

The evolution of word-order universals: Some word-order correlations are lineage specific - others might be universal

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December 15, 2017



WORDS BONES GENES TOOLS
Tracking Linguistic, Cultural, and Biological Trajectories of the Human Past

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DFG

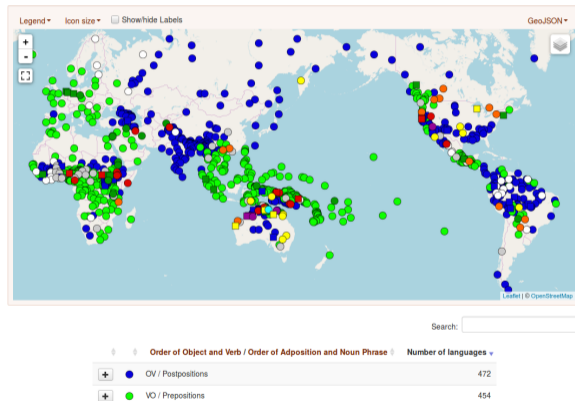


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Introduction

Word order correlations

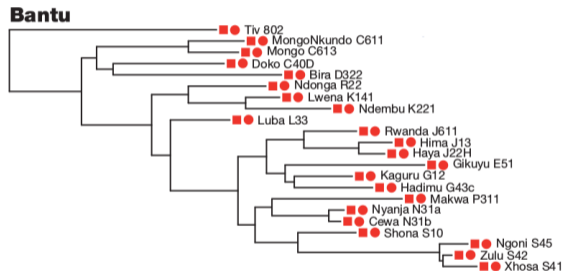
- Greenberg, Keenan, Lehmann etc.: general tendency for languages to be either consistently head-initial or consistently head-final
- alternative account (Dryer, Hawkins): phrases are consistently left- or consistently right-branching
- can be formalized as collection of implicative universals, such as
With overwhelmingly greater than chance frequency, languages with normal SOV order are postpositional. (Greenberg's Universal 4)
- both generativist and functional/historical explanations in the literature



Phylogenetic non-independence

- languages are phylogenetically structured
- if two closely related languages display the same pattern, these are not two independent data points

⇒ we need to control for phylogenetic dependencies



(from Dunn et al., 2011)

Phylogenetic non-independence

Maslova (2000):

“If the A-distribution for a given typology cannot be assumed to be stationary, a distributional universal cannot be discovered on the basis of purely synchronic statistical data.”

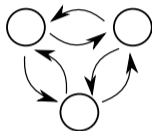
*“In this case, the only way to discover a distributional universal is to **estimate transition probabilities** and as it were to ‘predict’ the stationary distribution on the basis of the equations in (1).”*



The phylogenetic comparative method

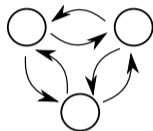
Modeling language change

Markov process



Modeling language change

Markov process

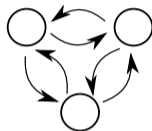


Phylogeny



Modeling language change

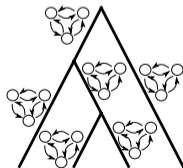
Markov process



Phylogeny

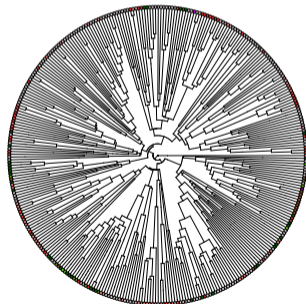


Branching process



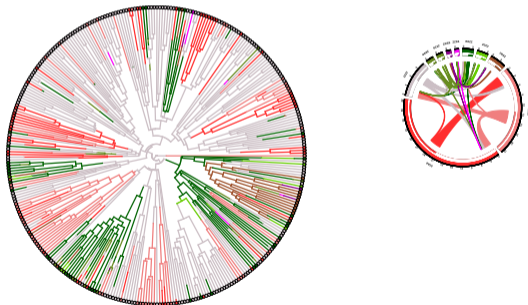
Estimating rates of change

- if phylogeny and states of extant languages are known...



Estimating rates of change

- if phylogeny and states of extant languages are known...
- ... transition rates, stationary probabilities and ancestral states can be estimated based on Markov model

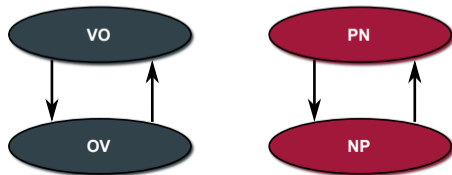


Correlation between features

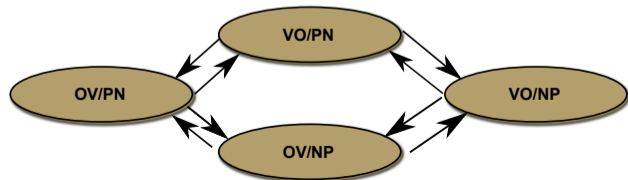
Pagel and Meade (2006)

- construct two types of Markov processes:
 - **independent:** the two features evolve according to independent Markov processes
 - **dependent:** rates of change in one feature depends on state of the other feature
- fit both models to the data
- apply statistical model comparison

Independent model



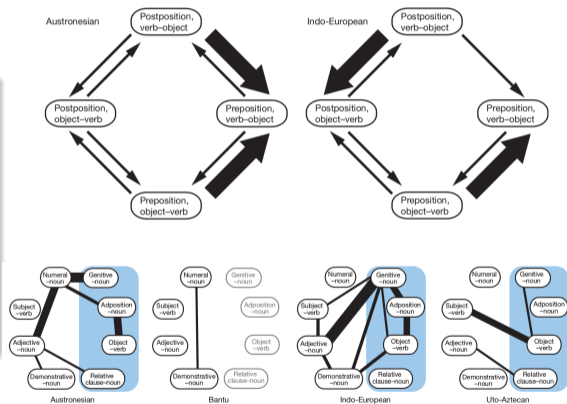
Dependent model



Dunn et al. (2011)

Dunn et al. (2011)

- all 28 pairs of 8 word-order features considered
- 4 language families: Austronesian, Bantu, Indo-European, and Uto-Aztecan
- main finding: wildly different results between families
- conclusion:
word-order correlations are lineage-specific



Universal and lineage-specific models

This study

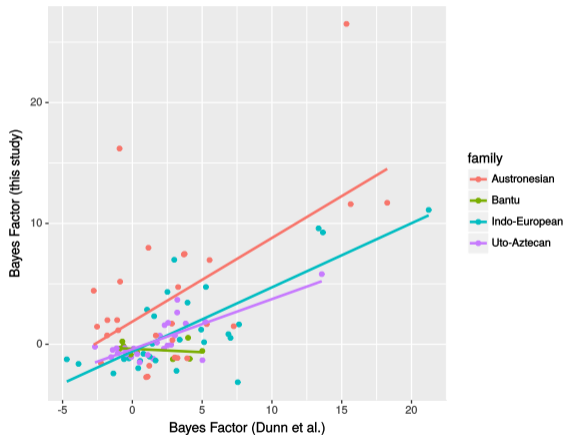
Experiments

- ① replication of Dunn et al. (2011) with different data
- ② model comparison: universal vs. lineage-specific correlations
- ③ word-order correlations across a world-tree of languages
- ④ automatically identifying lineage-specificity

Data

- **word-order data:** WALS
- **phylogeny:**
 - ASJP word lists (Wichmann et al., 2016)
 - feature extraction (automatic cognate detection, *inter alia*) \rightsquigarrow character matrix
 - Maximum-Likelihood phylogenetic inference with Glottolog (Hammarström et al., 2016) tree as backbone
 - advantages over hand-coded Swadesh lists
 - applicable across language families
 - covers more languages than those for which expert cognate judgments are available
 - 1004 languages in total
 - Austronesian: 123; Bantu: 41; Indo-European: 53; Uto-Aztecan: 13

Replication of Dunn et al.

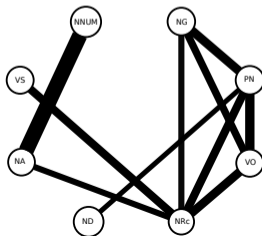


Comparing universal and lineage-specific models

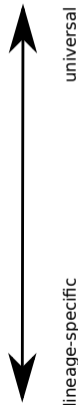
- so far: fitting a separate model for each language family
 - **advantage:** good fit of the lineage-specific data
 - **disadvantage:** many parameters (8 per family for a dependent model)
- statistical model comparison: quantifying to what degree the data support the excess parameters of lineage-specific models
- models to be compared:
 - **universal:** one set of rates (8 parameters), applying to all 4 families
 - **lineage specific:** a separate set of rates for each family
- comparison via **Bayes Factor**
(implementation with RevBayes; Höhna et al. 2016)

Results

- very strong evidence for universality:
 - noun-adjective \leftrightarrow noun-numeral
 - adposition-noun \leftrightarrow verb-object
- strong evidence for universality:
 - adposition-noun \leftrightarrow verb-object \leftrightarrow noun-genitive \leftrightarrow noun-relative clause
- strong or very strong evidence for lineage specificity:
 - behavior of noun-adjective and noun-numeral

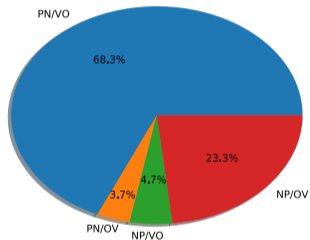
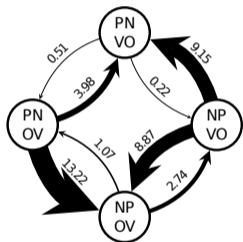


feature pair	Bayes Factor
NA-NNum	16.24
PN-VO	15.22
PN-NG	9.45
VO-NRc	9.21
PN-NRc	8.69
NRc-VS	8.18
NG-VO	7.92
NG-NRc	6.55
NA-NRc	6.49
PN-ND	5.42
ND-NRc	4.32
VO-VS	3.15
PN-VS	1.71
NA-ND	0.54
ND-VO	0.37
NA-VO	-2.07
ND-NG	-3.17
NA-PN	-3.40
NNum-VS	-8.13
NNum-NRc	-8.40
NA-VS	-9.66
NG-VS	-9.84
NA-NG	-10.94
ND-NNum	-12.12
ND-VS	-15.01
PN-NNum	-16.37
NNum-VO	-17.57
NG-NNum	-28.63

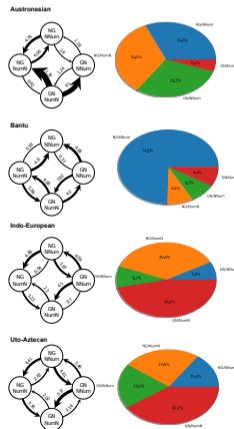


Results

universal (PN/VO)



lineage-specific (NG/NNum)



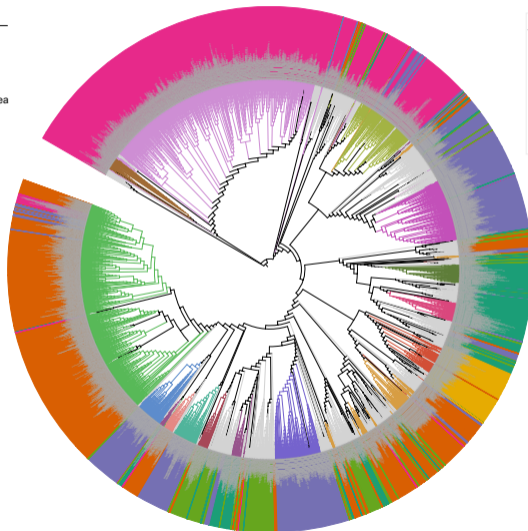
Using the world tree

Glottolog family

- Atlantic-Congo
- Mande
- Afro-Asiatic
- Nuclear_Trans_New_Guinea
- Pama-Nyungan
- Timor-Alor-Pantar
- Otomanguean
- Indo-European
- Uto-Aztecan
- Tai-Kadai
- Mayan
- Austronesian
- Austroasiatic
- Sino-Tibetan
- Quechuan

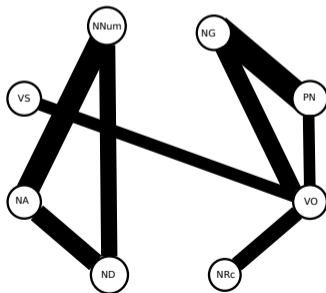
Macro-Area

- Africa
- Papunesia
- Eurasia
- South America
- North America
- Australia

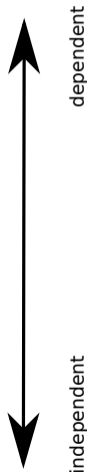


Results

- strong evidence for dependent model for 21 out of 28 feature pairs
- no evidence for independent model
- strongest evidence ($BF > 100$) supports Dryer (1992)

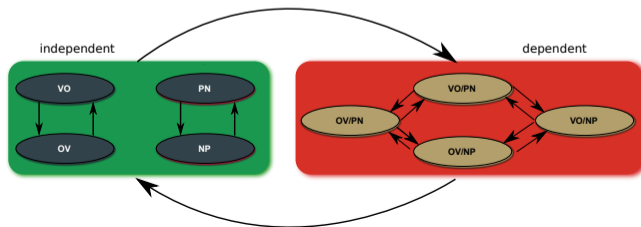


feature pair	Bayes Factor
PN-VO	267.83
PN-NG	220.74
NA-NNum	192.78
NA-ND	163.62
NG-VO	152.64
ND-NNum	140.17
VO-NRc	129.74
VO-VS	105.73
NG-NRc	99.82
PN-NRc	99.28
NA-NRc	84.36
NG-VS	83.68
ND-NRc	71.32
PN-VS	57.51
NNum-VS	37.25
NNum-NRc	36.54
NRc-VS	17.28
ND-NG	16.75
NA-NG	16.55
ND-VO	14.00
NNum-VO	12.43
PN-ND	6.99
NA-VS	5.91
NA-PN	3.84
NA-VO	3.24
ND-VS	1.25
PN-NNum	-0.75
NG-NNum	-2.38

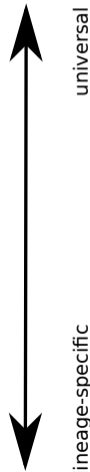


Automatically identifying lineage-specificity

- lineages with different dynamics can be inferred automatically on the world tree
- latest version of *BayesTraits* (v. 3) implements a model (“discrete covarion model”) where languages can be either in a dependent or an independent state
- statistical model comparison between universal and lineage-dependent model (in this sense)

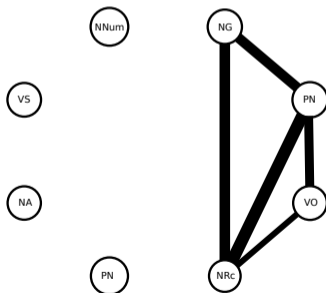


feature pair	Bayes Factor
PN-NRc	0.42
NG-NRc	-0.90
PN-NG	-1.37
PN-VO	-2.29
VO-NRc	-4.86
NA-ND	-11.66
NA-NRc	-21.42
ND-NNum	-22.86
ND-NRc	-23.16
NG-VO	-25.20
PN-VS	-25.70
ND-VS	-28.63
NG-VS	-29.05
VO-VS	-29.74
PN-ND	-30.35
ND-VO	-30.90
NA-NNum	-31.42
ND-NG	-37.75
NA-VS	-40.18
NRc-VS	-44.06
NA-PN	-44.25
NNum-VS	-45.30
NA-VO	-49.34
NNum-NRc	-53.38
PN-NNum	-55.88
NA-NG	-58.86
NNum-VO	-64.76
NG-NNum	-66.61

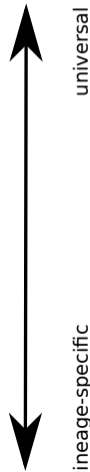


Automatically identifying lineage-specificity

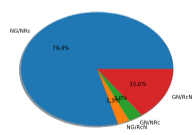
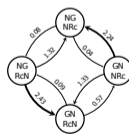
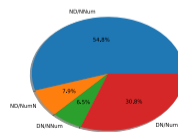
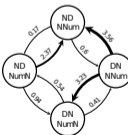
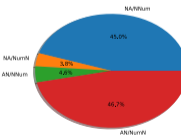
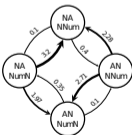
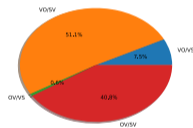
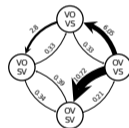
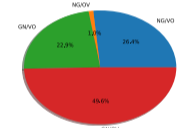
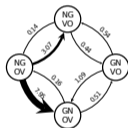
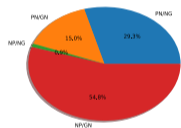
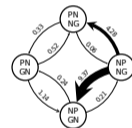
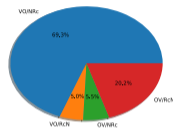
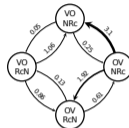
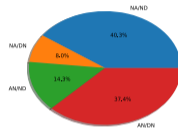
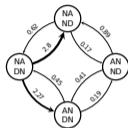
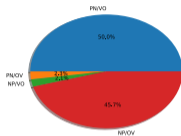
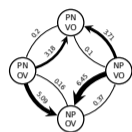
- no evidence for truly universal dependent model
- equivocal evidence for 5 feature pairs
- define a cluster for which there was strong evidence for universality in experiment 2



feature pair	Bayes Factor
PN-NRc	0.42
NG-NRc	-0.90
PN-NG	-1.37
PN-VO	-2.29
VO-NRc	-4.86
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What the dependencies look like



Conclusion

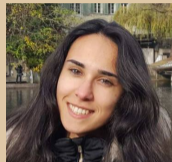
Conclusion

- empirical
 - *universal vs. lineage-specific* is not an absolute distinction, but a matter of degree
 - some “classical” word-order correlation fall very close to the universal end
- methodological
 - important to fit statistical model across language-families

Our co-authors



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- Matthew S. Dryer. The Greenbergian word order correlations. *Language*, 68(1):81–138, 1992.
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