Tracking the change that leads to typological variation

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

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DFG

Typological distributions

- common practice since Greenberg (1963):
  - collect a sample of languages
  - classify them according to some typological feature

  ⇒ skewed distribution indicates something interesting going on
- Problem: languages are not independent samples
- skewed distribution may reflect
  - skewed diversification rate across families
  - properties of an ancestral bottleneck
- balanced sampling mitigates the first, but not the second problem

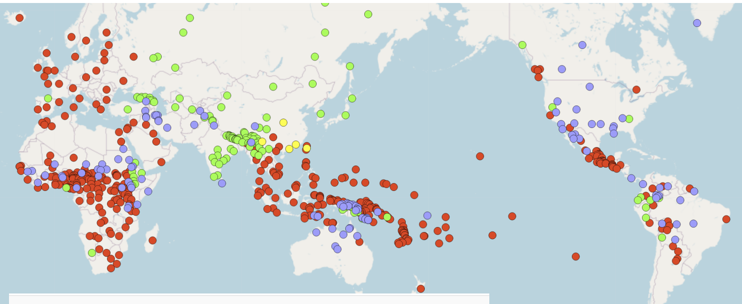
Maslova (2000):

> *“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).”*

A case study: Typological word order correlations

Distribution of verb-object/object verb vs. noun-relative clause/relative clause-noun

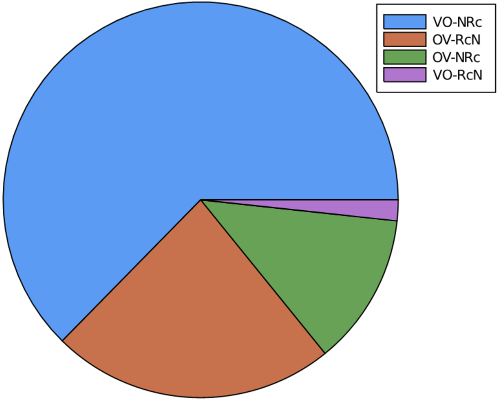


🔴	VO / Noun-Relative clause	415
🟢	OV / Relative clause-Noun	132
🔵	OV / Noun-Relative clause	113
🟡	VO / Relative clause-Noun	5

VO vs. NRc

this study:

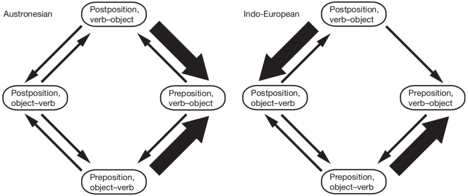
- word-order data from WALS
- 1,060 languages
- 94 families + 81 isolates = 175 lineages

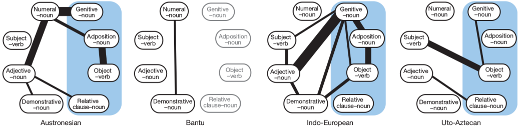


Dunn et al. (2011)

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





“*Evolved structure of language shows lineage-specific trends in word-order universals*”

Steps of (Bayesian) model validation

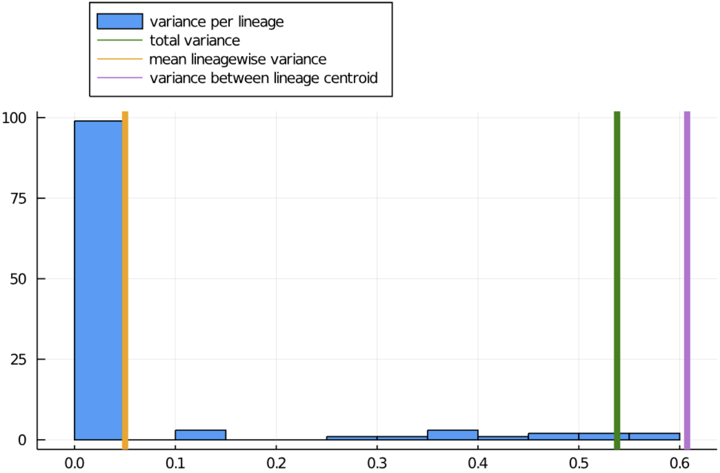
- exploratory data analysis → descriptive statistics
- specification of (a) generative probabilistic model(s)
- prior predictive simulation
- model fitting
- posterior predictive simulation
- model comparison

(cf., eg., Gelman et al. 2014)

Descriptive statistics

- each language can be represented as a binary vector over 4 variables (for the four combinations of OV/VO and NRc/RcN)
- the **total variance** is the sum of the variance of those four binary variables
- the **mean lineage-wise variance** is the average total variance per lineage
- the **between-family variance** is the total variance between the centroids for each family

Descriptive statistics



Defining models

- feature values evolve according to a *continuous time Markov chain* (CTMC)
- evolution along a phylogeny
- phylogenetic tree is only partially known - represented here as posterior distribution of Bayesian phylogenetic inference from lexical data (from ASJP)

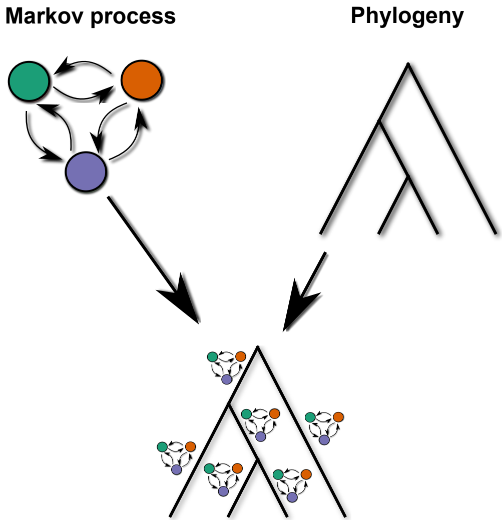


Figure: Schematic structure of the phylogenetic CTMC model. Independent but identical instances of a CTMC run on the branches of a phylogeny

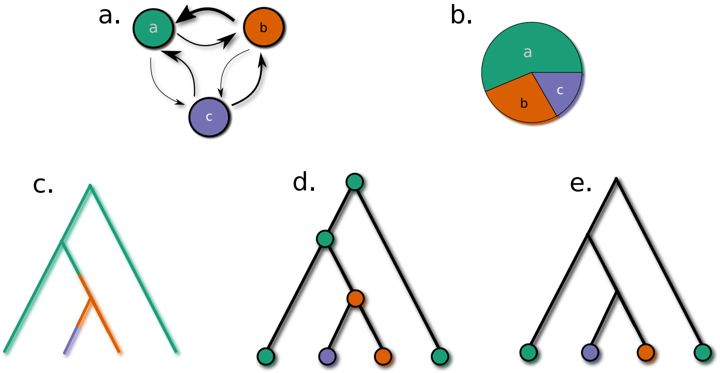
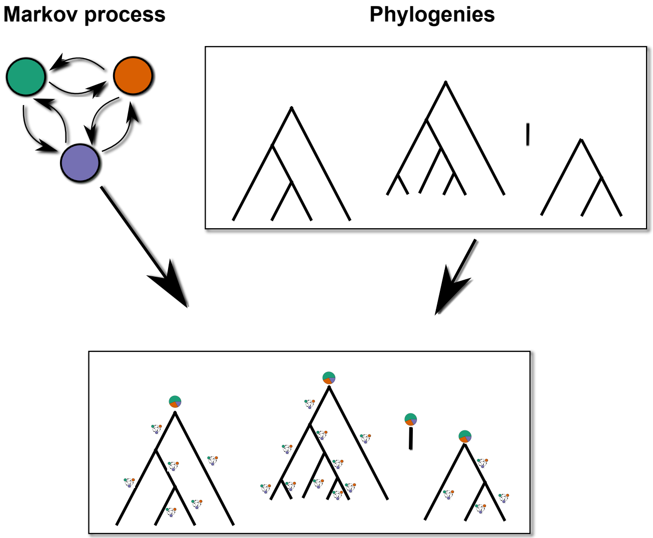


Figure: a. CTMC b. Equilibrium distribution c. Fully specified history of a phylogenetic Markov chain d. Marginalizing over events at branches e. Marginalizing over states at internal nodes



Markov process

Phylogenies

Figure: Phylogenetic Markov CTMC with a collection of phylogenies

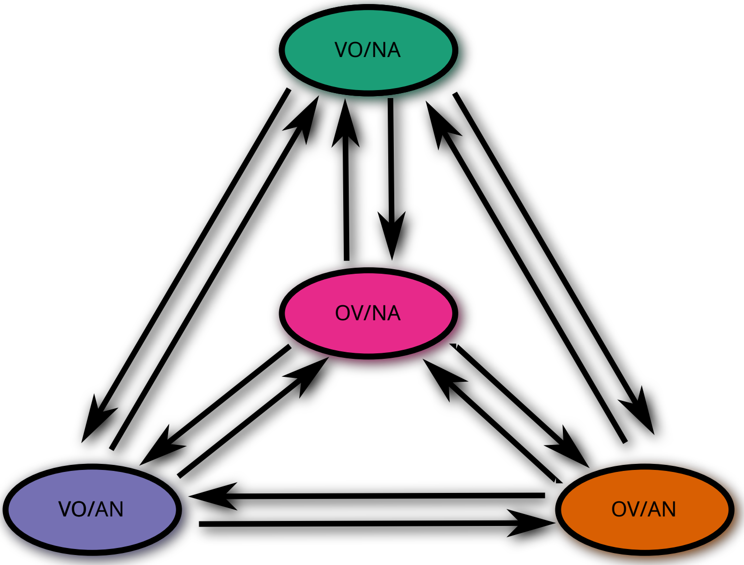


Figure: CTMC for a possibly correlated feature pair

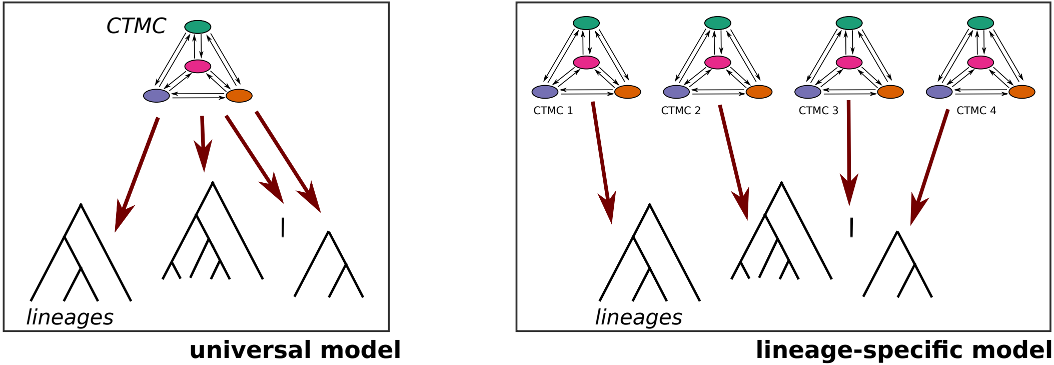
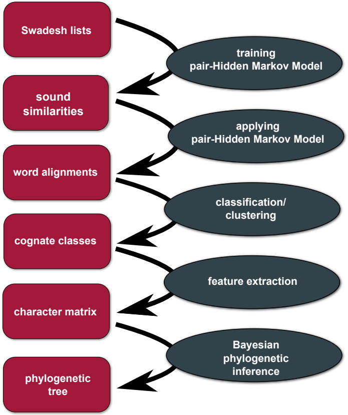


Figure: Universal vs. lineage-specific model

From words to trees



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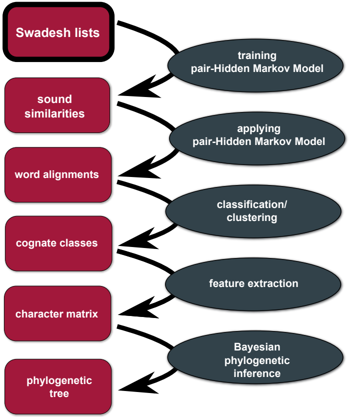


Swadesh lists

training
pair-Hidden Markov Model

sound
similarities

applying
pair-Hidden Markov Model

word alignments

classification/
clustering

cognate classes

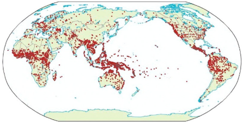
feature extraction

character matrix

Bayesian
phylogenetic
inference

phylogenetic
tree

concept	Latin	English
I	ego	Ei
you	tu	yu
we	nos	wi
one	unus	w3n
two	duo	tu
person	persona, homo	pers3n
fish	piskis	fiS
dog	kanis	dag
louse	pedikulus	laus
tree	arbor	tri
leaf	foly∼u*	lif
skin	kutis	skin
blood	saNgw∼is	bl3d
bone	os	bon
horn	kornu	horn
ear	auris	ir
eye	okulus	Ei



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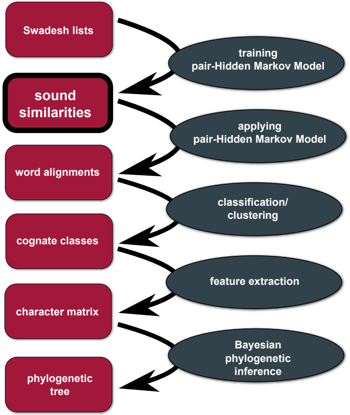

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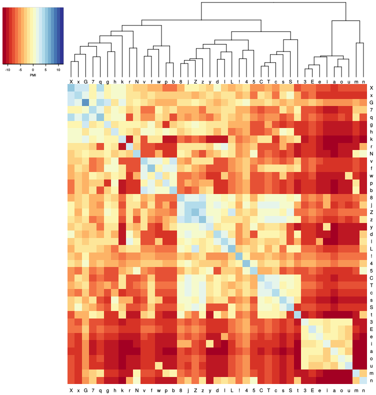
Bayesian phylogenetic inference

phylogenetic tree



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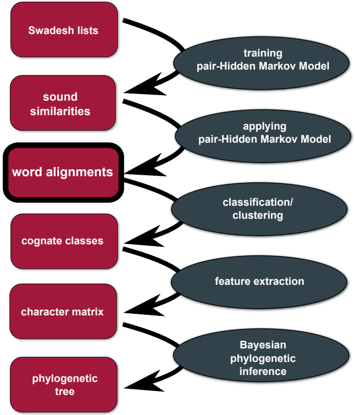
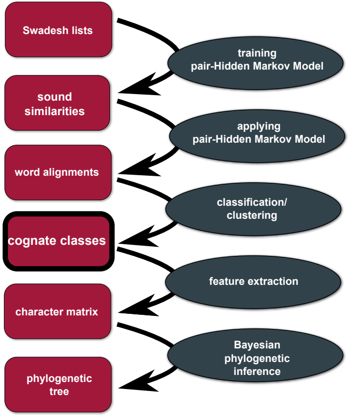


Language	*fish:z*	*tongue:1*	*smoke:1*
Abui-Atangmelang	-af-u		
Abui-Fuimelang	-af-u	tal-i-fi--	
Adang	aab--	tal-E-b---	awai--b-a-n-o-7o-
Blagar-Bakalang	-ab--	--j-e-bur-	--ad--b-a-n-aNka-
Blagar-Bama	aab--	teg-e-bur-	------b-e-n-a-xa-
Blagar-Kulijahi	-ab--	tej-e-bur-	------b-e-n-aNka-
Blagar-Nule	aab--	tej-e-bur-	--ad--b-e-n-aNka-
Blagar-Tuntuli	aab--	tej-e-bur-	a-adgeb-a-n-a-q--
Blagar-Warsalelang	-ab--	tel-e-bur-	a-ad--b-a-n-a-x--
Bunaq			------b-o-t-o-h--
Deing	haf--		------buu-n------
Hamap	7ab--	nar-ø-buN-	------b-a-n-o-7--
Kabola	hab--	tal-e-b---	awal--b-e-n-e-7o-
Kaera-Padangsul	-ab--	talee-b---	a-ad--b-e-naa-x--
Kafoa	-afUi	tal-i-p---	------f-o-n-a----
Kamang	-ap-i	nal---pu--	------p-u-n----a-
Kiraman	-Eb--	nal-i-bar-	--ar--b-a-n-o-kan
Klon	-eb-i	gel-E-b---	--ed-ab-o-n------
Kui	-eb--	tal-i-ber-	--ar--b-o-n-o-k--
Kula	-ap-i	-il-I-p---	------p---n-ekka-
Nedebang	aaf-i	gel-e-fu--	--ar-ab-u-n------
Reta	aab--	nal-e-bul-	a-ad--b-o-n-a----
Sar-Adiabang	haf--	--p-e-fal-	--ar--buu-n------
Sar-Nule	haf--	nal-e-faj-	
Sawila	-ap-i	gal-impuru	------p-u-n-a-ka-
Teiwa-Madar	xaf--	gel-i-vi--	------buu-n------
Wersing	-ap-i	nej-e-bur-	--ad-ap-u-n-a-k--
Wpantar	hap--	nal-e-bu--	------b-unn-a----

From words to trees



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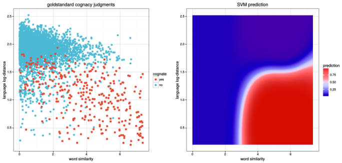

	English	Spanish	Modern Greek	Standard German
I	Ei:A	yo:B	exo:C	iX:D
you	yu:A	ustet:B, tu:C	esi:D	du:E
we	wi:A	nosotros:B	emis:C	vir:A
one	w3n:A	uno:B	enas:C, ena:C	ains:D
two	tu:A	dos:B	8y∼o:C, 8io:D	cvai:E
person	pers3n:A	persona:A	an8∼ropos:B	mEnS:C
fish	fiS:A	peskado:A, pes:A	psari:B	fiS:A
dog	dag:A	pero:B	sTili:C, sTilos:C	hunt:D
come	k3m:A	veni:B	erx∼o:C	kh∼om3n:A
sun	s3n:A	sol:B	ily∼os:C, iLos:C	zon3:A
star	star:A	estreya:A	asteri:A, astro:A	StErn:A
water	wat3r:A	agw∼a:B	nero:C	vas3r:A
stone	ston:A	piedra:B	petra:B	Stain:A
fire	fEir:A	fuego:B	foty∼a:C	foia:D
path	pE8:A	senda:B	8romos:C	pf∼at:A, vek:D
mountain	maunt3n:A	sero:B, monta5a:A	vuno:C, oros:D	bErk:E
full	ful:A	yeno:B	yematos:C, pliris:D	fol:A
new	nu:A	nuevo:A	neos:A, Tenury∼os:B	noi:A
name	nem:A	nombre:A	onoma:A	nam3:A

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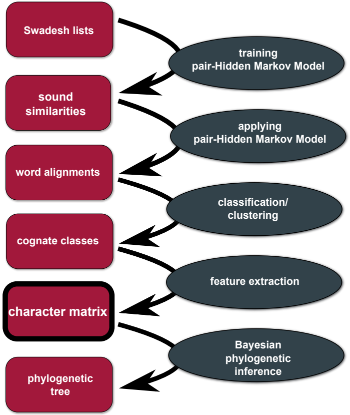
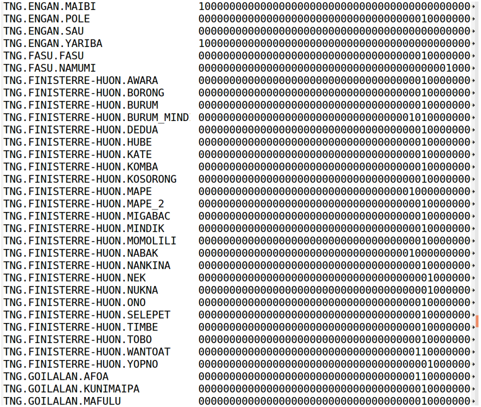
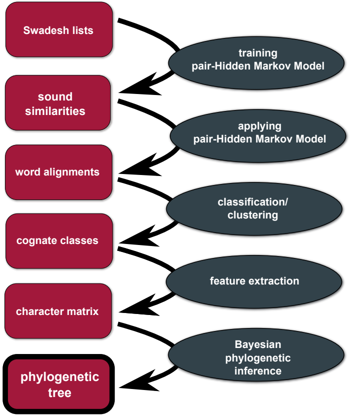




```
TNG.ENGAN.MAIBI                 10000000000000000000000000000000000000000000→
TNG.ENGAN.POLE                  00000000000000000000000000000000000010000000→
TNG.ENGAN.SAU                   00000000000000000000000000000000000000000000→
TNG.ENGAN.YARIBA                10000000000000000000000000000000000000000000→
TNG.FASU.FASU                   00000000000000000000000000000000000010000000→
TNG.FASU.NAMUMI                 00000000000000000000000000000000000000001000→
TNG.FINISTERRE-HUON.AWARA       00000000000000000000000000000000000010000000→
TNG.FINISTERRE-HUON.BORONG      00000000000000000000000000000000000010000000→
TNG.FINISTERRE-HUON.BURUM       00000000000000000000000000000000000010000000→
TNG.FINISTERRE-HUON.BURUM_MIND  00000000000000000000000000000000001010000000→
TNG.FINISTERRE-HUON.DEDUA       00000000000000000000000000000000000010000000→
TNG.FINISTERRE-HUON.HUBE        00000000000000000000000000000000000010000000→
TNG.FINISTERRE-HUON.KATE        00000000000000000000000000000000000010000000→
TNG.FINISTERRE-HUON.KOMBA       00000000000000000000000000000000000010000000→
TNG.FINISTERRE-HUON.KOSORONG    00000000000000000000000000000000000010000000→
TNG.FINISTERRE-HUON.MAPE        00000000000000000000000000000000000100000000→
TNG.FINISTERRE-HUON.MAPE_2      00000000000000000000000000000000000010000000→
TNG.FINISTERRE-HUON.MIGABAC     00000000000000000000000000000000000010000000→
TNG.FINISTERRE-HUON.MINDIK      00000000000000000000000000000000000010000000→
TNG.FINISTERRE-HUON.MOMOLILI    00000000000000000000000000000000000010000000→
TNG.FINISTERRE-HUON.NABAK       00000000000000000000000000000000000100000000→
TNG.FINISTERRE-HUON.NANKINA     00000000000000000000000000000000000010000000→
TNG.FINISTERRE-HUON.NEK         00000000000000000000000000000000000001000000→
TNG.FINISTERRE-HUON.NUKNA       00000000000000000000000000000000000001000000→
TNG.FINISTERRE-HUON.ONO         00000000000000000000000000000000000010000000→
TNG.FINISTERRE-HUON.SELEPET     00000000000000000000000000000000000010000000→
TNG.FINISTERRE-HUON.TIMBE       00000000000000000000000000000000000010000000→
TNG.FINISTERRE-HUON.TOBO        00000000000000000000000000000000000010000000→
TNG.FINISTERRE-HUON.WANTOAT     00000000000000000000000000000000000110000000→
TNG.FINISTERRE-HUON.YOPNO       00000000000000000000000000000000000001000000→
TNG.GOILALAN.AFOA               00000000000000000000000000000000000110000000→
TNG.GOILALAN.KUNIMAIPA          00000000000000000000000000000000000010000000→
TNG.GOILALAN.MAFULU             00000000000000000000000000000000000010000000→
```

From words to trees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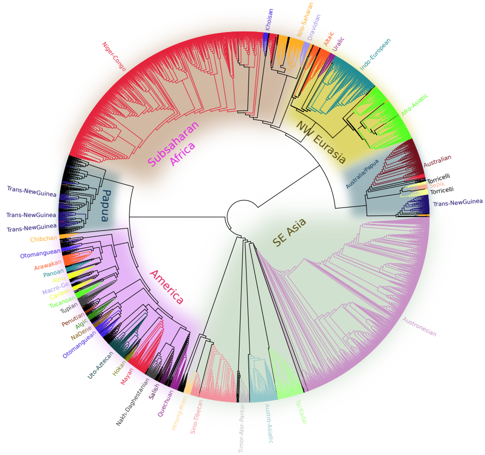
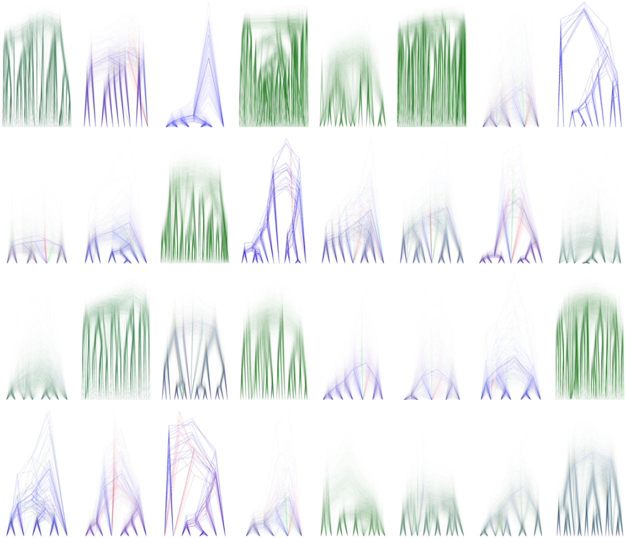


Workflow

(data from all 94 families in data base; ca. 1,060 languages in total)

- estimate posterior tree distributions with MrBayes for each family, using Glottolog as constraint tree
- estimate transition rates
- estimate stationary distribution of major word order categories

Phylogenetic tree sample



Prior predictive check

- all models use the same prior for rates:

$$\mathrm{rate_i} \sim \mathrm{LogNormal}(0, 1)$$

- universal models: one set of rates across lineages
- lineage-dependent models: different set of rates for each lineage
- dependent features model: 8 rates per set
- independent features model: 4 rates per set

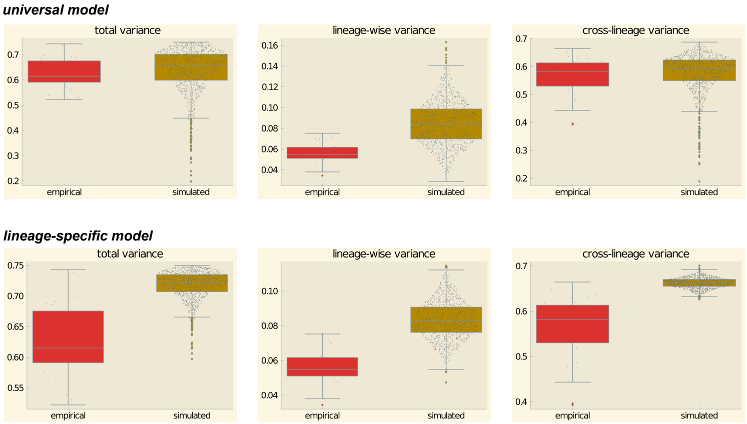


Figure: Prior predictive simulations

Run MCMC to infer posterior distribution

- here: done with Johannes Wahle's *Julia* package *MCPhylo*
- based on *Mamba* (https://mambajl.readthedocs.io/en/latest/)
- `https://github.com/erathorn/MCPhylo.jl`

Posterior predictive check

- use parameters from posterior sample
- simulate mock data using these parameters

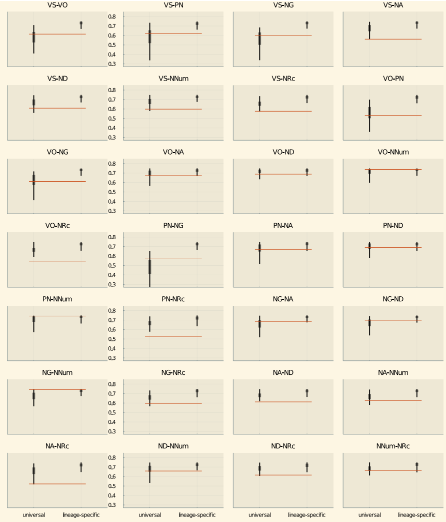
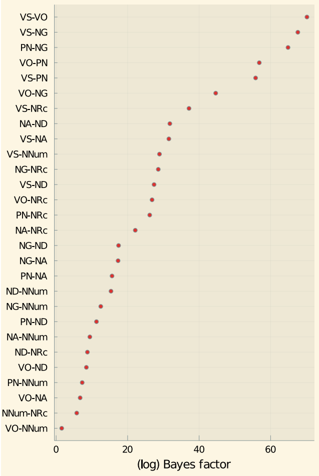


Figure: Posterior predictive simulations: total variance. Horizontal lines indicate the empirical value. The thick vertical lines show the 50% highest-density intervals and the thin lines the 95% highest-density intervals of the posterior predictive distributions.

Model comparison



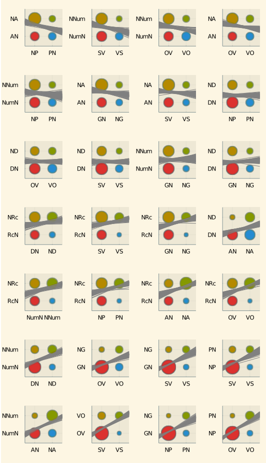


Figure: Posterior equilibrium probabilities and linear regression

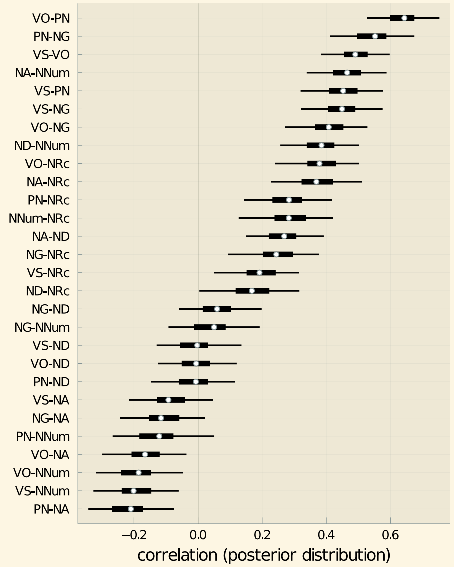


Figure: Correlation coefficients for feature pairs. White dots indicate the median, thick lines the 50% and thin lines the 95% HPD intervals.

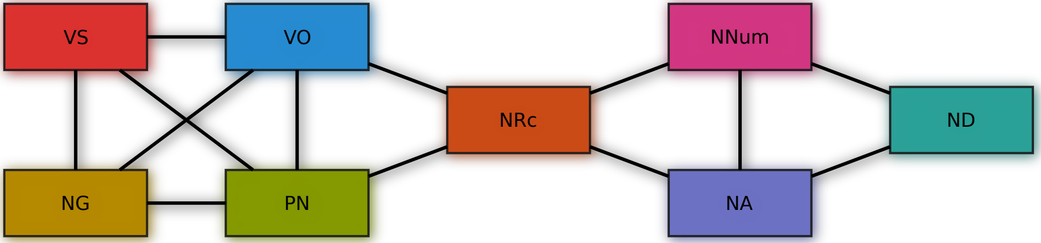


Figure: Feature-pairs with credible evidence for a correlation.

Reflections

- All these techniques assess the **predictive performance** of models
- A good predictive model may be a poor scientific model though.
- Good predictive performance is a necessary but not a sufficient condition for model evaluation.

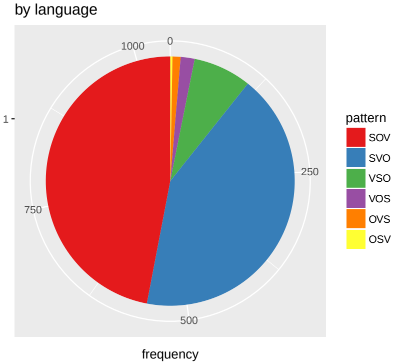
Major word orders

Statistics of major word order distribution

- data: WALS intersected with ASJP
- 1,045 languages, 211 lineages, 32 families with at least 5 languages

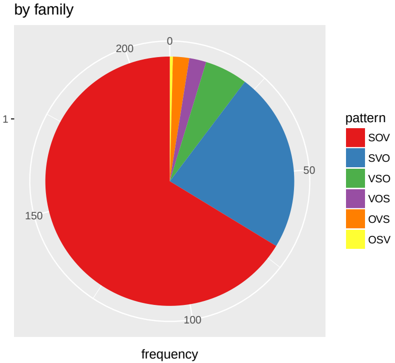
Raw numbers

SOV	SVO	VSO	VOS	OVS	OSV
491 47.0%	442 42.3%	79 7.6%	19 1.8%	11 1.1%	3 0.3%



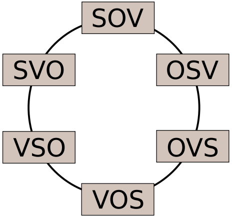
Weighted by lineages

SOV	SVO	VSO	VOS	OVS	OSV
139.1 66.3%	49.3 23.4%	11.8 5.6%	4.7 2.2%	4.5 2.1%	0.8 0.4%



Previous approaches

- Gell-Mann and Ruhlen (2011):
  - Proto-world was SOV
  - general pathway: SOV → SVO ↔ VSO/VOS
  - minor pathway: SOV → OVS/OSV
  - exceptions due to diffusion
- Ferrer-i-Cancho (2015):



SOV

SVO

OSV

VSO

OVS

VOS

  - permutation circle
  - transition probability inversely related to path length

Previous approaches

- Maurits and Griffiths (2014):
  - Bayesian rate estimation, based on five families and NJ-trees

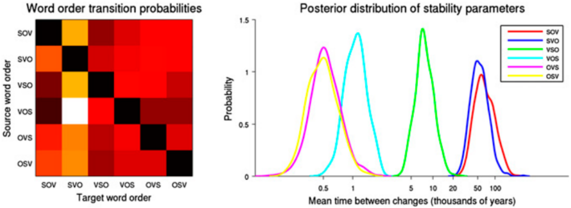
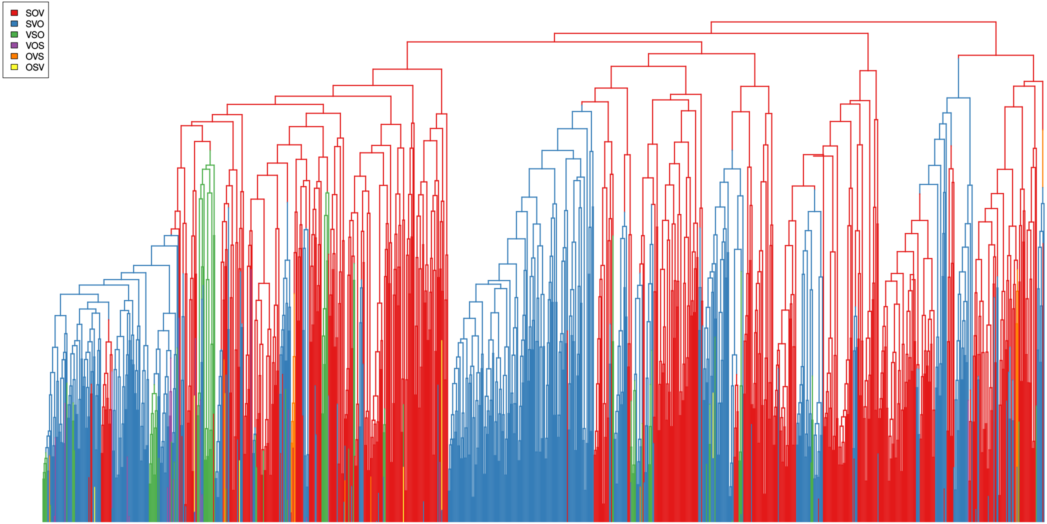


Fig. 1. Results of inferring a single mutation matrix Q for all six language families. (*Left*) Heat map showing the transition probabilities between word orders. Higher intensity (white, yellow) indicates more-probable transitions compared with lower intensity (red, brown), so SOV is most likely to transition to SVO and SVO to SOV. VSO is much more likely to transition to SVO than to SOV. (*Right*) Inferred posterior distributions of stability parameters for each word order. The horizontal axis shows the stability parameter, expressed as the mean time between transitions; i.e., higher values indicate a more stable word order.

Phylogenetic non-independence



Estimating word-order transition patterns

Workflow

(data from all 32 families with $\geq$ 5 languages in data base; 778 languages in total)

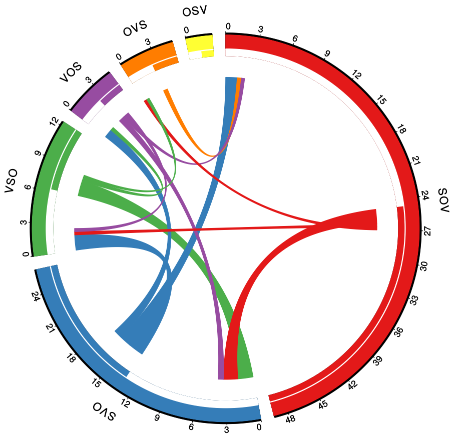
- estimate posterior tree distributions with MrBayes for each family, using Glottolog as constraint tree
- test whether universal or lineage-specific model gives a better fit
- estimate transition rates with best model
- estimate stationary distribution of major word order categories
- apply *stochastic character mapping* (SIMMAP; Bollback 2006)
- estimate expected number of mutations for each transition type

Estimating posterior tree distributions

- using characters extracted from ASJP data (Jäger 2018)
- Glottolog as constraint tree
- Γ-distributed rates
- ascertainment bias correction
- relaxed molecular clock (IGR)
- uniform tree prior
- stop rule: 0.01, samplefreq=1000
- if convergence later than after 1,000,000 steps, sample 1,000 trees from posterior

Estimating transition rates

- totally unrestricted model, all 30 transition rates are estimed independently
- implementation using RevBayes (Höhna et al., 2016)



Reconstruction history with SIMMAP

- estimated frequency of mutations within the 32 families under consideration (posterior mean, 100 iterations)

	SOV	**SVO**	**VSO**	**VOS**	**OVS**	**OSV**
SOV	–	20.2	3.2	0.5	3.3	0.4
SVO	17.6	–	23.9	14.5	1.5	1.1
VSO	1.5	19.9	–	2.5	1.8	0.4
VOS	1.0	5.4	2.3	–	0.9	0.3
OVS	2.8	0.9	0.6	0.4	–	0.2
OSV	0.5	0.5	0.4	0.3	0.5	–

Refining the model with Reversibly Jump MCMC

- Estimating 30 transition rates is a tall order, given that the data possibly only reflect about 130 transition events
- hand-crafted sub-model construction: time consuming, subjective and error prone
- solution: posterior sampling over sub-models using *Reversible Jump Markov Chain Monte Carlo* (RJMCMC, Green 1995)

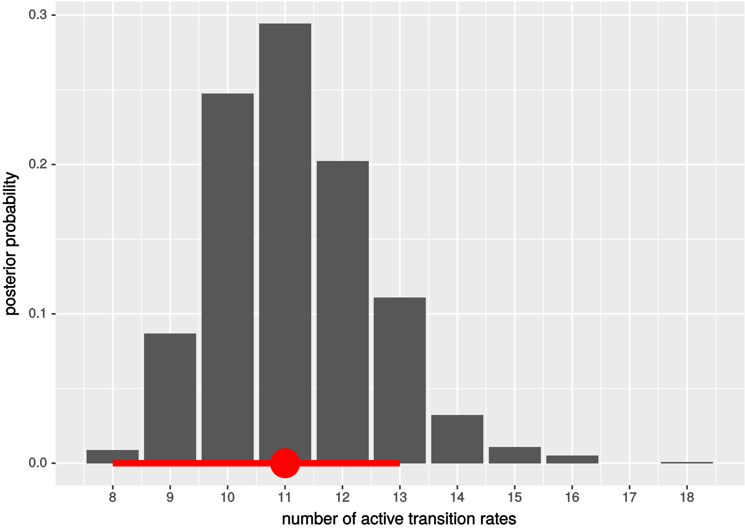
RJMCMC

RJMCMC assumes a prior distribution over sub-models (where some transition rates are set to 0) and simultaneously samples from the set of sub-models and the parameter spaces of the sub-models.

Model comparison

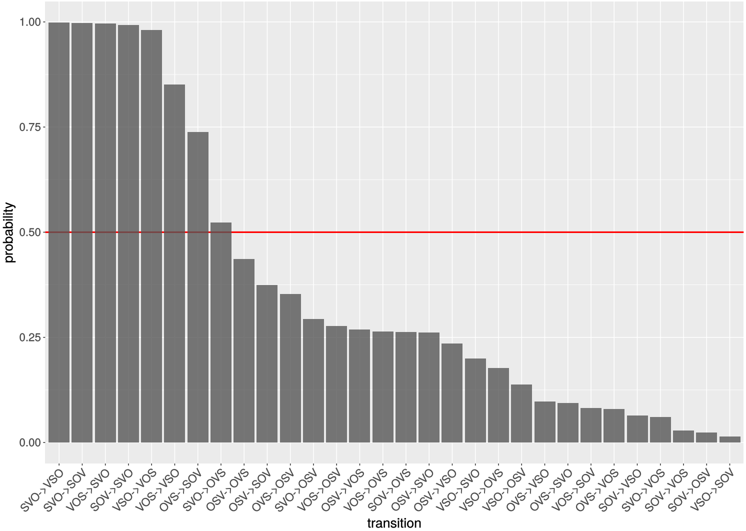
model	**marginal likelihood**	**AICM**
lineage-specific	−423.0 ± 0.08	926.4 ± 0.5
circular GTR	−420.0 ± 1.72	851.7 ± 1.6
circular	−414.2 ± 0.72	851.6 ± 2.1
RJ/GTR	−413.4 ± 2.96	855.9 ± 4.7
unrestricted	−406.7 ± 0.78	846.4 ± 2.5
unrestricted GTR	−404.4 ± 0.89	843.5 ± 3.6
RJ	−398.0 ± 0.57	827.2 ± 2.1

Number of active transition rates: posterior distribution



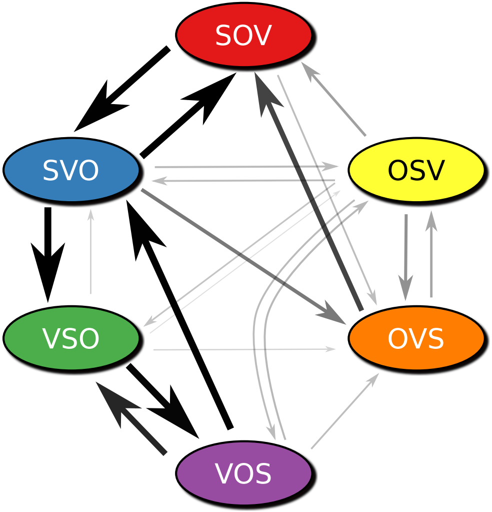
Refining the model with Reversibly Jump MCMC

Probabilities of active transition rates: posterior distribution



Refining the model with Reversibly Jump MCMC

Probabilities of active transition rates: posterior distribution

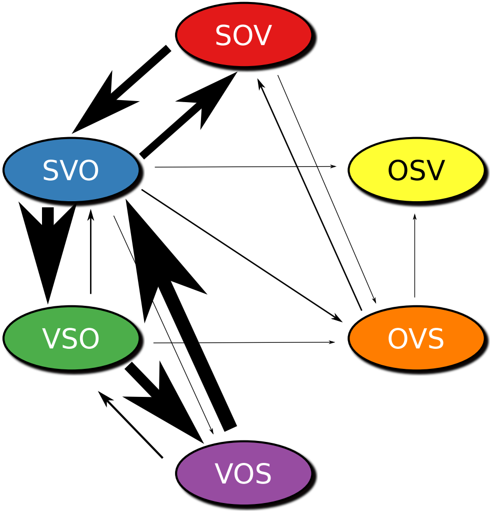


Reconstruction history with SIMMAP

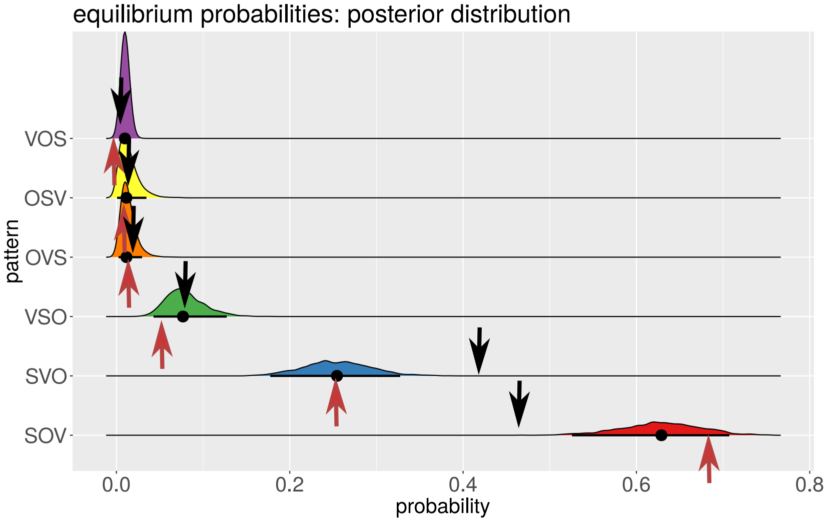
- estimated frequency of mutations within the 32 families under consideration (posterior mean, 99 iterations)

	SOV		SVO		VSO		VOS		OVS		OSV	
SOV	–		23.1	[14; 30]	0.5	[0; 6]	0.1	[0; 0]	1.9	[0; 9]	0.1	[0; 0]
SVO	20.3	[16; 28]	–		33.0	[20; 45]	2.2	[0; 29]	3.4	[0; 11]	1.2	[0; 7]
VSO	0.0	[0; 0]	3.8	[0; 25]	–		29.7	[0; 46]	1.5	[0; 9]	0.5	[0; 4]
VOS	0.1	[0; 0]	38.3	[19; 54]	6.2	[0; 13]	–		0.9	[0; 5]	0.4	[0; 2]
OVS	4.0	[0; 10]	0.5	[0; 3]	0.9	[0; 6]	0.2	[0; 1]	–		1.1	[0; 6]
OSV	0.7	[0; 6]	0.3	[0; 3]	0.4	[0; 3]	0.6	[0; 5]	0.9	[0; 7]	–	

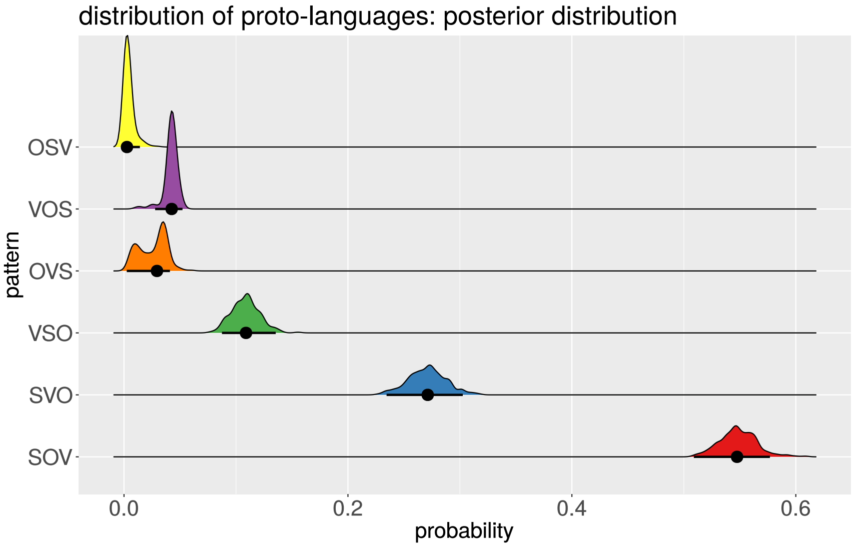
Expected frequencies of transitions: posterior mean



Empirical vs. estimated distribution

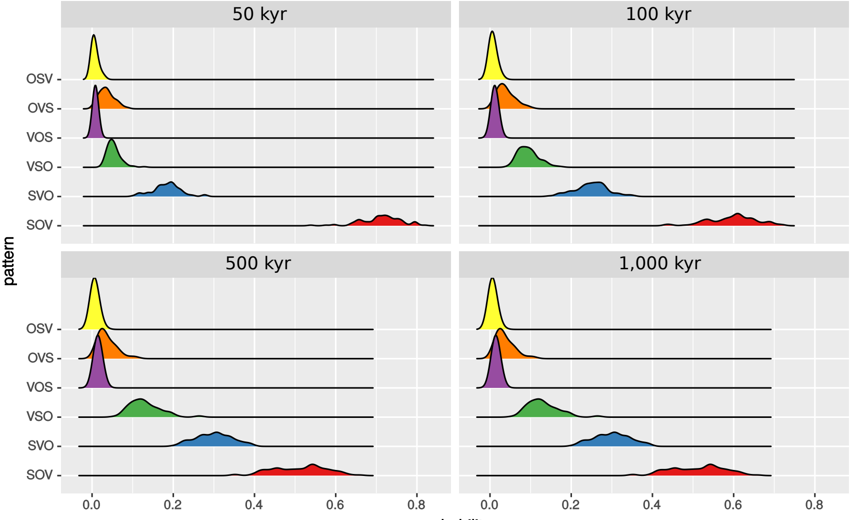


Expected distribution of Proto-languages

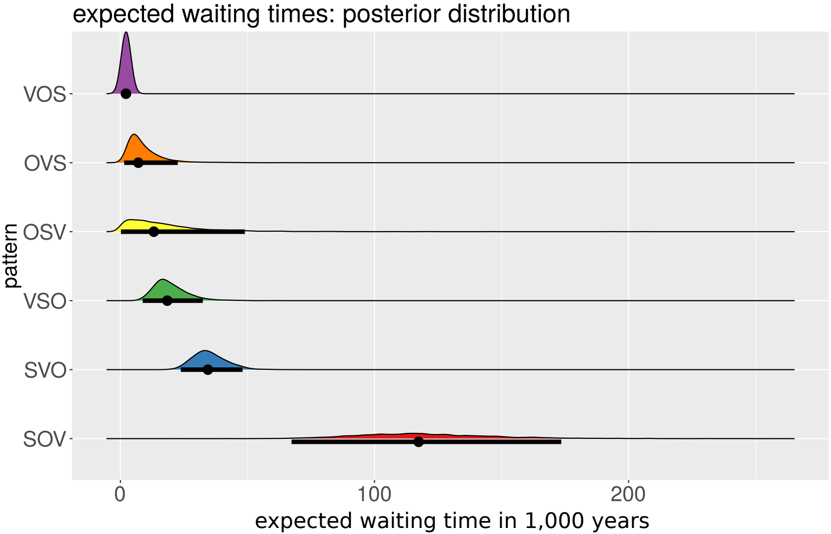


Posterior distributions

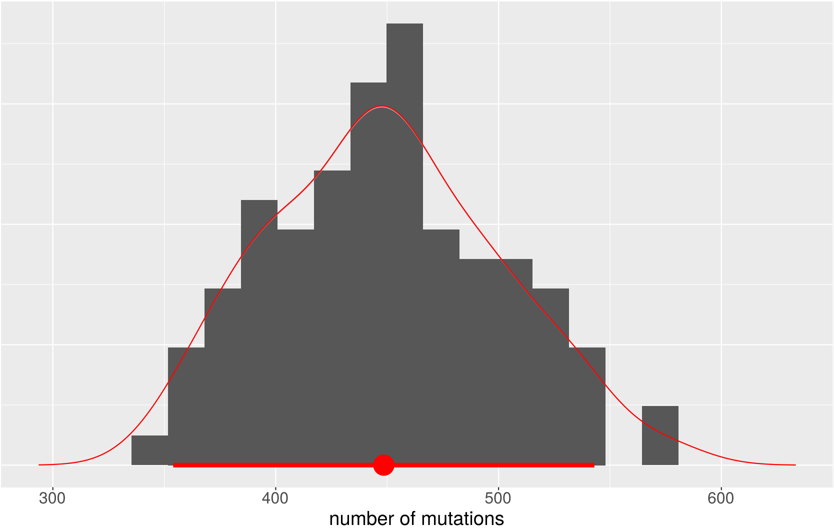
Expected probabilities of Proto-World, given that we can demonstrate SOV for all proto-languages



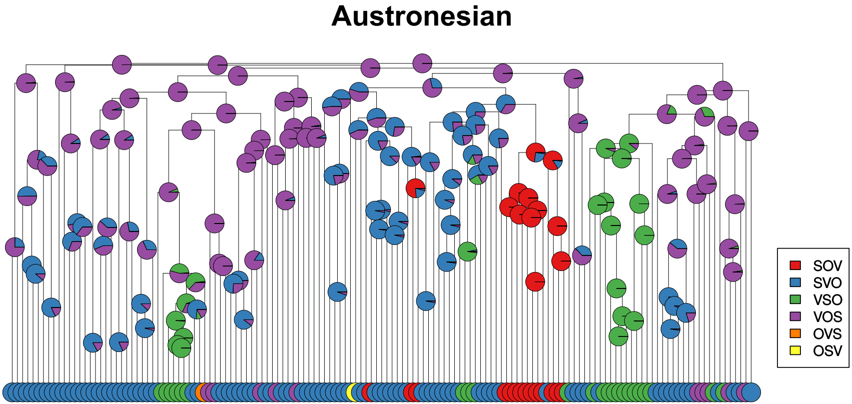
Waiting times



Number of state changes

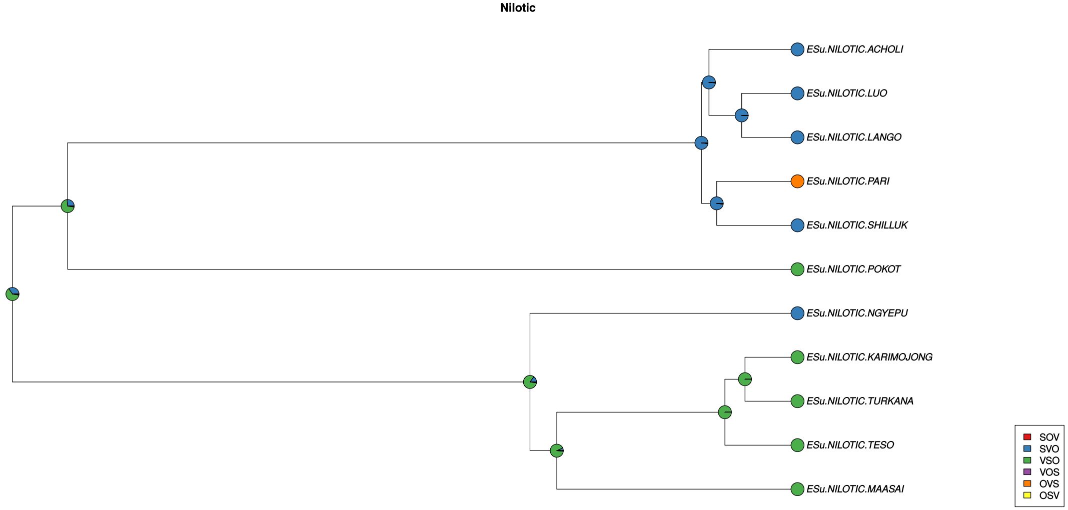


Ancestral state reconstruction



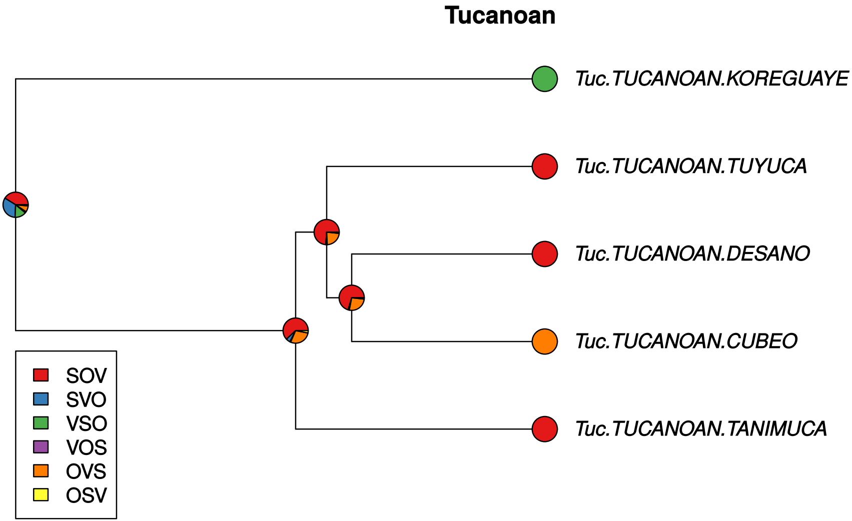
Examples for unexpected transitions

SVO → OVS



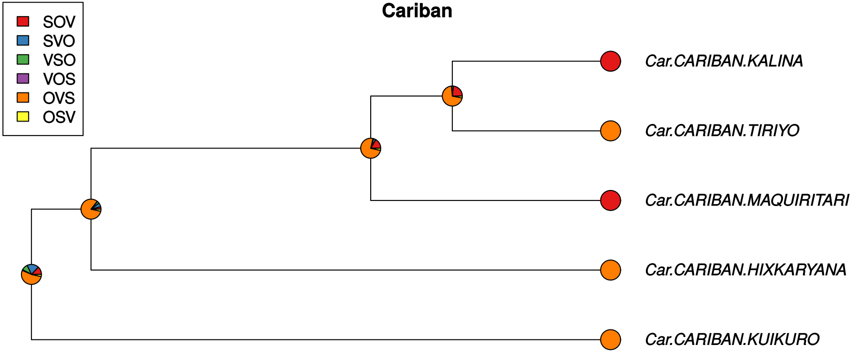
Examples for unexpected transitions

OVS → SOV



Examples for unexpected transitions

OVS → SOV



Summary

- no evidence for general preference of SOV → SVO over the reverse
- SVO is currently over-represented due to recent spread of Austronesian and Atlantic-Congo, but not excessively so
- multiple counter-evidence to Ramon-i-Ferrer's and Gell-Mann & Ruhlen's models

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