Horizontal transfer and phylogenetic calibration in linguistics: a Bayesian approach

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Introduction & Summary

- Dating language divergence poses a challenge in linguistics
- Bayesian methods and results of historical-comparative linguistics together help answer the challenge.
- Absolute calibrations are usually used to obtain divergence times of a linguistic subfamilies in calendar years. However, they are hard to establish[1], especially for families without written records.
 Most linguistic datasets contain results of horizontal transfer, e.g. loanwords, due to language contacts.

Materials

Uralex 1.0. and its tagged borrowings

- Basic vocabulary dataset of 26
 Uralic languages [3]
- Known borrowings tagged using etymological literature [4]

Results & Conclusion

- Our relative calibration method estimates Proto-Uralic divergence at approx 5,250 YBP (95% HPD 4,000-6,600)
- Analysing same data with absolute calibrations based on loanwords

- Although often thought of as "noise", loanwords carry valuable timing information as contact happens between contemporaneous languages.
- Uralic has long-standing contacts with Indo-European, a family which has been extensively researched and whose timing is better understood.
- We test "relative calibration" of linguistic phylogenies using Indo-European loanwords acquired into the Uralic family and the effects on dating Proto-Uralic and intermediate protolanguages.



 Certainty estimate given using evaluative literature

Example: borrowings in Standard Estonian



Figure 3: Proportion of borrowings, source languages and certainty estimations in the Uralex Standard Estonian sample

Indo-European timings

 The Indo-European language family is well-studied and has written records, which has enabled thoroughly calibrated phylogenetic analyses to estimate divergence

- yields a much older date of approx 6,700 YBP[6].
- Both estimates older than a recent popular hypothesis in Uralic linguistics of ca. 4000 YBP[7, 8].





Figure 6: Posterior age estimates for different Uralic subfamilies for relative vs absolute calibrations.

 The histories of language families known to have been in contact should be co-estimated to ensure

Figure 1: The Uralic language family. Map by T. Rantanen (BEDLAN)



Methods

- Simultaneous sampling of Uralic and IE trees in a single MCMC chain using BEAST 2.
- Uralic tree includes UraLex data, whose evolution is modelled with a relaxed lognormal clock.
- The Indo-European tree has no data, but interior node times are constrained to match published posteriors.
- Sampling is constrained so that trees are only accepted if there is some non-zero overlap in the lifespan of the ancestors of each pair of subfamilies with identified

consistency with linguistic knowledge and make use of all available data.

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Acknowledgements

Figure 2: An example of a calibrated phylogeny of the Uralic language family using narrow distribution priors for absolute calibrations only[2]

borrowings.

Figure 4: Compatible trees

Figure 5: Incompatible trees

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