers/

Recent years have seen growth in the study of comparative lexical semantics, especially but not limited to the "colexification" paradigm (François 2008). Colexification research investigates, for example, the distribution of languages that either distinguish HAND from ARM, or "colexify" HAND/ARM. Much more research is still required to understand how such distributions are shaped by phylogenetic inheritance and areal contact.

A special issue of *Linguistic Typology* on Areal Semantics (Schapper & Koptjevskaja-Tamm 2022) has highlighted the need for more systematic research on areal clustering of lexical meanings. For example languages of the Hindu Kush area use kinship terms that group into geographic clusters, while cross-cutting phylogenetic clades (Liljegren 2022). Similarly, a region of western Africa exhibits particular colexifications of colour terms with natural colour sources (e.g. YELLOW = LOCUST BEAN), though the presence of many unrelated lexemes indicates conceptual patterns that have spread through multilingual interaction, as opposed to purely lexical inheritance (Segerer & Vanhove 2022). These studies highlight that inheritance in lexical semantics can be considered either in terms of phylogenetic clades, specific etymologies, or cognate sets.

Other studies have focused more on the diachronic dimension. Various studies have investigated common semantic changes in etymological chains (e.g. Wilkins 1996; Traugott & Dasher 2001), and several projects are now underway to investigate these effects more systematically, including EvoSem (François & Kalyan 2023) and DiACL (Carling et al. 2023).

Both areal and phylogenetic dimensions can also be studied against the background of universal patterns in lexical semantics. Semantic research here intersects with cognitive science and theories of communicative efficiency, with key findings on kinship (Kemp & Regier 2012), colour (Zaslavsky et al. 2020), numbers (Calude & Verkerk 2016), and the natural environment (Regier et al. 2016). This intersection has led to a burst of research on global colexification patterns, focusing especially on general cognitive biases relating to efficiency, similarity and association. These biases drive similar colexification patterns among languages of the world (Srinivasan & Rabagliati 2015; Youn et al. 2016; Xu et al. 2020; Brochhagen & Boleda 2022; Tjuka et al. 2024), as well as child language (Brochhagen et al. 2023) and artificial language learning (Karjus et al. 2021).

While systematic global studies have tended to focus on lexical semantic universals, in this workshop we are seeking submissions that pay particular attention to how universals are modulated by areal and phylogenetic effects, and especially studies that aim to disentangle the two. In typological research more generally, there have been significant recent advances in distinguishing contact vs inheritance (e.g. Ranacher et al. 2021; Allassonnière-Tang et al. 2021; Neureiter et al. 2022; Guzmán Naranjo & Mertner 2023). An obvious next step is to apply such methods to lexical semantics, which will provide a more robust test for claims of universals, while also investigating claims of areality in a more rigorous way.

We particularly seek submissions characterised by:

1. Methodological innovation and statistical techniques;
2. Investigation of large datasets such as Lexibank;
3. Use of corpora or large language models for comparative lexical semantics;
4. Regional case studies compared against global baselines;
5. Phylogenetic modelling;
6. Cluster detection based on geographic or genetic proximity.

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