

## The effect of priors on tree topologies

26. February 2021


The Phylogenetic Party


## Linguistics: Inferring Trees

- Inferring Language Family Trees

Grollemund et al. (2015); Bowern and Atkinson (2012)

- Dating Language Families

Rama (2018); Chang, Cathcart, Hall, and Garrett (2015); Gray and Atkinson (2003)

- Spread of Languages

Bouckaert et al. (2012)

## Linguistics: Using Trees

- Lexical Change

Greenhill et al. (2017)

- Reconstruction

Bouchard-Côté, Hall, Griffiths, and Klein (2013); Jäger and List (2018)

- Comparative Studies

Calude and Verkerk (2016); Dunn, Greenhill, Levinson, and Gray (2011); Cathcart, Hölzl, Jäger, Widmer, and Bickel (2020)

- Language Diversity

Bentz, Dediu, Verkerk, and Jäger (2018)

Checking Models!

- Models and Data

Yanovich (2018); Rama, List, Wahle, and Jäger (2018)

- The effect of Priors

Rama (2018)

- Probability of "false positive" results Rönchen \& Wiklund (2021, MaEiQCL)


## Priors over Priors



## Priors over Priors



## Different Priors

- Accross-Site Rate Variation
- Equal Rates
- Gamma Distributed
- Topology Priors
- unconstrained
- Birth Death Process + strict clock
- Birth Death Process + Relaxed clock (independent gamma)
- Uniform + strict clock
- Uniform + Relaxed clock (independent gamma)


## Data (c.f. Rama et al. (2018))

| Dataset | \# Meanings | \# Languages |
| :--- | :---: | :---: |
| Austronesian (Greenhill, Blust, \& Gray, 2008) | 210 | 45 |
| Austro-Asiatic (Sidwell, 2015) | 200 | 58 |
| Indo-European (Dunn, 2012) | 208 | 42 |
| Pama-Nyungan (Bowern \& Atkinson, 2012) | 183 | 67 |
| Sino-Tibetan (Peiros, 2004) | 110 | 64 |

Methods

- Mr. Bayes (Ronquist \& Huelsenbeck, 2003) + BEAGLE (Suchard \& Rambaut, 2009)
- 2 Runs, $4 \times 10^{6}$ generations, $25 \%$ burn-in, sample every 5000 generations
- spr-space (Whidden \& Matsen, 2015) + Cytoscape (Shannon et al., 2003)


## Analysis

|  | Austroasiatic | Austronesian | Indo-European | Pamanungian | Sino-Tibetean |
| :--- | ---: | ---: | ---: | ---: | ---: |
| eq rates, BD, strict clock | 0.02 | 0.11 | 0.02 | 0.13 | 0.06 |
| eq rates, BD, IGR clock | 0.01 | 0.11 | 0.03 | 0.14 | 0.07 |
| eq rates, CD | 0.01 | 0.06 | 0.04 | 0.14 | 0.08 |
| eq rates, uniform, strict clock | 0.02 | 0.11 | 0.02 | 0.13 | 0.07 |
| eq rates, uniform, IGR clock | 0.01 | 0.11 | 0.03 | 0.14 | 0.07 |
| $\gamma$ rates, BD, strict clock | 0.01 | 0.11 | 0.02 | 0.13 | 0.06 |
| $\gamma$ rates, BD, IGR clock | 0.01 | 0.11 | 0.03 | 0.14 | 0.05 |
| $\gamma$ rates, CD | 0.01 | 0.05 | 0.03 | 0.14 | 0.06 |
| $\gamma$ rates, uniform, strict clock | 0.01 | 0.11 | 0.02 | 0.13 | 0.06 |
| $\gamma$ rates, uniform, IGR clock | 0.01 | 0.11 | 0.03 | 0.14 | 0.06 |

Mean Generalized quartet distances between trees in the posterior distribution and the gold standard tree. (Pompei, Loreto, \& Tria, 2011)

GQDs


## GQDs



GQDs


## SPR spaces - Austro Asiatic

## SPR spaces - Austro Asiatic

## Topologies

$\gamma$ rates, BD, strict clock: 388
$\gamma$ rates, BD, IGR clock: 2795
$\gamma$ rates, CD: 475
$\gamma$ rates, uniform, strict clock: 672
$\gamma$ rates, uniform, IGR clock: 3881

## SPR spaces - Austro Asiatic

## SPR spaces - Austronesian

## SPR spaces - Austronesian



## SPR spaces - Austronesian

## SPR spaces - Indo European

## SPR spaces - Indo European

## Topologies

$\gamma$ rates, BD, strict clock: 256
$\gamma$ rates, BD, IGR clock: 1194
$\gamma$ rates, CD: 138
$\gamma$ rates, uniform, strict clock: 210
$\gamma$ rates, uniform, IGR clock: 2957

## SPR spaces - Indo European

## Summary

- In terms of the GQD (almost) all models/priors perform equally well
- However the posterior distributions of tree topologies differ
- Caveat: Relaxed Clock (IGR) models explore the most tree topologies
- Across Site rate variation shows a mixed picture
- We can investigate the posterior distribution of trees and detect pathological behavior or regions


## References

Bentz, C., Dediu, D., Verkerk, A., \& Jäger, G. (2018, nov). The evolution of language families is shaped by the environment beyond neutral drift. Nature Human Behaviour, 2(11), 816-821. doi: 10.1038/s41562-018-0457-6 Bouchard-Côté, A., Hall, D., Griffiths, T. L., \& Klein, D. (2013, feb). Automated reconstruction of ancient languages using probabilistic models of sound change. Proceedings of the National Academy of Sciences, 110(11), , Hall, D., Griffiths, T. L., \& Klein, D. (2013, feb)
4224-4229. doi: $10.1073 /$ pnas. 1204678110
Bouckaert, R., Lemey, P., Dunn, M., Greenhill, S. J., Alekseyenko, A. V., Drummond, A. J., Atkinson, Q. D. (2012), Mapping the origins and expansion of the Indo-European language family Science, 337(6097), 957-960. Bowern, C., \& Atkinson, Q. D. (2012). Computational phylogenetics of the internal structure of pama-nguyan. Language, 88(4), 817-845. doi: 10.1353/lan.2012.0081
Calude, A. S., \& Verkerk, A. (2016, apr). The typology and diachrony of higher numerals in Indo-European: a phylogenetic comparative study. Journal of Language Evolution, 1(2), 91-108. doi: 10.1093/jole/lzw003 Cathcart, C. A., Hölzl, A., Jäger, G., Widmer, P., \& Bickel, B. (2020, oct). Numeral classifiers and number marking in indo-iranian. Language Dynamics and Change, 1-53. doi: 10.1163/22105832-bja10013 Chang, W., Cathcart, C., Hall, D., \& Garrett, A. (2015). Ancestry-constrained phylogenetic analysis supports the indo-european steppe hypothesis. Language, 91(1), 194-244.
Dunn, M. (2012). Indo-european lexical cognacy database (ielex).
Dunn, M., Greenhill, S. J., Levinson, S. C., \& Gray, R. D. (2011, apr). Evolved structure of language shows lineage-specific trends in word-order universals. Nature, 473(7345), 79-82. doi: 10.1038/nature09923 Gray, R. D., \& Atkinson, Q. D. (2003, November). Language-tree divergence times support the anatolian theory of indo-european origin. Nature, 426(6965), 435-439
Greenhill, S. J. Blust R \& Gray R. D. (2008, November). The Austronesian Basic Vocabulary Database: from bioinformatics to lexomics. Evolutionary bioinformatics online 4 , $271-283$.
Greenhill, S. J., Wu, C.-H., Hua, X., Dunn, M., Levinson, S. C., \& Gray, R. D. (2017). Evolutionary dynamics of language systems. Proceedings of the National Academy of Sciences. Retrieved from
htts://www pnas.org/centent/early/2017/10/02/1700388114 doi: 10.1073/pnas. 1700388114
Grollemund, R., Branford, S., Bostoen, K., Meade, A., Venditti, C., \& Pagel, M. (2015, sep). Bantu expansion shows that habitat alters the route and pace of human dispersals. Proceedings of the National Academy of Sciences, 112(43), 13296-13301. doi: 10.1073/pnas.1503793112
Jäger, G., \& List, J.-M. (2018, jun). Using ancestral state reconstruction methods for onomasiological reconstruction in multilingual word lists. Language Dynamics and Change, 8(1), 22-54. doi: 10.1163/22105832-00801002 Peiros, I. (2004). Dataset on sino-tibetan languages encoded in starling.
Pompei, S., Loreto, V., \& Tria, F. (2011). On the accuracy of language trees. PloS one, 6(6), e20109
Rama, T. (2018). Three tree priors and five datasets. Language Dynamics and Change, 8(2), 182-218. doi: 10.1163/22105832-00802005
Rama, T., List, J.-M., Wahle, J., \& Jäger, G. (2018). Are automatic methods for cognate detection good enough for phylogenetic reconstruction in historical linguistics? In Proceedings of the north american chapter of the association of computational linguistics (p. 393-400). Retrieved from https ://aclanthology .coli . uni-saarland.de/papers/N18-2063/n18-2063 Ronquist, F., \& Huelsenbeck, J. P. (2003, August). MrBayes 3: Bayesian phylogenetic inference under mixed models. Bioinformatics (Oxford, England), 19, 1572-1574. Shannon, P., Markiel, A., Ozier, O., Baliga, N. S., Wang, J. T., Ramage, D., ... Ideker, T. (2003, nov). Cytoscape: A software environment for integrated models of biomolecular interaction networks. Genome Research, 13(11), 2498-2504. doi: 10.1101/gr. 1239303
Sidwell, P. (2015). Austroasiatic dataset for phylogenetic analysis: 2015 version. Mon-Khmer Studies (Notes, Reviews, Data-Papers), 44, Ixviii-ccclvii
Suchard, M. A., \& Rambaut, A. (2009, apr). Many-core algorithms for statistical phylogenetics. Bioinformatics, 25(11), 1370-1376. doi: 10.1093/bioinformatics/btp244 Whidden, C., \& Matsen, F. A. (2015, jan). Quantifying MCMC exploration of phylogenetic tree space. Systematic Biology, 64(3), 472-491. doi: 10.1093/sysbio/syv006 Yanovich, I. (2018, jun). The effect of dictionary omissions on phylogenies computationally inferred from lexical data. Language Dynamics and Change, 8(1), 78-107. doi: 10.1163/22105832-00801007

