Harnessing Bayesian phylogenetics to test a Greenbergian universal

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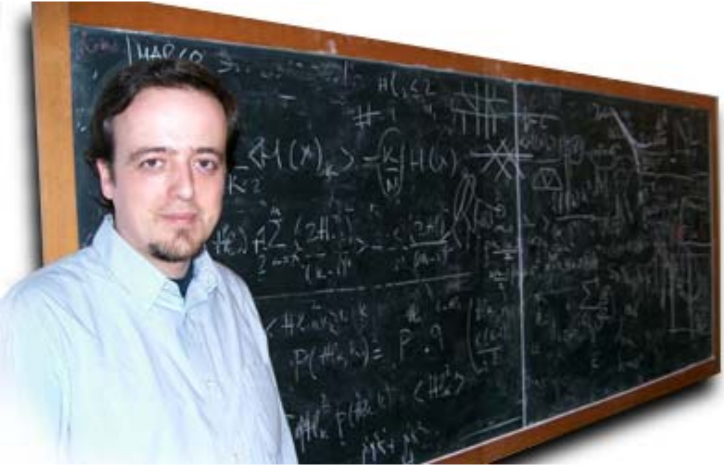
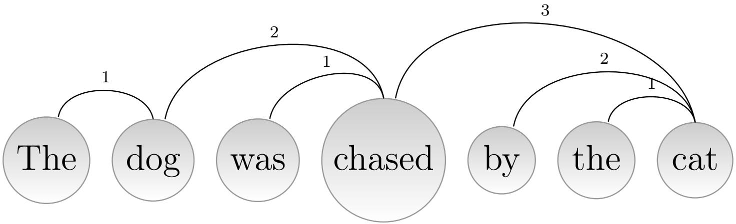


Greenberg's Universal 17

With overwhelmingly more than chance frequency, languages with dominant order VSO have the adjective after the noun. (Greenberg, 1963)

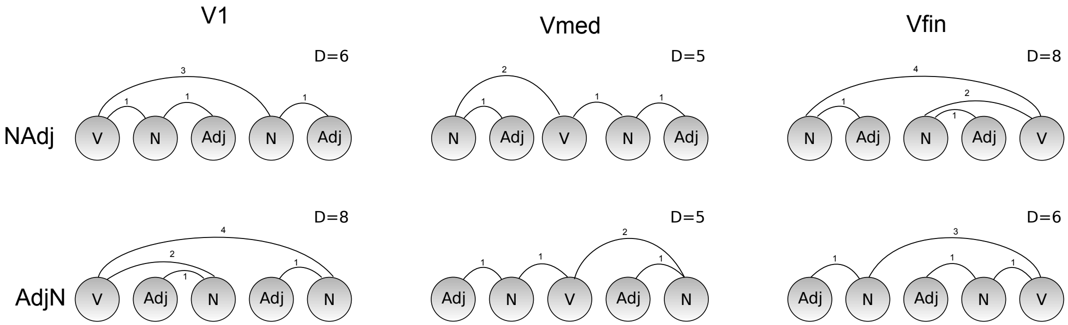
Mirror image: Verb-final languages prefer adjective-noun order.

But: Dryer (1992)



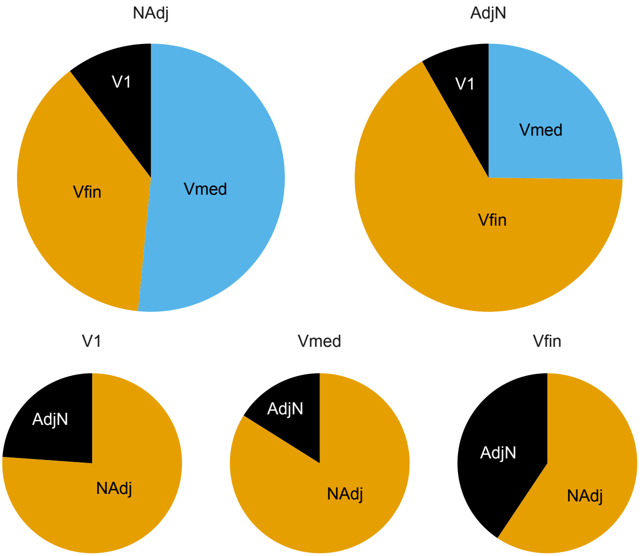
$n = 7,\ D = 10$

- Dependency distances.
- DDm: dependency distance minimization principle (Liu et al., 2017).
- Cognitive origins of DDm: interference and decay (Liu et al., 2017).
- The challenge of aggregating D over heterogeneous data: sentences of different lengths, multiple authors, ... (Ferrer-i-Cancho and Liu, 2014)

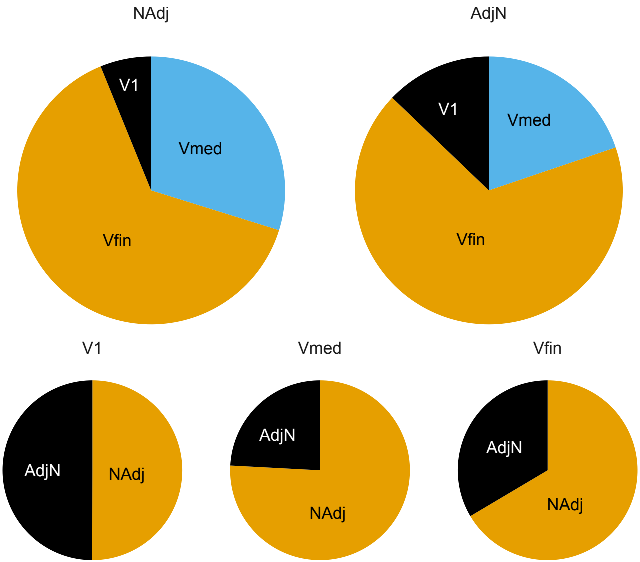


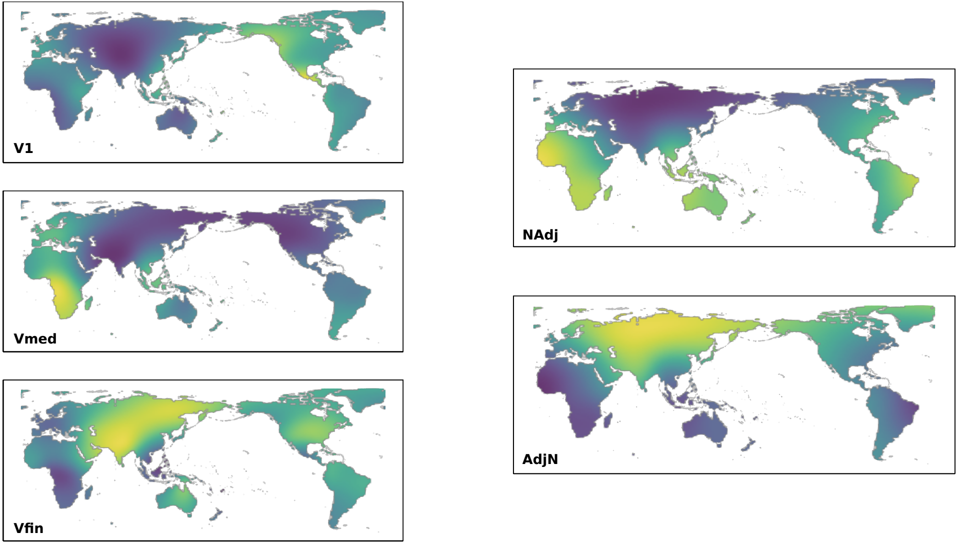
DDm provides functional motivation for Universal 17 and its mirror image.

Frequency distribution (WALS)



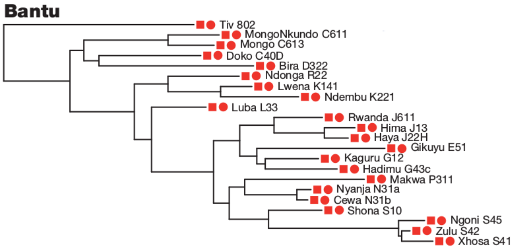
Frequency distribution, weighted by lineage




V1
Vmed
Vfin
NAdj
AdjN

- 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)

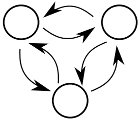
Maslova (2000):

> *"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."*

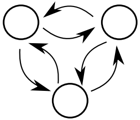
> *"In this case, the only way to discover a distributional universal is to* ***estimate transition probabilities*** *and as it were to 'predict' the stationary distribution on the basis of the equations in (1)."*

The phylogenetic comparative method

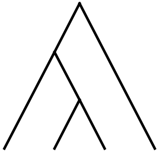
Markov process



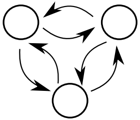
Markov process



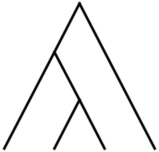
Phylogeny



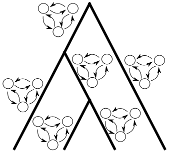
Markov process



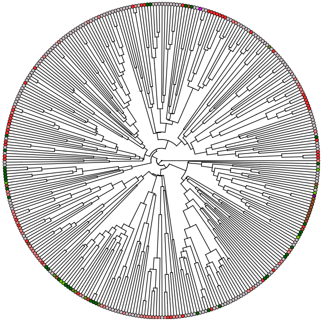
Phylogeny



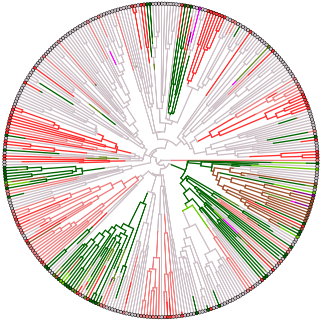
Branching process

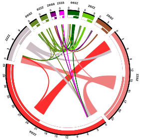


- if phylogeny and states of extant languages are known...



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



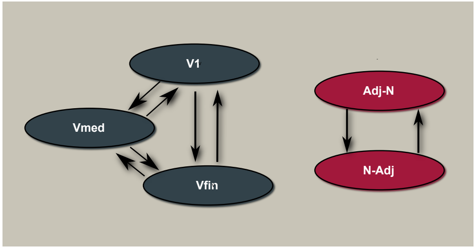


Correlation between features

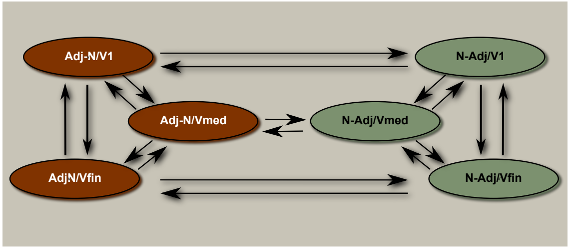
Pagel and Meade (2006)

- construct two types of Markov processes:
  - **independent:** the two features evolve according to independend 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

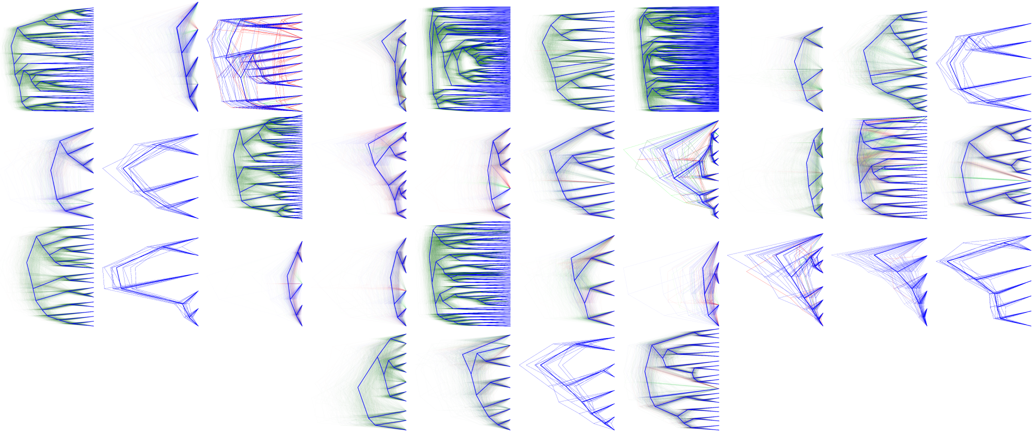
Independent model

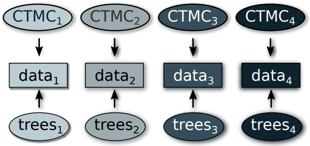


Dependent model

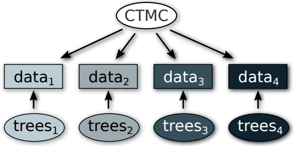


- **word-order data:** WALS
- **phylogeny:**
  - ASJP word lists (Wichmann et al., 2016)
  - feature extraction (automatic cognate detection, *inter alia*) $\rightsquigarrow$ character matrix
  - Bayesian phylogenetic inference with Glottolog (Hammarström et al., 2016) tree as backbone
  - advantages over hand-coded Swadesh lists
    - applicable across language familes
    - covers more languages than those for which expert cognate judgments are available
  - 902 languages in total
  - 76 families and 105 isolates

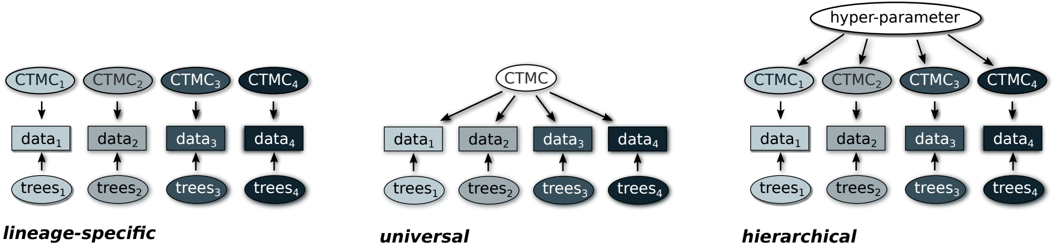




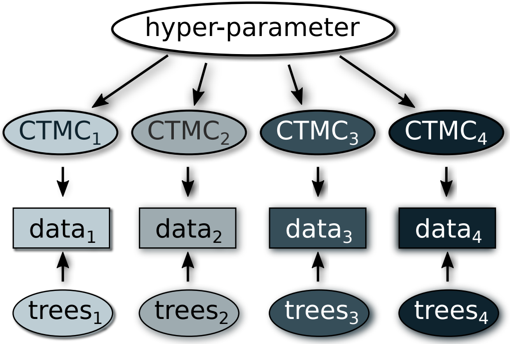
lineage-specific



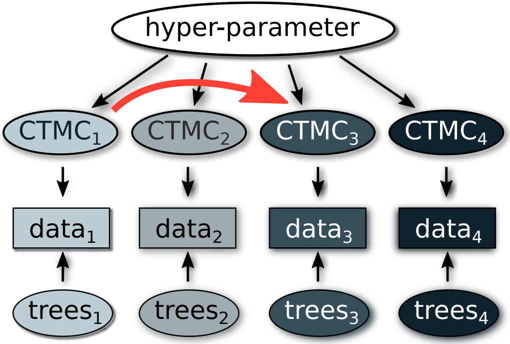
universal


CTMC1
CTMC2
CTMC3
CTMC4
data1
data2
data3
data4
trees1
trees2
trees3
trees4
lineage-specific
CTMC
data1
data2
data3
data4
trees1
trees2
trees3
trees4
universal
hyper-parameter
CTMC1
CTMC2
CTMC3
CTMC4
data1
data2
data3
data4
trees1
trees2
trees3
trees4
hierarchical

- each family 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-family variation $\rightarrow$ can be overwritten by the data



- each family 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-family variation $\rightarrow$ can be overwritten by the data
- enables **information flow across families**

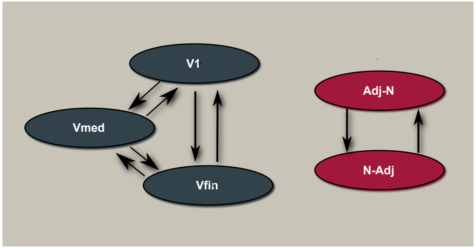


What about isolates?

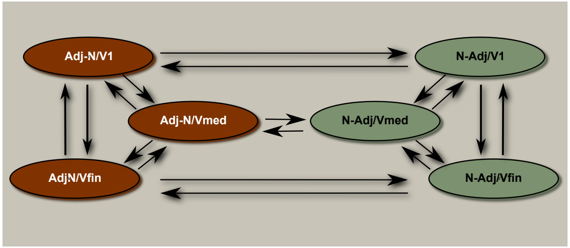
- Continuous Time Markov Chain defines a unique **equilibrium distribution**
- hierarchical model assumes a different CTMC, and thus a different equilibrium distribution for each lineage
- by modeling assumption, root state of a lineage is drawn from this distribution (Uniformity Principle)
- isolates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

Results

Independent model



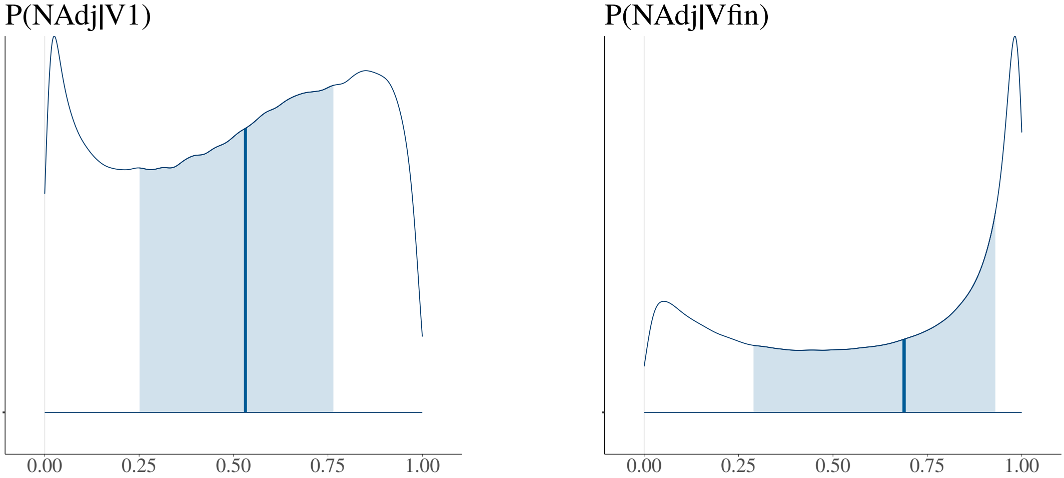
Dependent model



- **Bayes Factor:** 260 in favor of dependent model[1]

[1] In the abstract we reported the opposite conclusion, but there we used a non-hierarchical universal model.

17



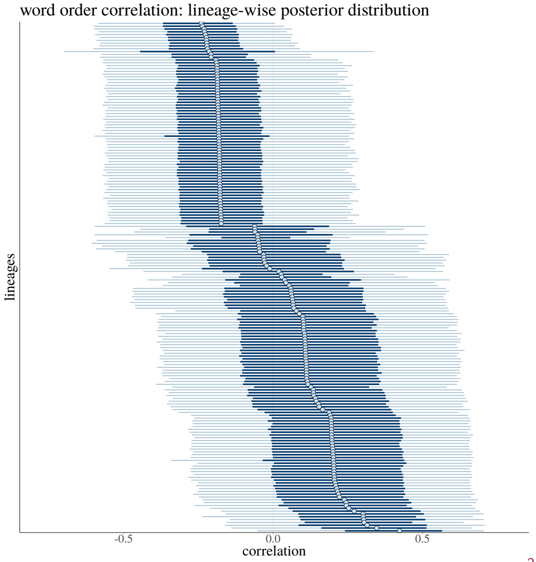
Correlation between verb order and adjective order

- lineages fall into two, about equally sized, groups:
  1. negative or no correlation

     Nuclear Macro-Je, Mande, Siouan, Pama-Nyungan, Austronesian, ...
  2. positive correlation

     Uto-Aztecan, Afro-Asiatic, Indo-Euroean, Dravidian, Austroasiatic,

     Otomanguean, ...



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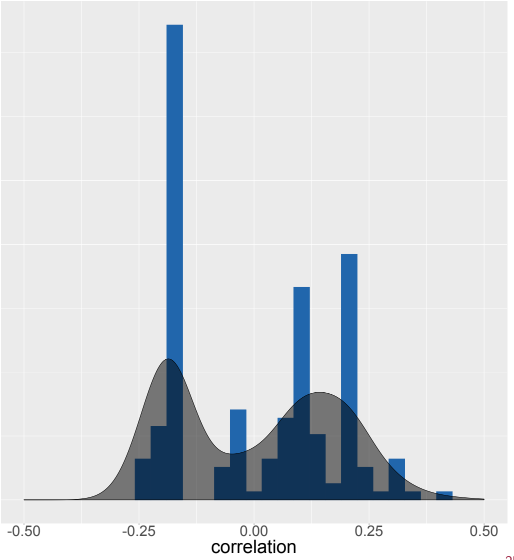
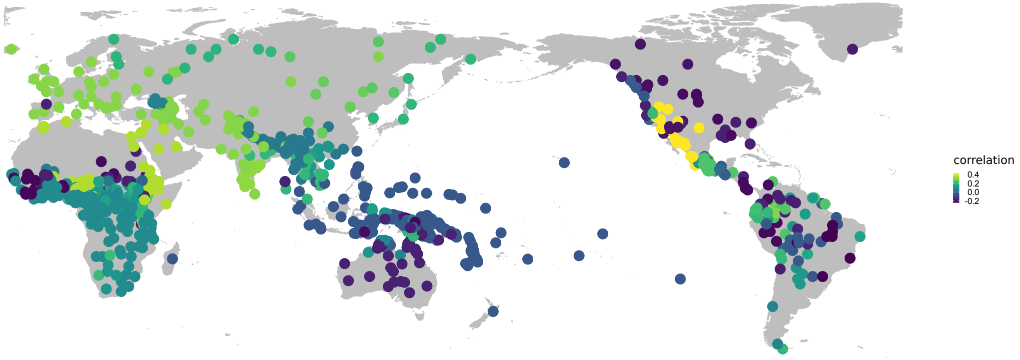
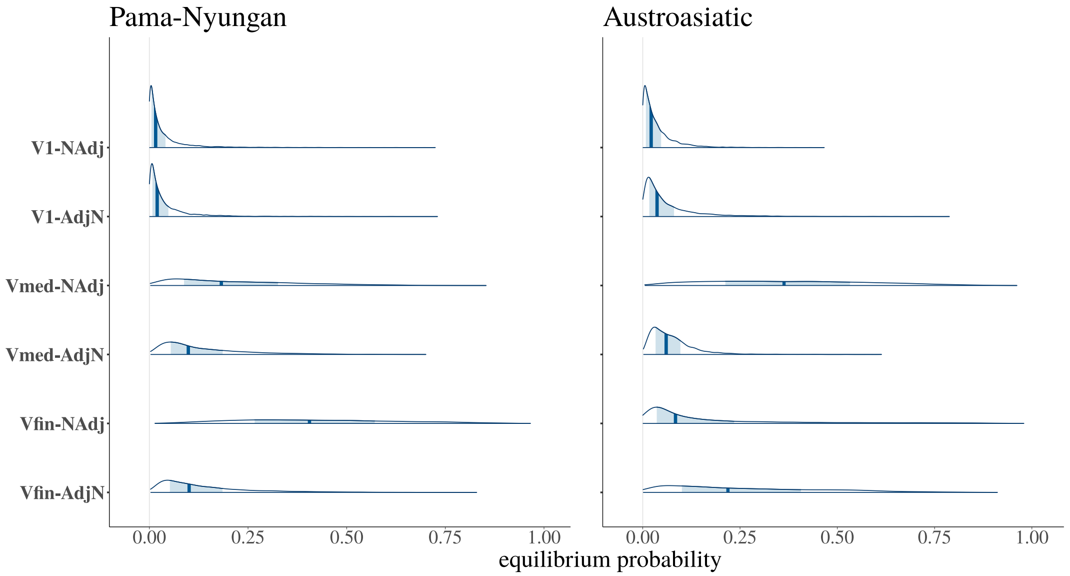


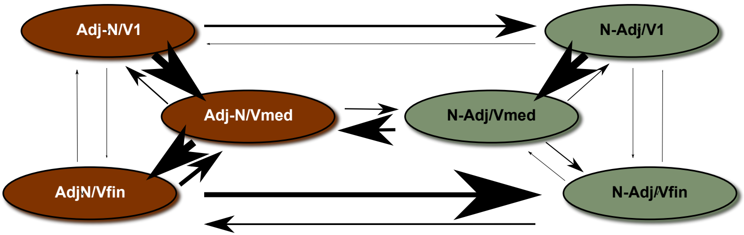
Correlation between verb order and adjective order



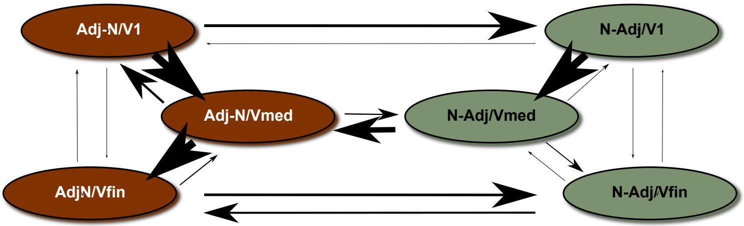
A representative family for each type



Pama-Nyungan



Austroasiatic



Conclusion

- no empirical support for Universal 17
- more nuanced picture for its mirror image:
  - two different possible dynamics governing relationship between verb-object and noun-adjective order
  - Dependency Length Minimization is operative in one dynamic, but not the other
  - reminds of an OT style pattern, with two competing constraints

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