

Referential scales and differential case marking: A study using hierarchical models in Bayesian phylogenetics

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

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DFG

Case alignment systems

Universal syntactic-semantic primitives

- three universal core roles

S: intransitive subject

A: transitive subject

O: transitive object

German

Der Junge ist dreckig.
the boy.NOM is dirty
'The boy is dirty.'

Der Junge wirft einen Stein.
DEF boy.NOM throw a.ACC stone
'The boy is throwing a stone.'

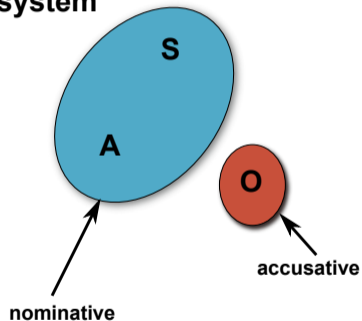
S
A
O

Kalkatungu (Australia)

Kaun muu-yan-ati
dress.ABS dirt-PROP-INCH
'The dress is dirty.'

Kuntu wampa-ngku kaun muu-yan-puni-mi.
not girl-ERG dress.ABS dirty-PROP-CAUS-FUT
'The girl will not dirty the dress.'

Accusative system



Latin

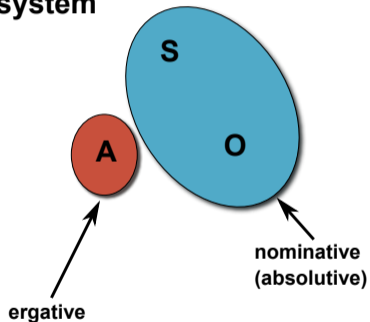
Puer puellam vidit.

boy.NOM girl.ACC saw *'The boy saw the girl.'*

Puer venit.

boy.NOM came *'The boy came.'*

Ergative system

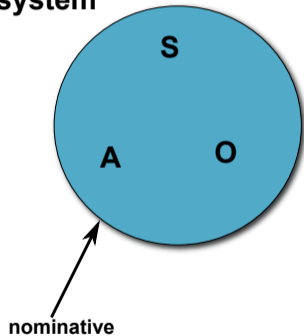


Dyirbal

ɲuma yabu-ɲgu bura-n.
father mother.ERG see-NONFUT
'The mother saw the father.'

ɲuma banaga-nu.
boy.NOM came *'The boy came.'*

Neutral system



Mandarin

rén lái le.

person come CRS

'The person has come.'

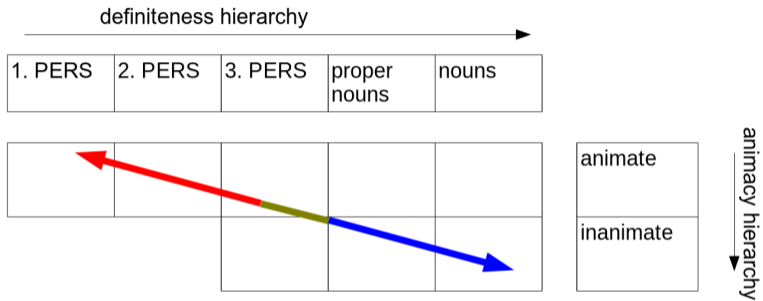
zhāngsān mà lǐsì le ma.

Zhangsan scold Lisi CRS Q

'Did Zhangsan scold Lisi?'

- many languages have mixed systems
- e.g., some NPs have accusative and some have neutral paradigm, such as Hebrew
 - (1) Ha-seret her?a ?et-ha-milxama
the-movie showed acc-the-war
'The movie showed the war.'
 - (2) Ha-seret her?a (*?et-)milxama
the-movie showed (*acc-)war
'The movie showed a war'
(from Aissen, 2003)

Differential case marking

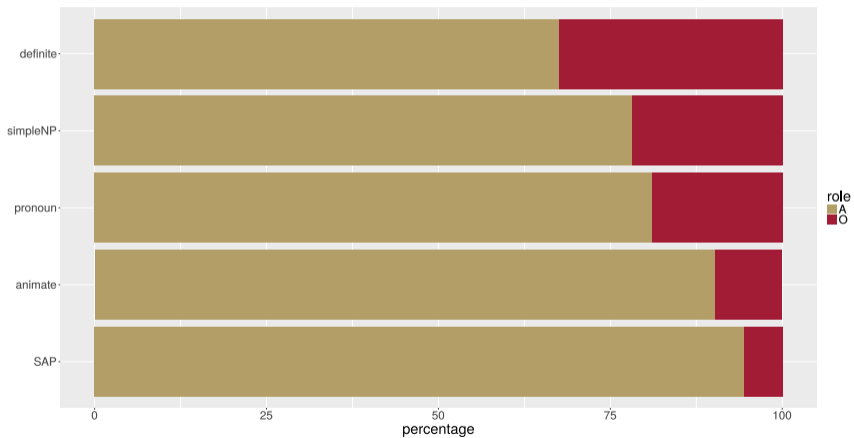


accusative

neutral or tripartite

ergative

probability $P(\text{syntactic role} | \text{prominence of NP})$



A is prominent	A is non-prominent	O is prominent	O is non-prominent
e(rgative)	e(rgative)	a(ccusative)	a(ccusative)
e	e	a	z(ero)
e	e	z	a
e	e	z	z
e	z	a	a
...
z	e	z	z
z	z	a	a
z	z	a	z
z	z	z	a
z	z	z	z

actually attested:

- ① **zzzz**: no case marking
- ② **zxaa**: non-differential object marking
- ③ **zzaz**: harmonic differential object marking
- ④ **ezzz**: non-differential subject marking
- ⑤ **zeaz**: split ergative
- ⑥ **eeaz**: non-differential subject marking plus differential object marking
- ⑦ **ezzz**: dis-harmonic differential subject marking
- ⑧ **zezz**: harmonic differential subject marking
- ⑨ **zeaa**: harmonic differential subject marking plus non-differential object marking
- ⑩ **zzza**: dis-harmonic differential object marking

Differential case marking and referential scales

- received wisdom (Silverstein, 1976; Comrie, 1981; Aissen, 2003, , *inter alia*):
 - if object-marking is differential, upper segments of a referential hierarchy receive accusative marking
 - if object-marking is differential, lower segments of a referential hierarchy receive accusative marking
- Bickel et al. (2015):
 - large differences between macro-areas
 - no universal effects of referential scales on differential case marking

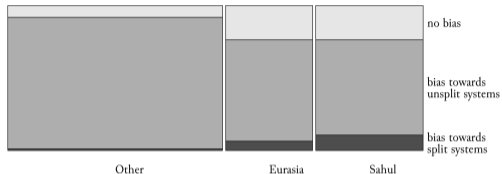


Figure 1: Estimated biases of families having split case marking for A across macro-areas. (The sizes of the individual tiles in the plot are proportional to frequencies, using the 'mosaic' plot technique provided by Meyer et al. 2006)

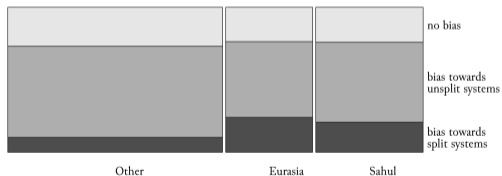
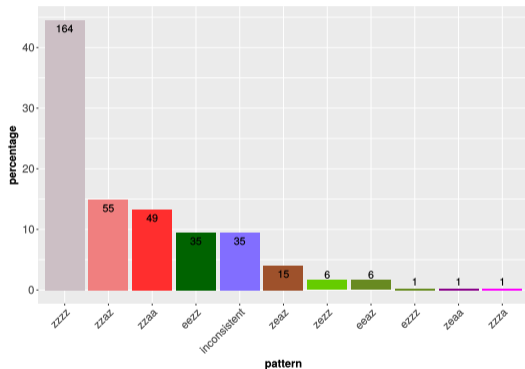


Figure 2: Estimated biases of families having split case marking for P across macro-areas (using the same mosaic plot techniques as in Figure 1)

Empirical distribution

- genetically diverse sample of 460 case marking systems
- used here: 368 systems
 - one system per language
 - only languages with ISO code
 - only languages present in ASJP
- 2 out of 333 systems (99.4%) are obey the Silverstein hierarchy (not counting inconsistent states)

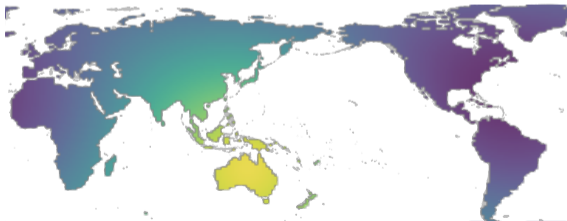


Differential object marking



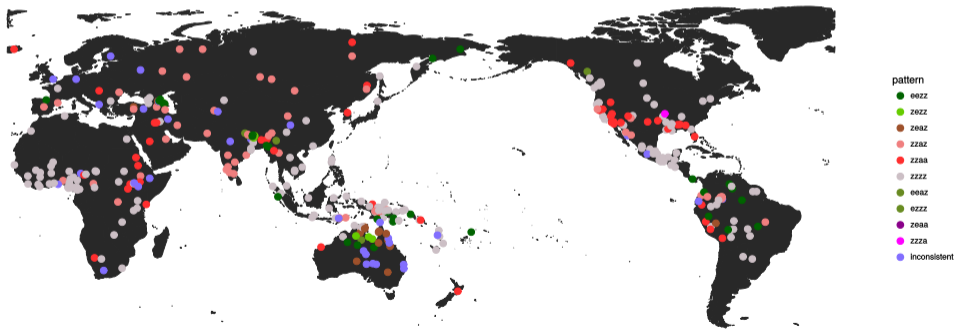
- differential object marking concentrated in Eurasia
- differential subject marking concentrated in Sahul
- only cases of anti-DOM and anti-DSM (one instance of each) in North America

Differential subject marking

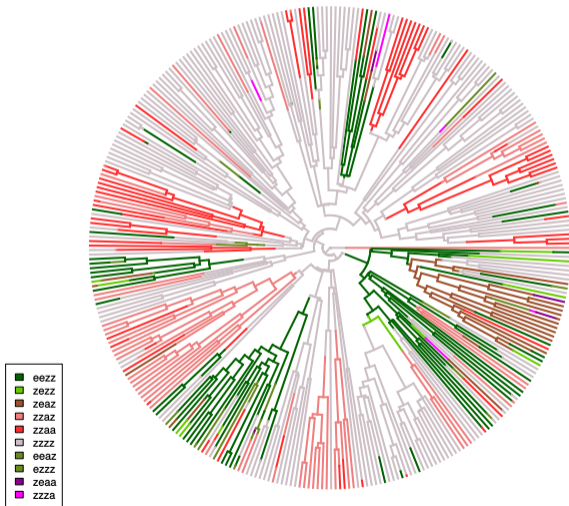


Phylogenetic non-independence

- 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



Phylogenetic non-independence



Maslova (2000):

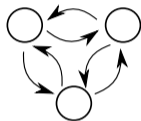
“If the A-distribution for a given typology cannot be assumed to be stationary, a distributional universal cannot be discovered on the basis of purely synchronic statistical data.”

*“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).”*

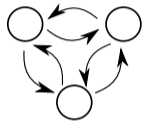


The phylogenetic comparative method

Markov process



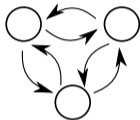
Markov process



Phylogeny



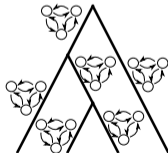
Markov process



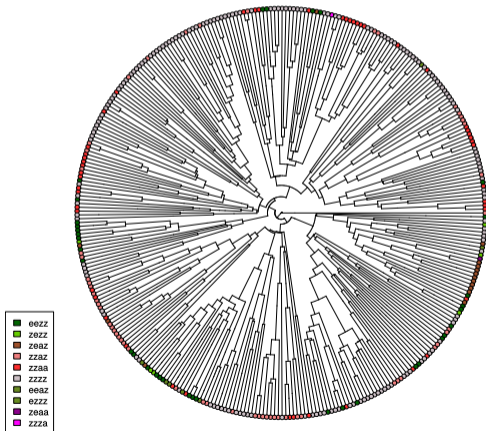
Phylogeny



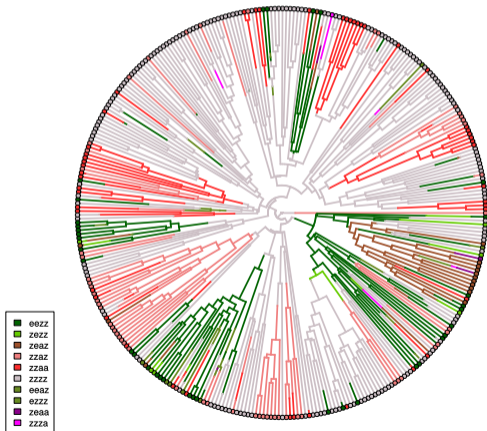
Branching process



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



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

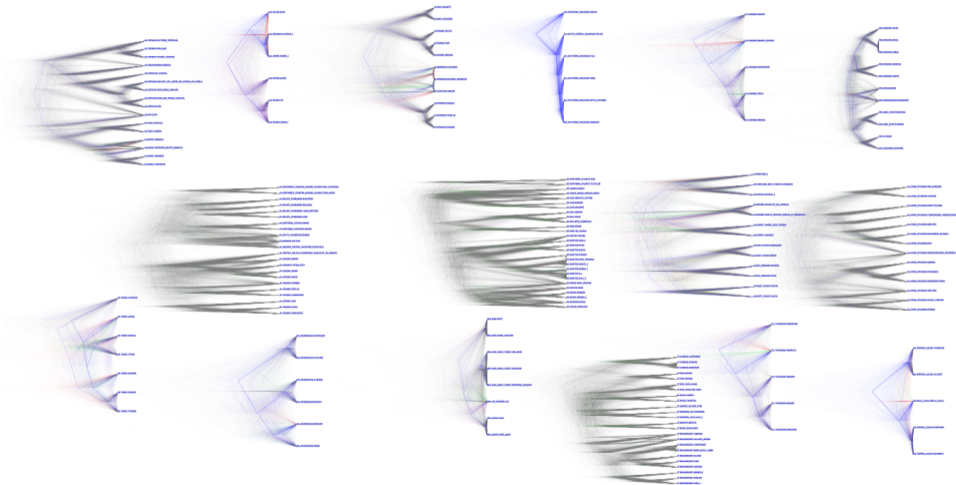


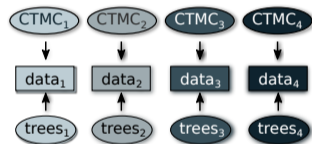
Cases in equilibrium

Phylogenetic trees for the case data

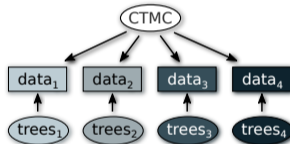
- 39 families and 63 isolates in the intersection of the Autotyp data and ASJP (Wichmann et al., 2018)
- for each of these families, I inferred a posterior distribution of 1,000 trees (using lexical data from ASJP) to reflect uncertainty in tree structure and branch length
- Glottolog tree was used as constraint tree

Phylogenetic trees for the case data



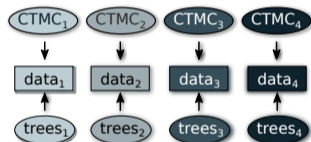


area-specific

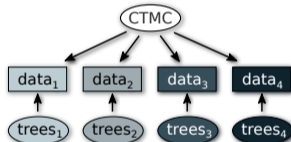


universal

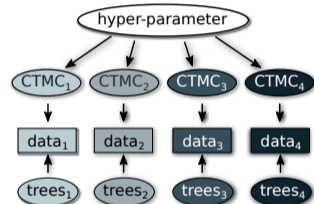
Hierarchical Bayesian models



area-specific



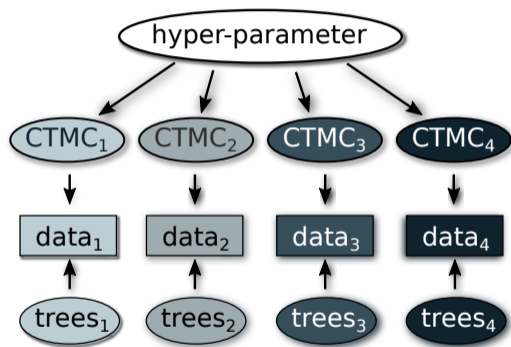
universal



hierarchical

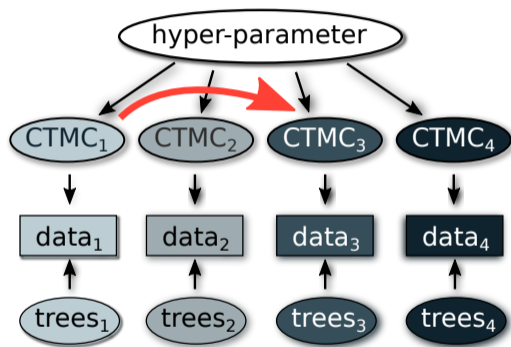
Hierarchical Models to capture areal effects

- each macro-area has its own parameters
- parameters are all drawn from the same distribution f
- shape of f is learned from the data
- prior assumption that there is little cross-area variation \rightarrow can be overwritten by the data



Hierarchical Models to capture areal effects

- each macro-area has its own parameters
- parameters are all drawn from the same distribution f
- shape of f is learned from the data
- prior assumption that there is little cross-area variation \rightarrow can be overwritten by the data
- enables **information flow across areas**

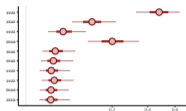


- Continuous Time Markov Chain defines a unique **equilibrium distribution**
- hierarchical model assumes a different CTMC, and thus a different equilibrium distribution for each lineage
- by modeling assumption, root state of a lineage is drawn from this distribution (Uniformity Principle)
- isolates are treated as families of size 1, i.e., they are drawn from their equilibrium distribution

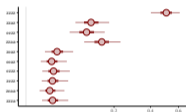
Results

Estimated equilibrium distributions

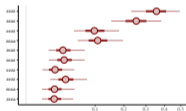
Africa



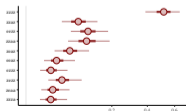
Americas



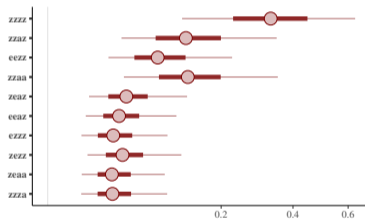
Eurasia



Sahul



posterior prediction



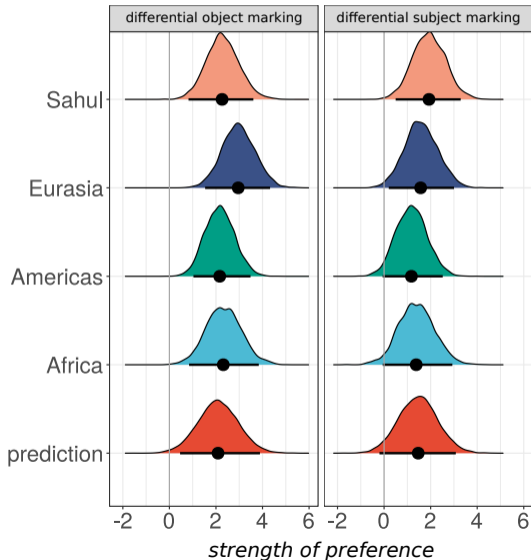
Preference for scale-respecting differential case marking

- **strength of preference** of DOM over anti-DOM:

$$\log \frac{P(..az)}{P(..za)}$$

- DSM over anti-DSM:

$$\log \frac{P(ze..)}{P(ez..)}$$



- considerable variation between macroareas concerning the dynamic process governing the diachrony of alignment systems, and the resulting long-term averages
- still, consistent preference for DOM/DSM over anti-DOM/DSM

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