

The world tree of languages: How to infer it from data, and what it is good for

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

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TÜBINGEN

DFG

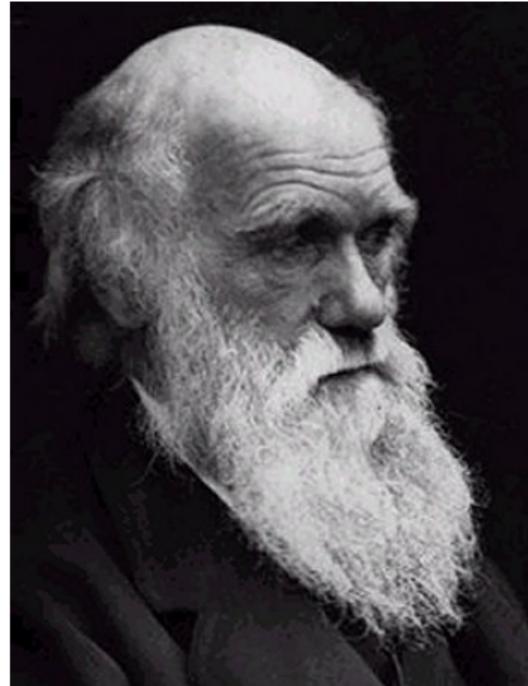


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Introduction

Language change and evolution

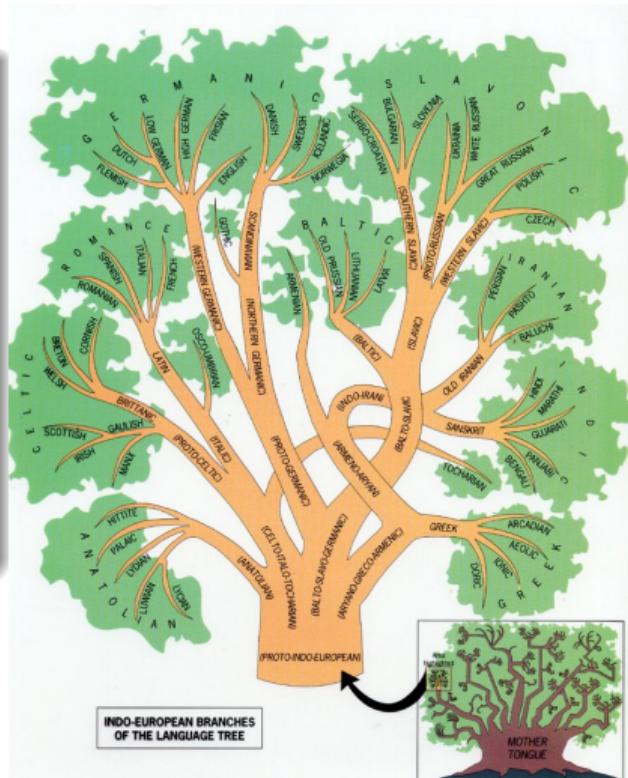
"If we possessed a perfect pedigree of mankind, a genealogical arrangement of the races of man would afford the best classification of the various languages now spoken throughout the world; and if all extinct languages, and all intermediate and slowly changing dialects, had to be included, such an arrangement would, I think, be the only possible one. Yet it might be that some very ancient language had altered little, and had given rise to few new languages, whilst others (owing to the spreading and subsequent isolation and states of civilisation of the several races, descended from a common race) had altered much, and had given rise to many new languages and dialects. The various degrees of difference in the languages from the same stock, would have to be expressed by groups subordinate to groups; but the proper or even only possible arrangement would still be genealogical; and this would be strictly natural, as it would connect together all languages, extinct and modern, by the closest affinities, and would give the filiation and origin of each tongue." (Darwin, The Origin of Species)



Language phylogeny

Comparative method

- ① identifying *cognates*, i.e. obviously related morphemes in different languages, such as *new/nowy*, *two/dwa*, or *water/voda*
- ② reconstruction of *common ancestor* and *sound laws* that explain the change from reconstructed to observed forms
- ③ applying this iteratively leads to phylogenetic language trees



Language phylogeny

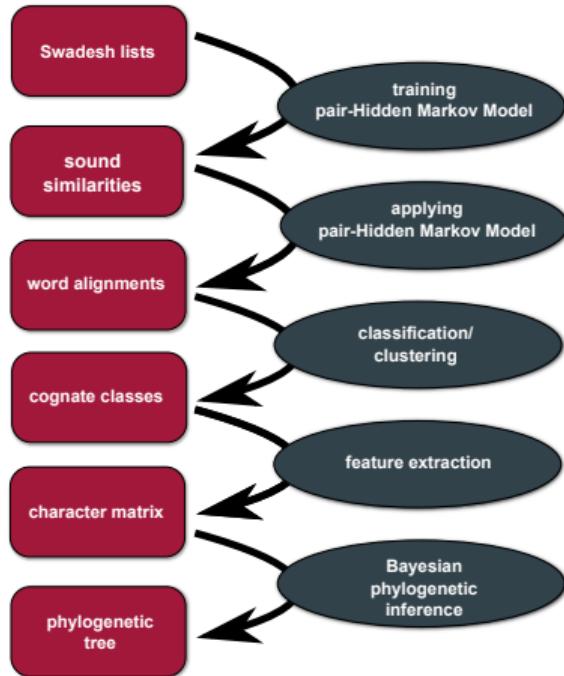
Scope of the method

- reconstructed vocabulary shrinks with growing time depth
- maximal time horizon seems to be about 8,000 years
- grammatical morphemes and categories arguably more stable and less apt to borrowing
- problem here: limited number of features, cross-linguistic variation constrained by language universals, frequently convergent evolution
- comparative method is hard to apply in regions with high linguistic diversity and without written documents (Paleo-America, Papua)
- tree structure might be inappropriate if there is a significant effect of language contact (cf. Australia)

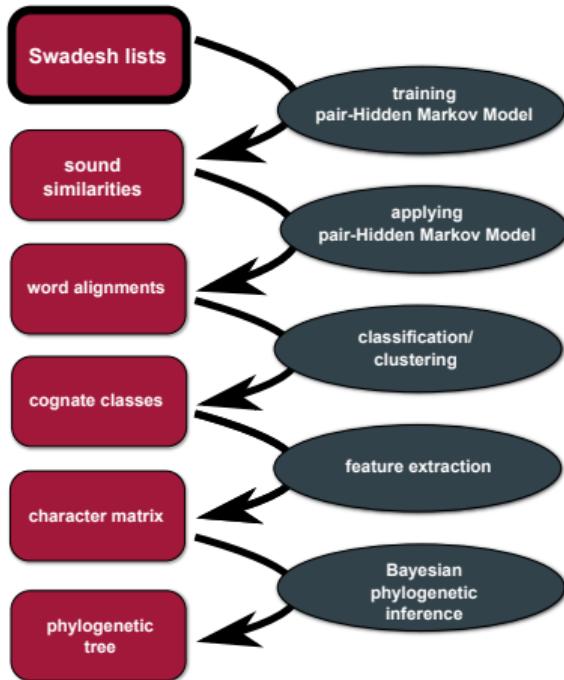
Computational Methods

- both cognate detection and tree construction lend themselves to algorithmic implementation
- Advantages:
 - easy to scale up
 - comparability of results
 - affords statistical evaluation
- Disadvantages:
 - cognacy judgments require lots of linguistic insight and experience
 - tree construction should be subject to historical (including archeological) and geographical plausibility

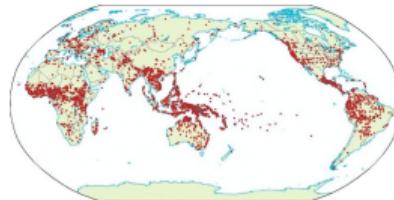
From words to trees



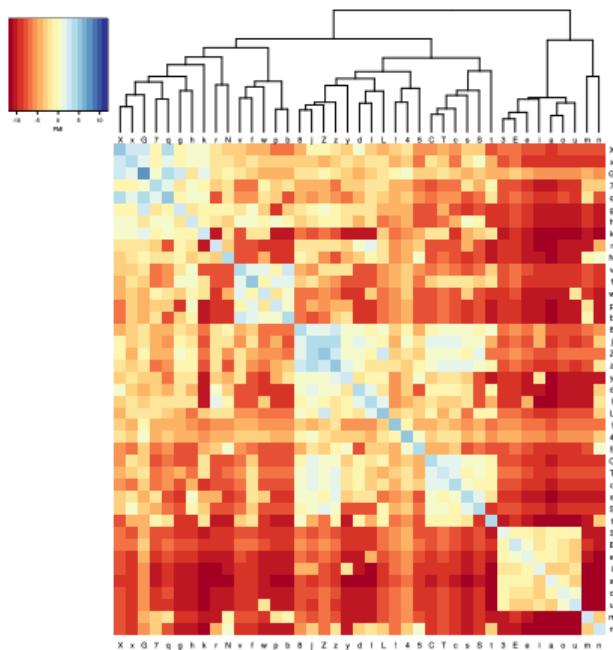
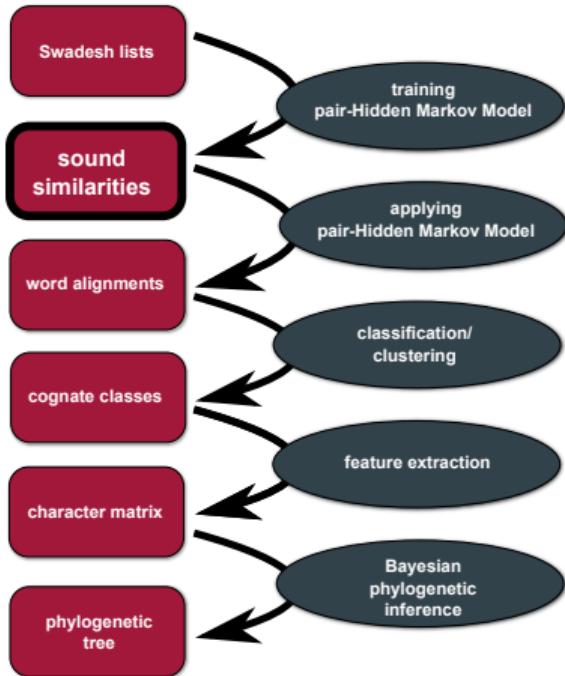
From words to trees



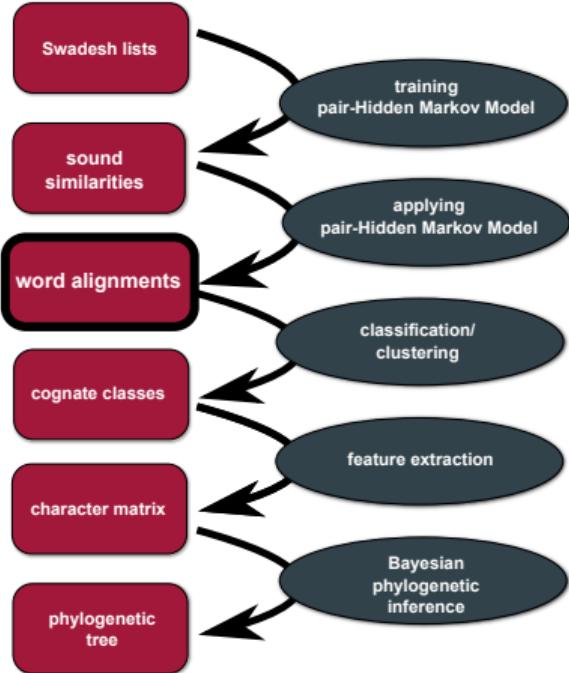
concept	Latin	English
I	ego	Ei
you	tu	yu
we	nos	wi
one	unus	w3n
two	duo	tu
person	persona, homo	pers3n
fish	piskis	fiS
dog	kanis	dag
louse	pedikulus	laus
tree	arbor	tri
leaf	foly~u*	lif
skin	kutis	skin
blood	saNgw~is	bl3d
bone	os	bon
horn	kornu	horn
ear	auris	ir
eye	okulus	Ei



From words to trees

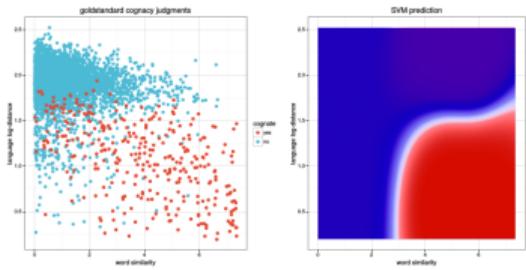
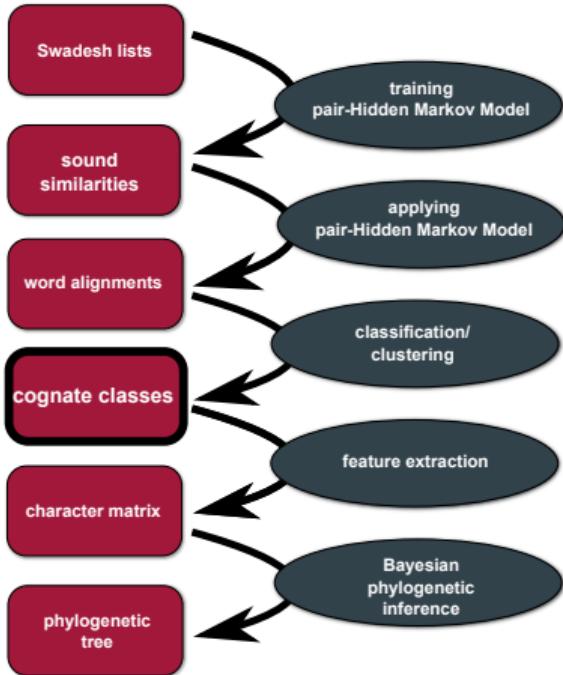


From words to trees



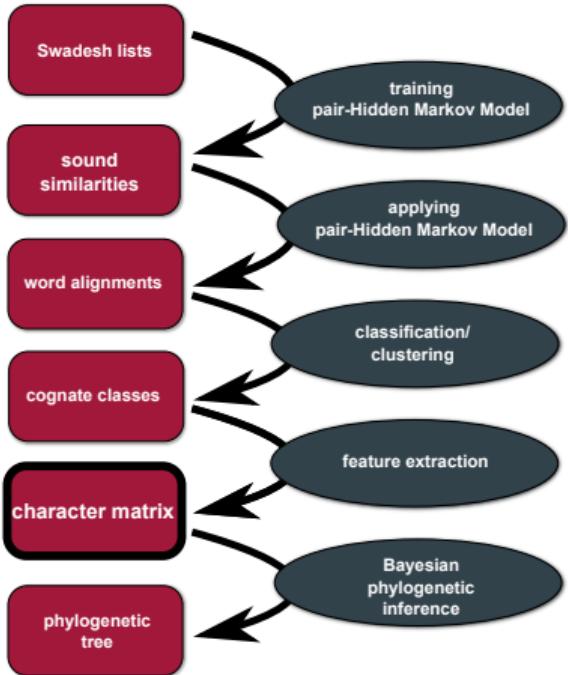
Language	<i>fish:z</i>	<i>tongue:i</i>	<i>smoke:i</i>
Abui-Atangmelang	-af-u	tal-i-fi--	
Abui-Fuimelang	-af-u		awai--b-a-n-o-7o-
Adang	aab--	tal-E-b---	--ad--b-a-n-a-nka-
Blagar-Bakalang	-ab--	--j-e-bur-	-----b-e-n-a-xa-
Blagar-Bama	aab--	teg-e-bur-	-----b-e-n-a-nka-
Blagar-Kulijahi	-ab--	tej-e-bur-	-----b-e-n-a-q--
Blagar-Nule	aab--	tej-e-bur-	--ad--b-e-n-a-nka-
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---	aval--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-impruru	-----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-unna----

From words to trees

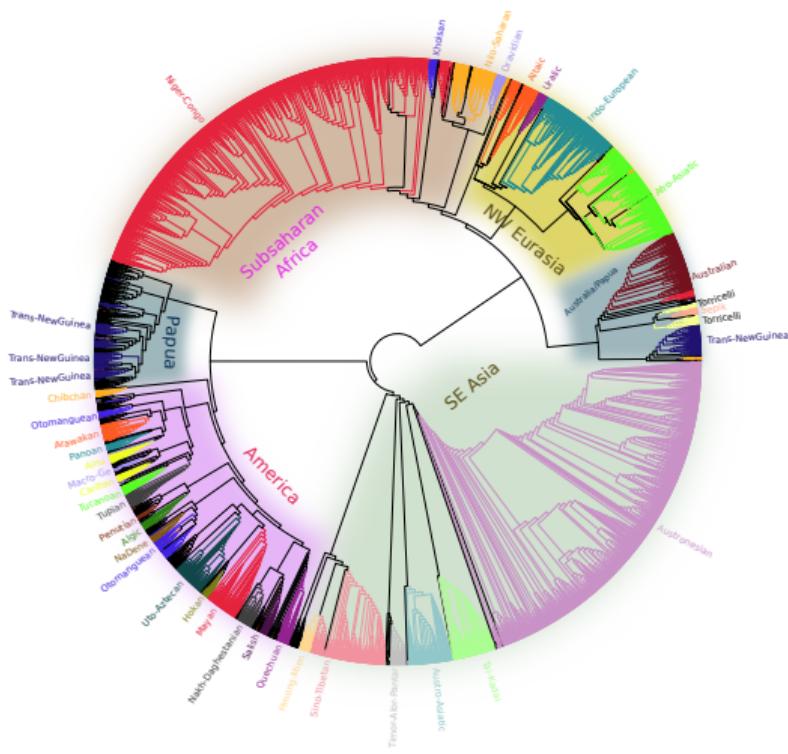
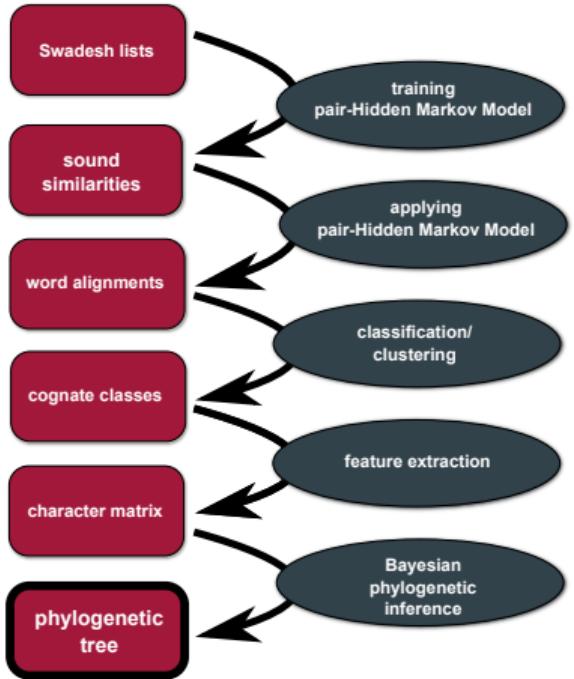


	English	Spanish	Modern Greek	Standard German
I	Ei:A	yo:B	exo:C	iX:D
you	yu:A	ustet:B, tu:C	esi:D	du:E
we	wi:A	nosotros:B	emis:C	vir:A
one	w3n:A	uno:B	enas:C, ena:C	ains:D
two	tu:A	dos:B	8y~o:C, 8io:D	cva:i:B
person	pers3n:A	persona:A	an8~ropos:B	mEnS:C
fish	fis:A	peskado:A, pes:A	psari:B	fi:S:A
dog	dag:A	pero:B	sTili:C, sTilos:C	hund:D
come	k3m:A	veni:B	erx~o:C	kh~om3n:A
sun	s3n:A	sol:B	ily~os:C, iLos:C	zon3:I
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	f8ir:A	fuego:B	foty~a:C	foia:D
path	p88: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, plirisis:D	fol:A
new	nu:A	nuevo:A	neos:A, Tenury~os:B	noi:A
name	nem:A	nombre:A	onoma:A	nam3:A

From words to trees



From words to trees



From word lists to distances

The Automated Similarity Judgment Program

- Started as project at MPI EVA in Leipzig around Søren Wichmann
- covers more than 7,000 languages and dialects
- basic vocabulary of 40 words for each language, in uniform phonetic transcription
- freely available

used concepts: *I, you, we, one, two, person, fish, dog, louse, tree, leaf, skin, blood, bone, horn, ear, eye, nose, tooth, tongue, knee, hand, breast, liver, drink, see, hear, die, come, sun, star, water, stone, fire, path, mountain, night, full, new, name*

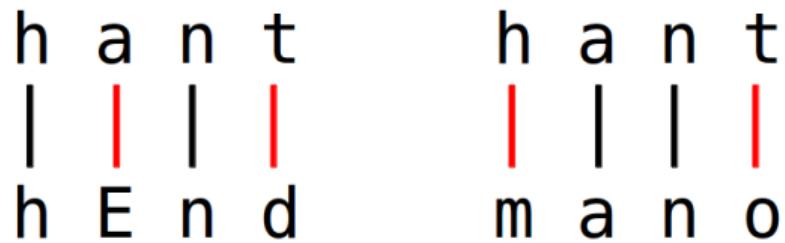
Automated Similarity Judgment Project

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

<i>concept</i>	Latin	English
<i>nose</i>	nasus	nos
<i>tooth</i>	dens	tu8
<i>tongue</i>	liNgw~E	t3N
<i>knee</i>	genu	ni
<i>hand</i>	manus	hEnd
<i>breast</i>	pektus, mama	brest
<i>liver</i>	yekur	liv3r
<i>drink</i>	bibere	drink
<i>see</i>	widere	si
<i>hear</i>	audire	hir
<i>die</i>	mori	dEi
<i>come</i>	wenire	k3m
<i>sun</i>	sol	s3n
<i>star</i>	stela	star
<i>water</i>	akw~a	wat3r
<i>stone</i>	lapis	ston
<i>fire</i>	iNnis	fEir

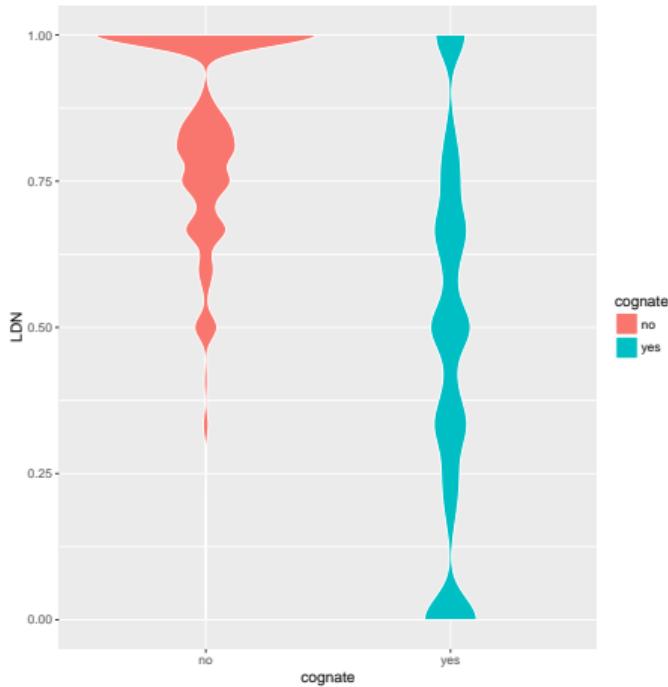
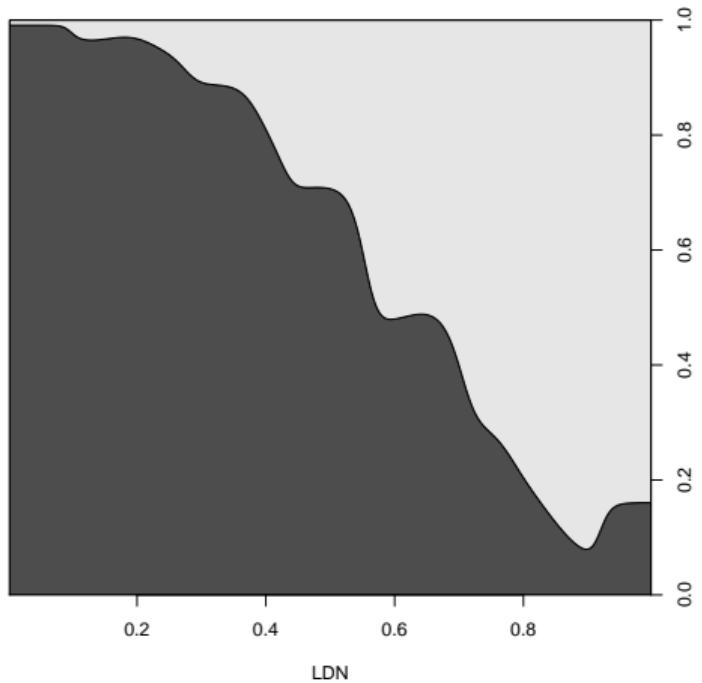
Word distances

- based on string *alignment*
- baseline: Levenshtein alignment ⇒ count matches and mis-matches



- too crude as it totally ignores sound correspondences

How well does normalized Levenshtein distance predict cognacy?



Problems

- binary distinction: match vs. non-match
- frequently genuine sound correspondences in cognates are missed:

c	v	a	i	n	a	z	3	-	-	-	f	i	S
-	-	t	u	n	-	o	s	p	i	s	k	i	s

- corresponding sounds count as mismatches even if they are aligned correctly

h	a	n	t	h	a	n	t
h	E	n	d	m	a	n	o

- substantial amount of chance similarities

Capturing sound correspondences

- weighted alignment using **Pointwise Mutual Information** (PMI, a.k.a. *log-odds*):

$$s(a, b) = \log \frac{p(a, b)}{q(a)q(b)}$$

- $p(a, b)$: probability of sound a being etymologically related to sound b in a pair of cognates
- $q(a)$: relative frequency of sound a
- **Needleman-Wunsch algorithm:** given a matrix of pairwise PMI scores between individual symbols and two strings, it returns the alignment that maximizes the aggregate PMI score
- but first we need to estimate $p(a, b)$ and $q(a), q(b)$ for all soundclasses a and b
- $q(a)$: relative frequency of occurrence of segment a in all words in ASJP
- $p(a, b)$: that's a bit more complicated...

Substitution matrix for the ASJP data

1. identify large sample of pairs of closely related languages (using expert information or heuristics based on aggregated Levenshtein distance)

An.NORTHERN_PHILIPPINES.CENTRAL_BONTOC
 An.MESO-PHILIPPINE.NORTHERN_SORSOGON

WF.WESTERN_FLY.IAMEGA
 WF.WESTERN_FLY.GAMAEWE

Pan.PANOAN.KASHIBO_BAJO_AGUAYTIA
 Pan.PANOAN.KASHIBO_SAN_ALEJANDRO

AA.EASTERN_CUSHITIC.KAMBAATA_2
 AA.EASTERN_CUSHITIC.HADIYYA_2

ST.BAI.QILIQIAO_BAI_2
 ST.BAI.YUNLONG_BAI

An.SULAWESI.MANDAR
 An.OCEANIC.RAGA

An.SULAWESI.TANETE
 An.SAMA-BAJAW.BOE PINANG_BAJAU

An.SOUTHERN_PHILIPPINES.KAGAYANEN
 An.NORTHERN_PHILIPPINES.LIMOS_KALINGA

An.MESO-PHILIPPINE.CANIPAAN_PALAWAN
 An.NORTHWEST_MALAYO-POLYNESIAN.LAHANAN

NC.BANTOID.LIFONGA
 NC.BANTOID.BOMBOMA_2

IE.INDIC.WAD_PAGGA
 IE.INDIC.TALAGANG_HINDKO

NC.BANTOID.LINGALA
 NC.BANTOID.LIFONGA

An.CENTRAL_MALAYO-POLYNESIAN.BALILEDO
 An.CENTRAL_MALAYO-POLYNESIAN.PALUE

AuA.MUNDA.HO
 AuA.MUNDA.KORKU

Substitution matrix for the ASJP data

2. pick a concept and a pair of related languages at random
 - languages: Pen.MAIDUAN.MAIDU_KONKAU, Pen.MAIDUAN.NE_MAIDU
 - concept: *one*
3. find corresponding words from the two languages:
 - nisam, niSem
4. do Levenshtein alignment

n	i	s	a	m
n	i	S	e	m

5. for each sound pair, count number of correspondences
 - nn: 1; ii: 1; sS; 1; ae: 1; mm: 1

Finding the best alignment

- Dynamic Programming

	—	m	E	n	S
—	0	-2.5	-4.1	-5.7	-7.3
m	-2.5				
e	-4.1				
n	-5.7				
E	-7.3				
s	-8.9				

Finding the best alignment

- Dynamic Programming

	—	m	E	n	S
—	0	-2.5	-4.1	-5.7	-7.3
m	-2.5				
e	-4.1				
n	-5.7				
E	-7.3				
s	-8.9				

Finding the best alignment

- Dynamic Programming

	—	m	E	n	S
—	0	-2.5	-4.1	-5.7	-7.3
m	-2.5				
e	-4.1				
n	-5.7				
E	-7.3				
s	-8.9				

Finding the best alignment

- Dynamic Programming

	—	m	E	n	S
—	0	-2.5	-4.1	-5.7	-7.3
m	-2.5	4.13			
e	-4.1				
n	-5.7				
E	-7.3				
s	-8.9				

Finding the best alignment

- Dynamic Programming

	–	m	E	n	S
–	0	-2.5	-4.1	-5.7	-7.3
m	-2.5	4.13			
e	-4.1				
n	-5.7				
E	-7.3				
s	-8.9				

Finding the best alignment

- Dynamic Programming

	–	m	E	n	S
–	0	-2.5	-4.1	-5.7	-7.3
m	-2.5	4.13			
e	-4.1				
n	-5.7				
E	-7.3				
s	-8.9				

Finding the best alignment

- Dynamic Programming

	—	m	E	n	S
—	0	-2.5	-4.1	-5.7	-7.3
m	-2.5	4.13	1.53		
e	-4.1				
n	-5.7				
E	-7.3				
s	-8.9				

Finding the best alignment

- Dynamic Programming

	—	m	E	n	S
—	0	-2.5	-4.1	-5.7	-7.3
m	-2.5	4.13	1.53	0.03	
e	-4.1				
n	-5.7				
E	-7.3				
s	-8.9				

Finding the best alignment

- Dynamic Programming

	–	m	E	n	S
–	0	-2.5	-4.1	-5.7	-7.3
m	-2.5	4.13	1.53	0.03	-1.47
e	-4.1				
n	-5.7				
E	-7.3				
s	-8.9				

Finding the best alignment

- Dynamic Programming

	–	m	E	n	S
–	0	-2.5	-4.1	-5.7	-7.3
m	-2.5	4.13	1.53	0.03	-1.47
e	-4.1	1.53			
n	-5.7				
E	-7.3				
s	-8.9				

Finding the best alignment

- Dynamic Programming

	–	m	E	n	S
–	0	-2.5	-4.1	-5.7	-7.3
m	-2.5	4.13	1.53	0.03	-1.47
e	-4.1	1.53	5.65		
n	-5.7				
E	-7.3				
s	-8.9				

Finding the best alignment

- Dynamic Programming

	–	m	E	n	S
–	0	-2.5	-4.1	-5.7	-7.3
m	-2.5	4.13	1.53	0.03	-1.47
e	-4.1	1.53	5.65	3.05	
n	-5.7				
E	-7.3				
s	-8.9				

Finding the best alignment

- Dynamic Programming

	–	m	E	n	S
–	0	-2.5	-4.1	-5.7	-7.3
m	-2.5	4.13	1.53	0.03	-1.47
e	-4.1	1.53	5.65	3.05	1.55
n	-5.7				
E	-7.3				
s	-8.9				

Finding the best alignment

- Dynamic Programming

	–	m	E	n	S
–	0	-2.5	-4.1	-5.7	-7.3
m	-2.5	4.13	1.53	0.03	-1.47
e	-4.1	1.53	5.65	3.05	1.55
n	-5.7	0.03			
E	-7.3				
s	-8.9				

Finding the best alignment

- Dynamic Programming

	–	m	E	n	S
–	0	-2.5	-4.1	-5.7	-7.3
m	-2.5	4.13	1.53	0.03	-1.47
e	-4.1	1.53	5.65	3.05	1.55
n	-5.7	0.03	3.05		
E	-7.3				
s	-8.9				

Finding the best alignment

- Dynamic Programming

	–	m	E	n	S
–	0	-2.5	-4.1	-5.7	-7.3
m	-2.5	4.13	1.53	0.03	-1.47
e	-4.1	1.53	5.65	3.05	1.55
n	-5.7	0.03	3.05	9.2	
E	-7.3				
s	-8.9				

Finding the best alignment

- Dynamic Programming

	–	m	E	n	S
–	0	-2.5	-4.1	-5.7	-7.3
m	-2.5	4.13	1.53	0.03	-1.47
e	-4.1	1.53	5.65	3.05	1.55
n	-5.7	0.03	3.05	9.2	6.6
E	-7.3				
s	-8.9				

Finding the best alignment

- Dynamic Programming

	–	m	E	n	S
–	0	-2.5	-4.1	-5.7	-7.3
m	-2.5	4.13	1.53	0.03	-1.47
e	-4.1	1.53	5.65	3.05	1.55
n	-5.7	0.03	3.05	9.2	6.6
E	-7.3	-1.47			
s	-8.9				

Finding the best alignment

- Dynamic Programming

	–	m	E	n	S
–	0	-2.5	-4.1	-5.7	-7.3
m	-2.5	4.13	1.53	0.03	-1.47
e	-4.1	1.53	5.65	3.05	1.55
n	-5.7	0.03	3.05	9.2	6.6
E	-7.3	-1.47	4.75		
s	-8.9				

Finding the best alignment

- Dynamic Programming

	–	m	E	n	S
–	0	-2.5	-4.1	-5.7	-7.3
m	-2.5	4.13	1.53	0.03	-1.47
e	-4.1	1.53	5.65	3.05	1.55
n	-5.7	0.03	3.05	9.2	6.6
E	-7.3	-1.47	4.75	6.6	
s	-8.9				

Finding the best alignment

- Dynamic Programming

	–	m	E	n	S
–	0	-2.5	-4.1	-5.7	-7.3
m	-2.5	4.13	1.53	0.03	-1.47
e	-4.1	1.53	5.65	3.05	1.55
n	-5.7	0.03	3.05	9.2	6.6
E	-7.3	-1.47	4.75	6.6	7.62
s	-8.9				

Finding the best alignment

- Dynamic Programming

	–	m	E	n	S
–	0	-2.5	-4.1	-5.7	-7.3
m	-2.5	4.13	1.53	0.03	-1.47
e	-4.1	1.53	5.65	3.05	1.55
n	-5.7	0.03	3.05	9.2	6.6
E	-7.3	-1.47	4.75	6.6	7.62
s	-8.9	-2.97			

Finding the best alignment

- Dynamic Programming

	–	m	E	n	S
–	0	-2.5	-4.1	-5.7	-7.3
m	-2.5	4.13	1.53	0.03	-1.47
e	-4.1	1.53	5.65	3.05	1.55
n	-5.7	0.03	3.05	9.2	6.6
E	-7.3	-1.47	4.75	6.6	7.62
s	-8.9	-2.97	2.15		

Finding the best alignment

- Dynamic Programming

	–	m	E	n	S
–	0	-2.5	-4.1	-5.7	-7.3
m	-2.5	4.13	1.53	0.03	-1.47
e	-4.1	1.53	5.65	3.05	1.55
n	-5.7	0.03	3.05	9.2	6.6
E	-7.3	-1.47	4.75	6.6	7.62
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Finding the best alignment

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Finding the best alignment

- Dynamic Programming

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m	-2.5	4.13	1.53	0.03	-1.47
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s	-8.9	-2.97	2.15	5.1	8.84

- memorizing in each step which of the three cells to the left and above gave rise to the current entry lets us recover the corresponding optimal alignment

Finding the best alignment

- Dynamic Programming

	–	m	E	n	S
–	0	-2.5	-4.1	-5.7	-7.3
m	-2.5	4.13	1.53	0.03	-1.47
e	-4.1	1.53	5.65	3.05	1.55
n	-5.7	0.03	3.05	9.2	6.6
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- memorizing in each step which of the three cells to the left and above gave rise to the current entry lets us recover the corresponding optimal alignment

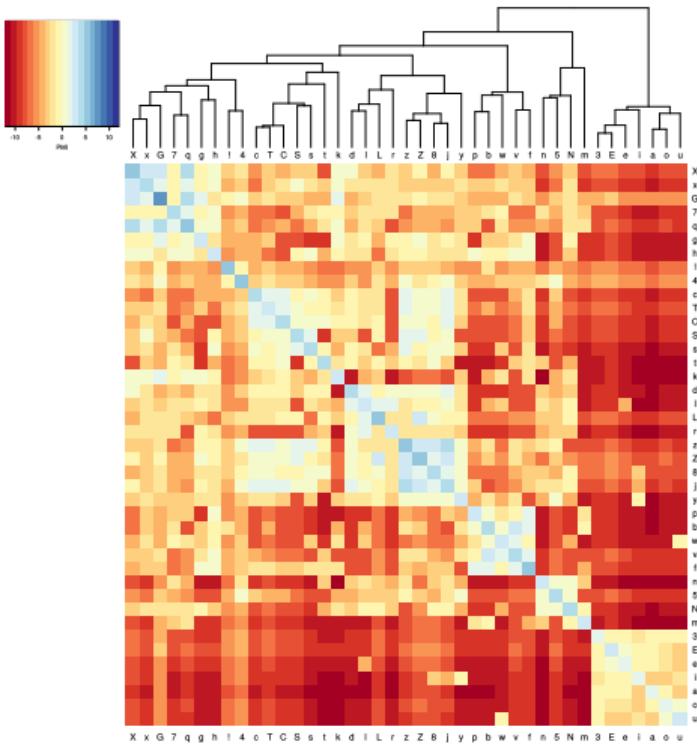
Finding the best alignment

- Dynamic Programming

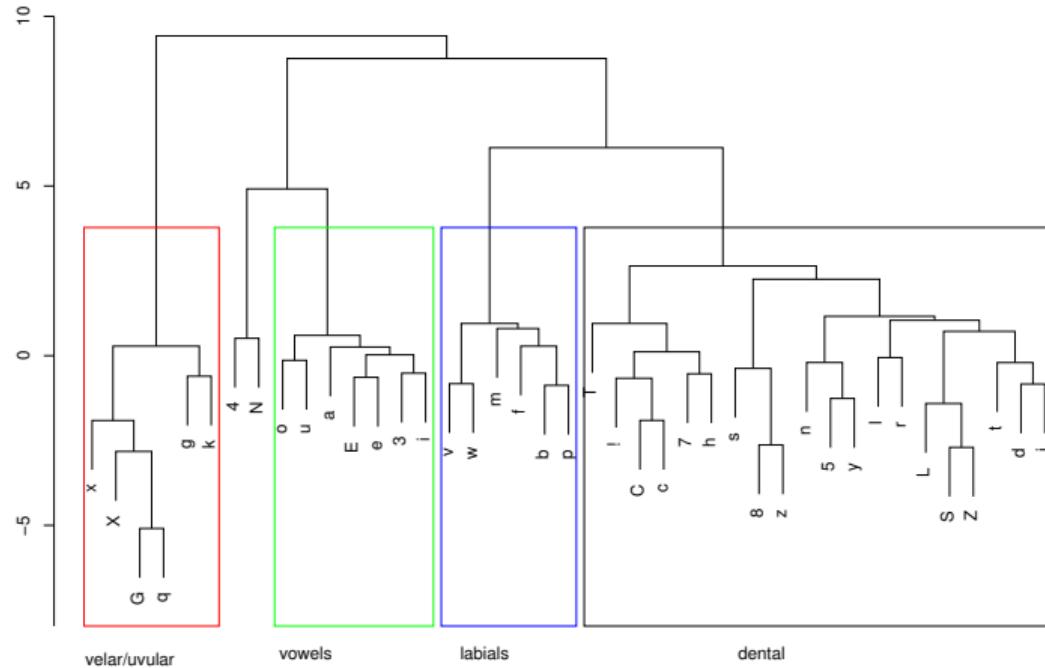
	–	m	E	n	S
–	0	-2.5	-4.1	-5.7	-7.3
m	-2.5	4.13	1.53	0.03	-1.47
e	-4.1	1.53	5.65	3.05	1.55
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- memorizing in each step which of the three cells to the left and above gave rise to the current entry lets us recover the corresponding optimal alignment

Evaluation

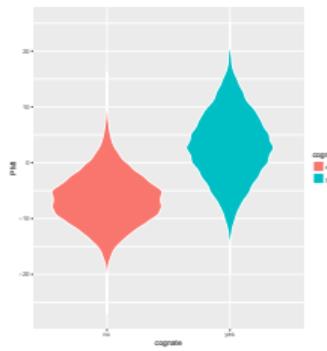
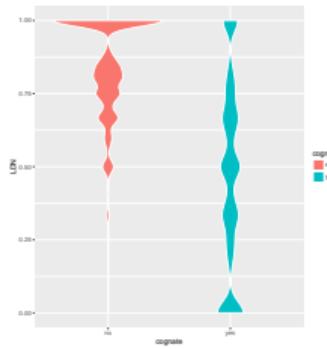
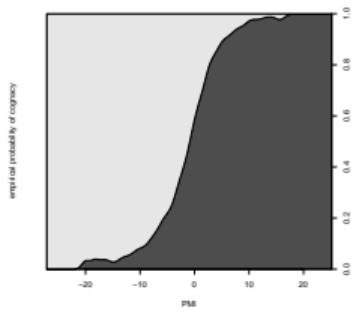
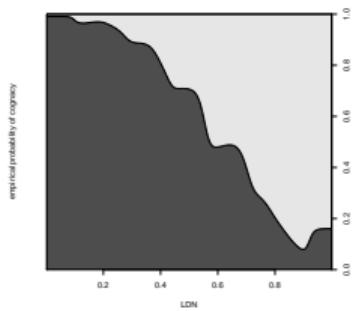


Evaluation



How well does PMI similarity predict cognacy?

expert cognacy judgments used as gold standard



Calibrated PMI similarity

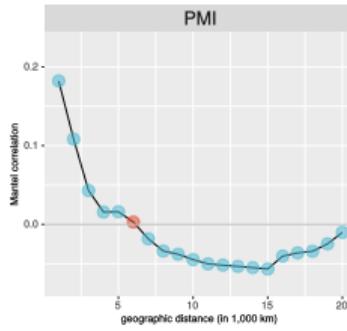
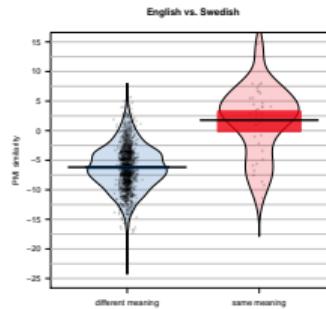
English / Swedish

	Ei	yu	wi	w3n	tu	fiS	...
yog	-7.77	0.75	-7.68	-7.90	-8.57	-10.50	
du	-7.62	0.33	-5.71	-7.41	2.66	-8.57	
vi	-2.72	-2.83	4.04	-1.34	-6.45	0.70	
et	-5.47	-7.87	-5.47	-6.43	-1.83	-4.70	
tvo	-7.91	-4.27	-3.64	-4.57	0.39	-6.98	
fisk	-7.45	-11.2	-3.07	-9.97	-8.66	7.58	
:							

- values along diagonal give similarity between candidates for cognacy (possibility of meaning change is disregarded)
- values off diagonal provide sample of similarity distribution between non-cognates

Calibrated PMI similarity

- let s be the PMI-similarity between the English and Swedish word for concept c
- calibrated string similarity:** $-\log(\text{probability that random word pairs are more similar than } s)$
- language similarity:** average word similarity for all concepts



Cognate clustering

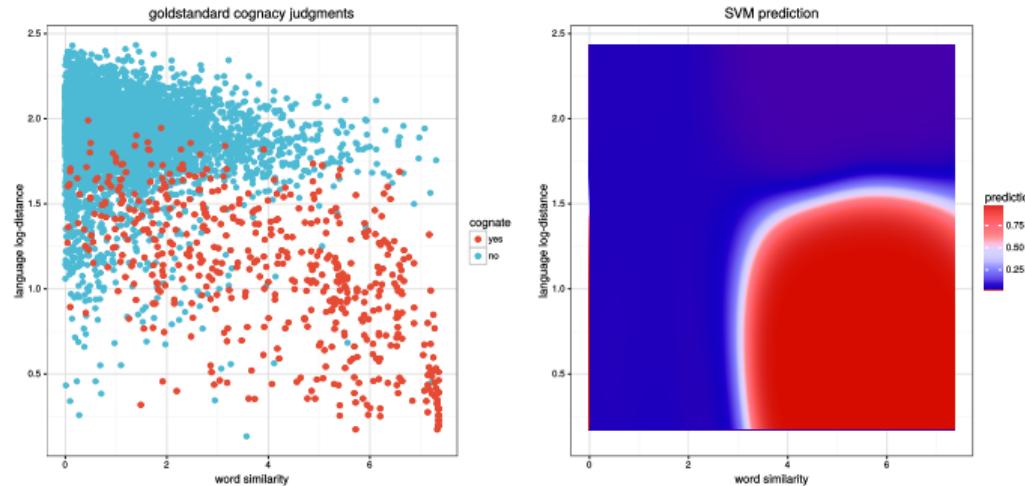
Cognate clustering

- clustering of ASJP strings into *automatically inferred cognate classes* (Jäger and Sofroniev, 2016; Jäger et al., 2017) (take “cognate” with a grain of salt)
- supervised learning, based on expert cognacy judgments as goldstandard
- sources (only the 40 ASJP concepts were used)

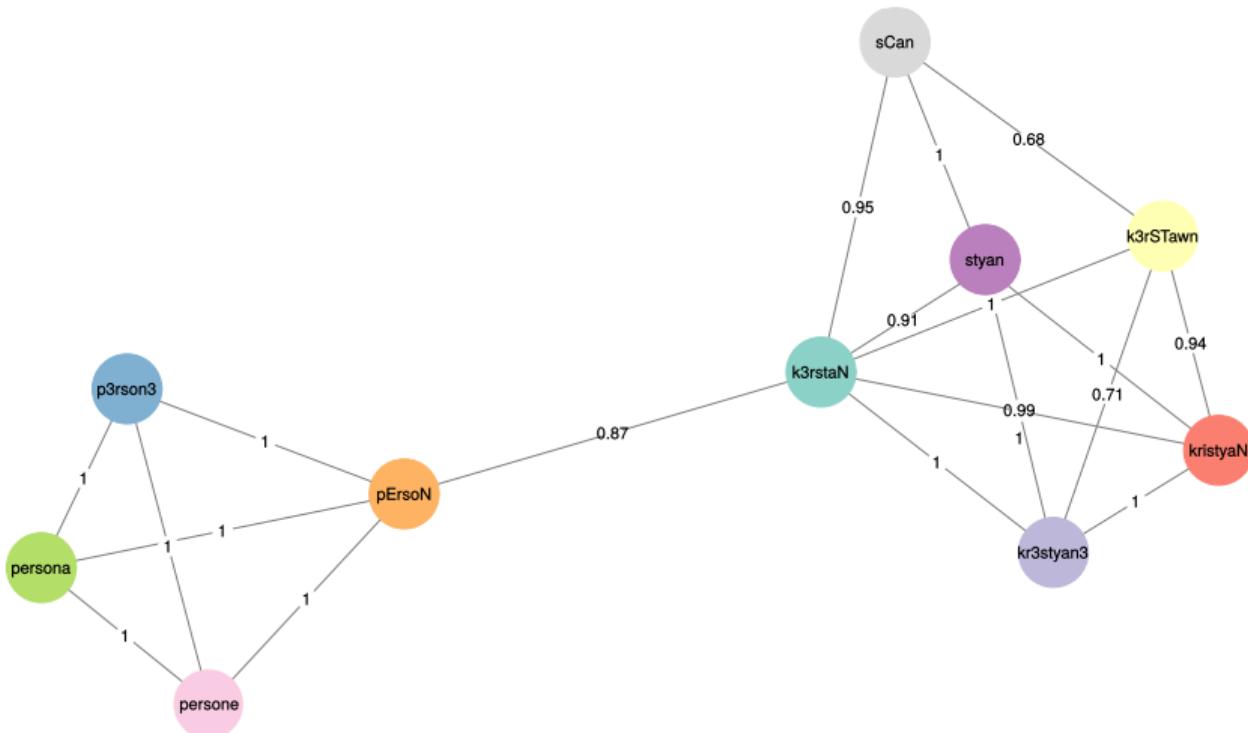
Dataset	Source	Words	Concepts	Languages	Families	Cognate classes
ABVD	Greenhill et al. (2008)	2,306	34	100	Austronesian	409
Afrasian	Militarev (2000)	770	39	21	Afro-Asiatic	351
Chinese	Běijing Dàxué (1964)	422	20	18	Sino-Tibetan	126
Huon	McElhanon (1967)	441	32	14	Trans-New Guinea	183
IELex	Dunn (2012)	2,089	40	52	Indo-European	318
Japanese	Hattori (1973)	387	39	10	Japonic	74
Kadai	Peiros (1998)	399	40	12	Tai-Kadai	102
Kamasau	Sanders and Sanders (1980)	270	36	8	Torricelli	59
Mayan	Brown et al. (2008)	1,113	40	30	Mayan	241
Miao-Yao	Peiros (1998)	206	36	6	Hmong-Mien	69
Mixe-Zoque	Cysouw et al. (2006)	355	39	10	Mixe-Zoque	79
Mon-Khmer	Peiros (1998)	579	40	16	Austroasiatic	232
ObUgrian	Zhvlov (2011)	769	39	21	Uralic	68
total		10,106	40	318		2,311

Cognate clustering

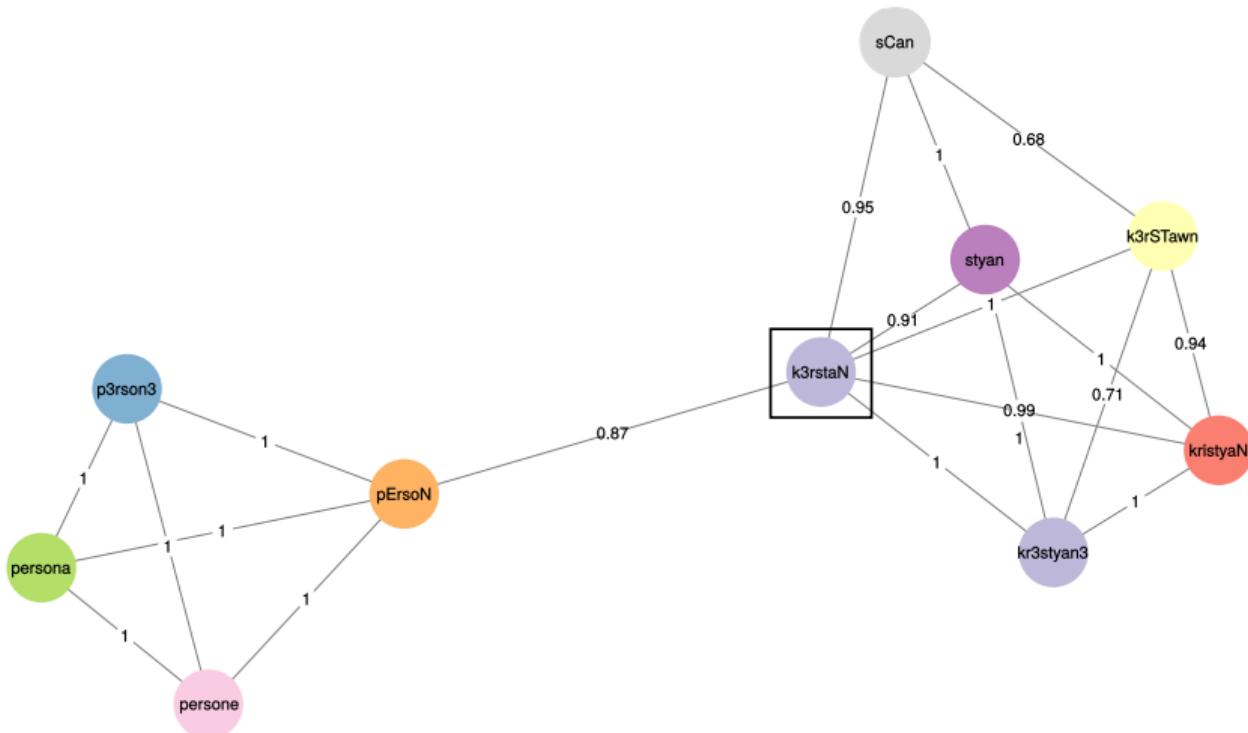
- calibrated word similarity and language similarity were used as predictors to train a *Support Vector Machine* → probability of being cognate for each pair of synonymous ASJP entries
- *Label Propagation* (Raghavan et al., 2007) for clustering
- 0.84 B-cubed F-score with cross-validation on goldstandard data



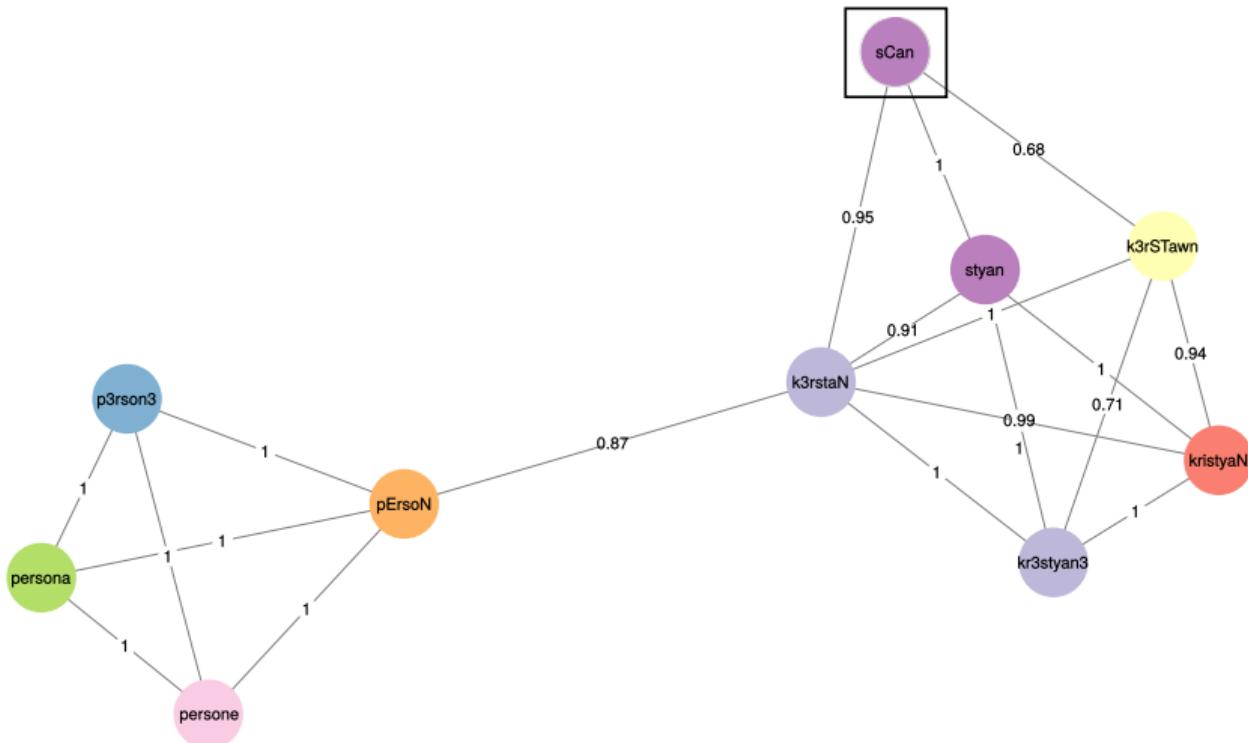
Clustering via Label Propagation



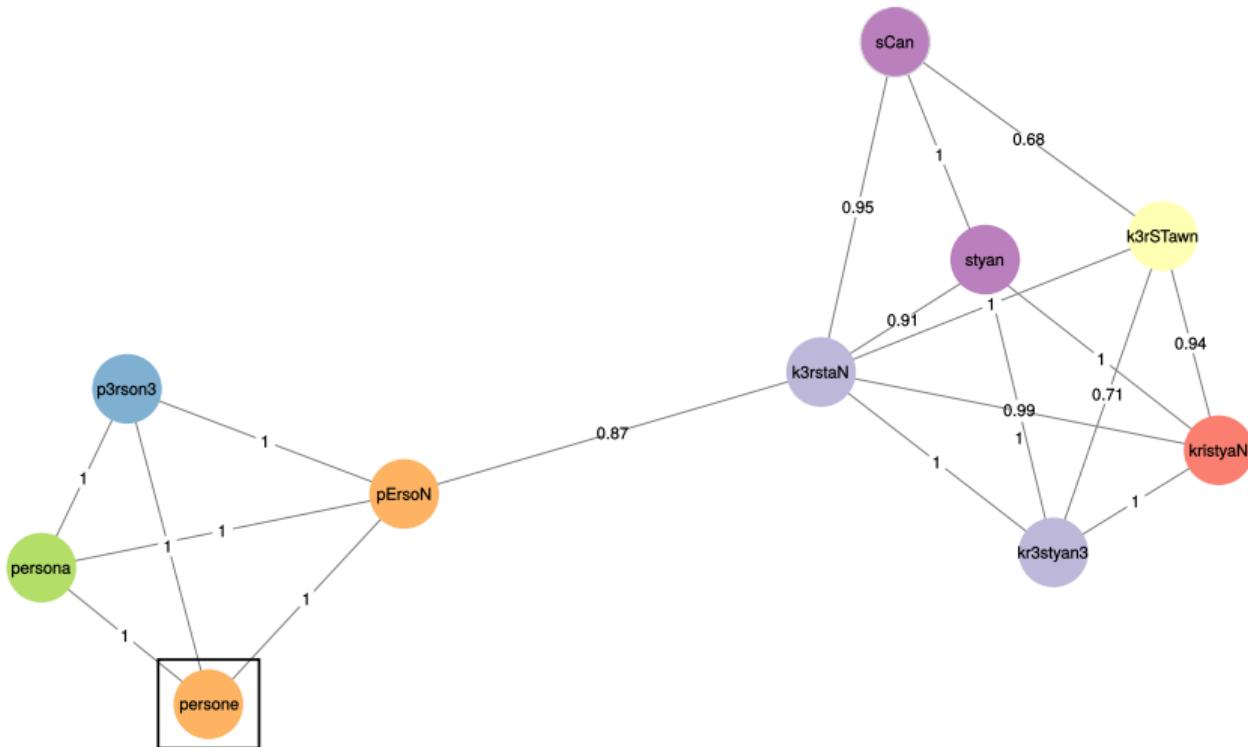
Clustering via Label Propagation



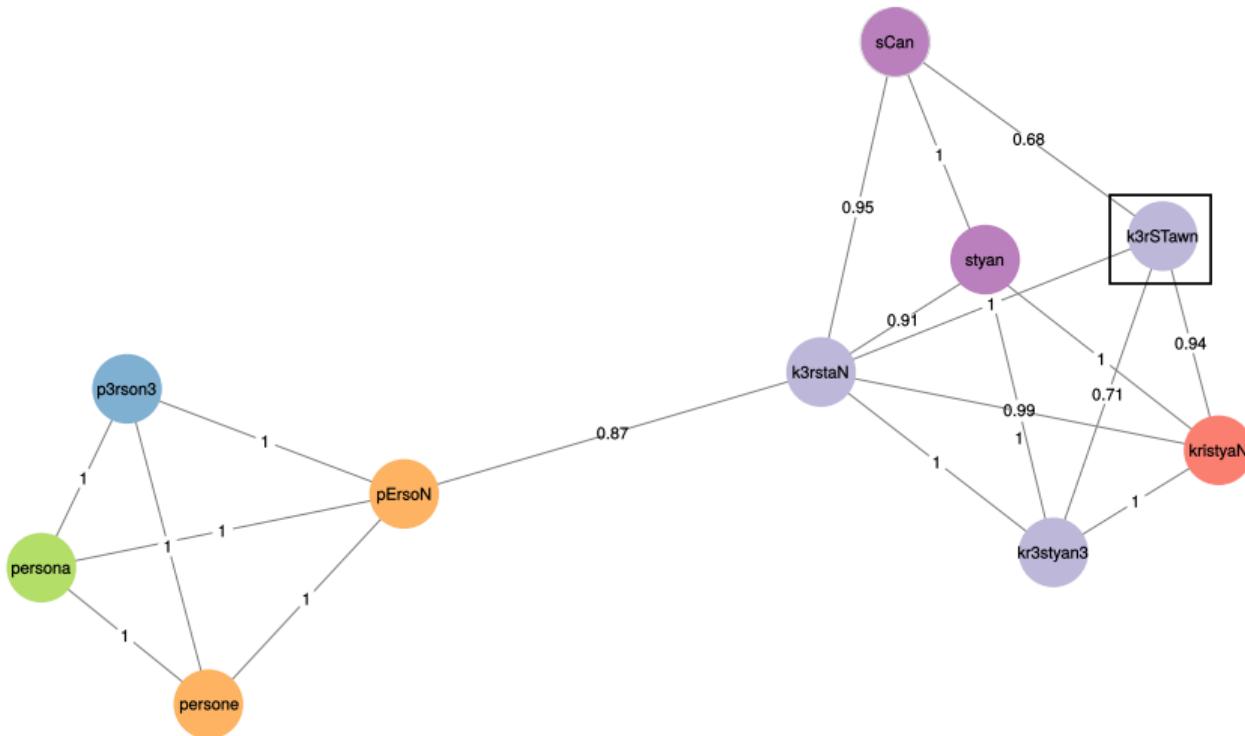
Clustering via Label Propagation



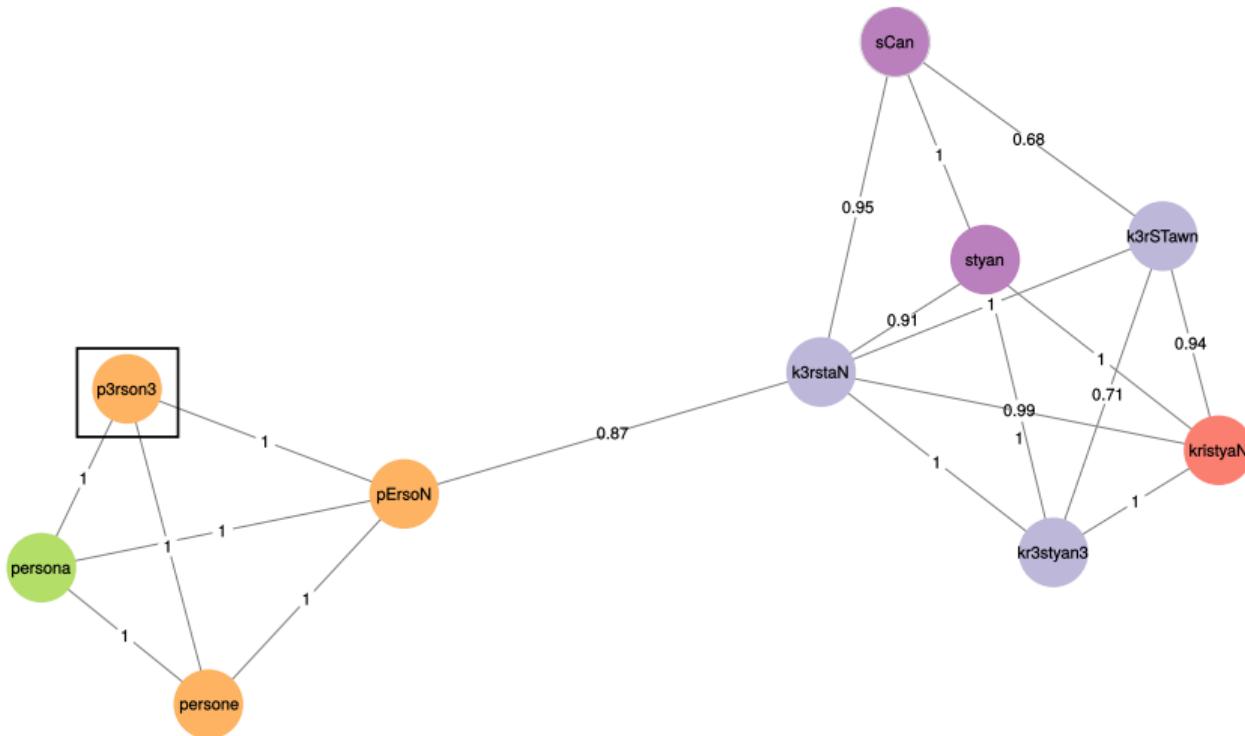
Clustering via Label Propagation



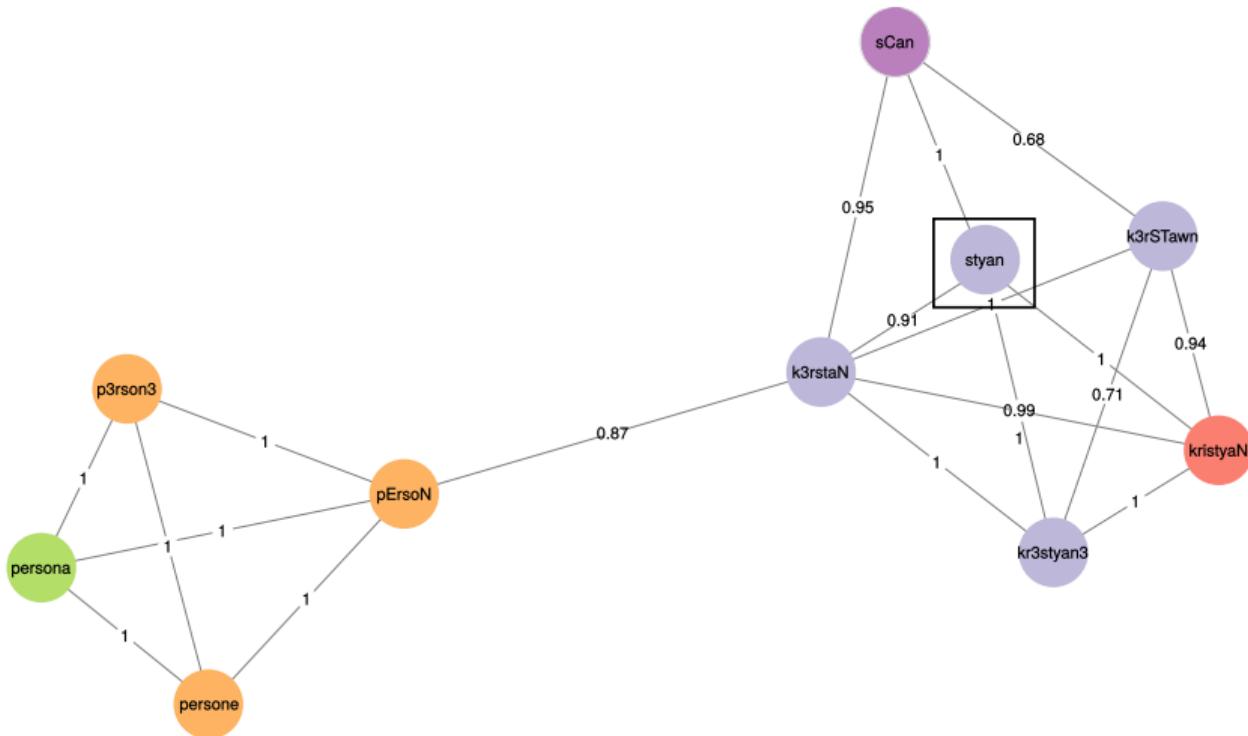
Clustering via Label Propagation



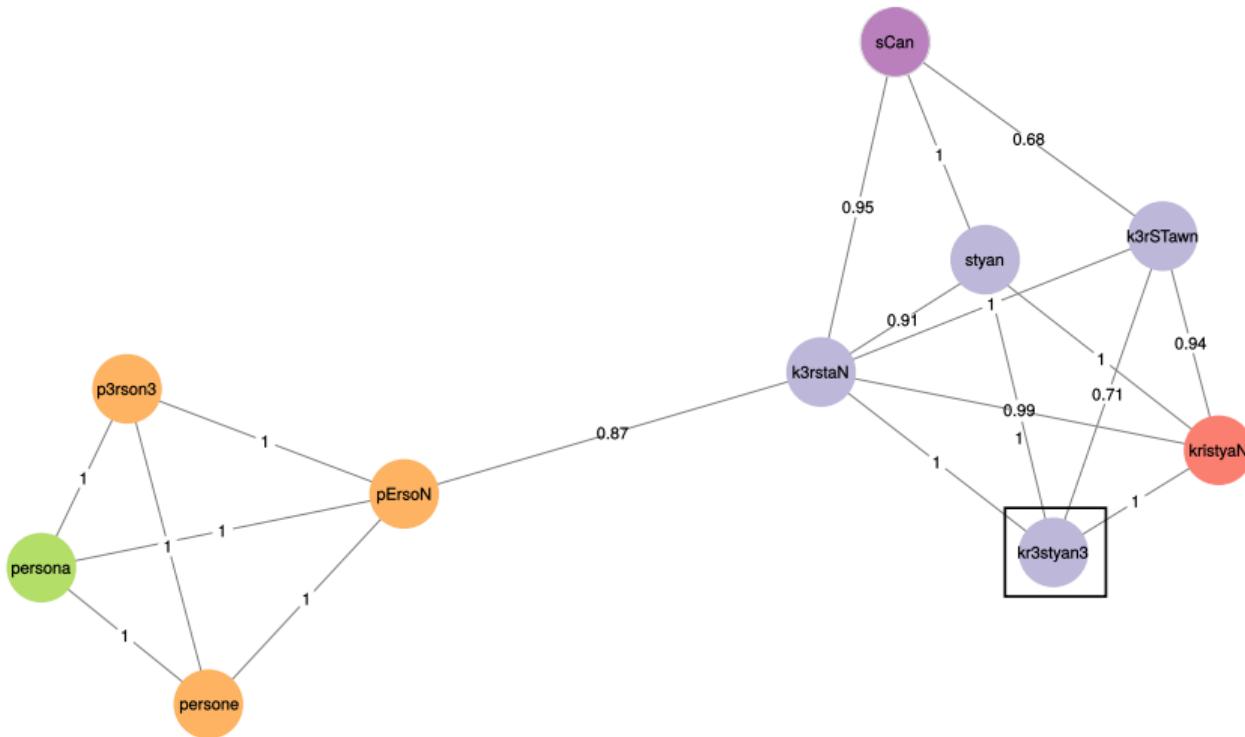
Clustering via Label Propagation



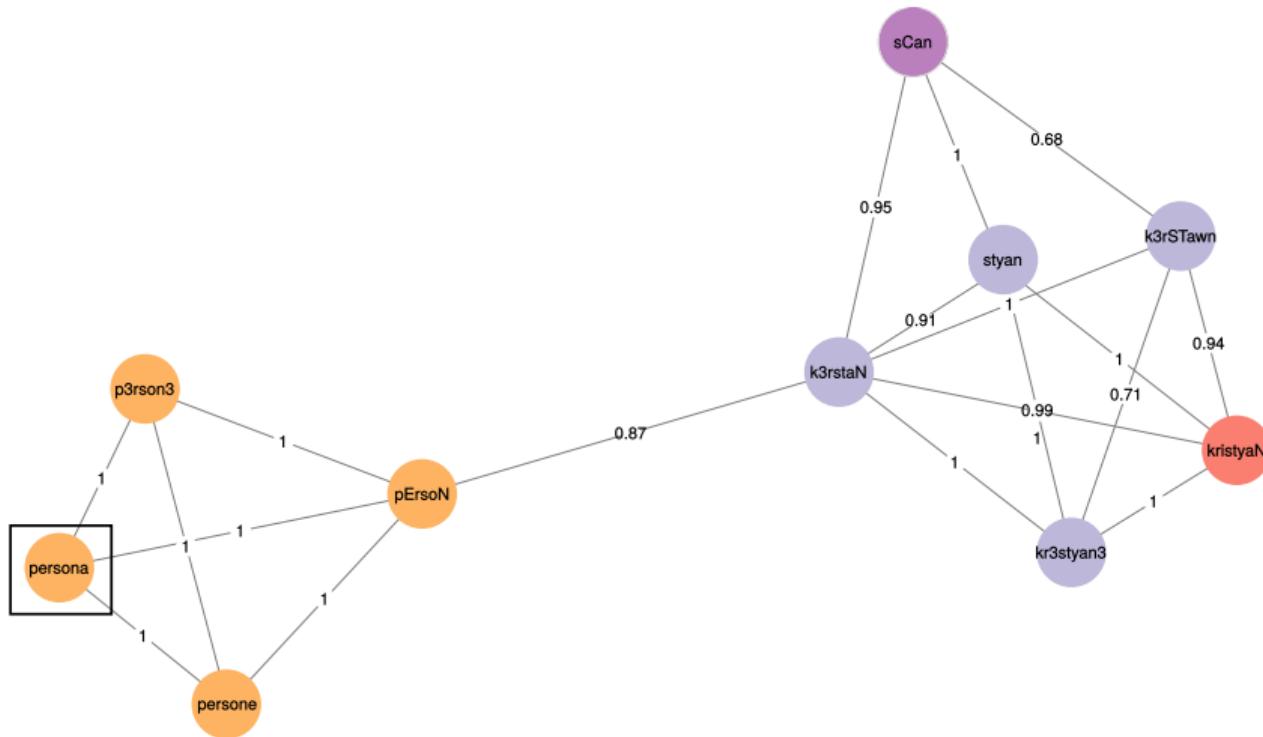
Clustering via Label Propagation



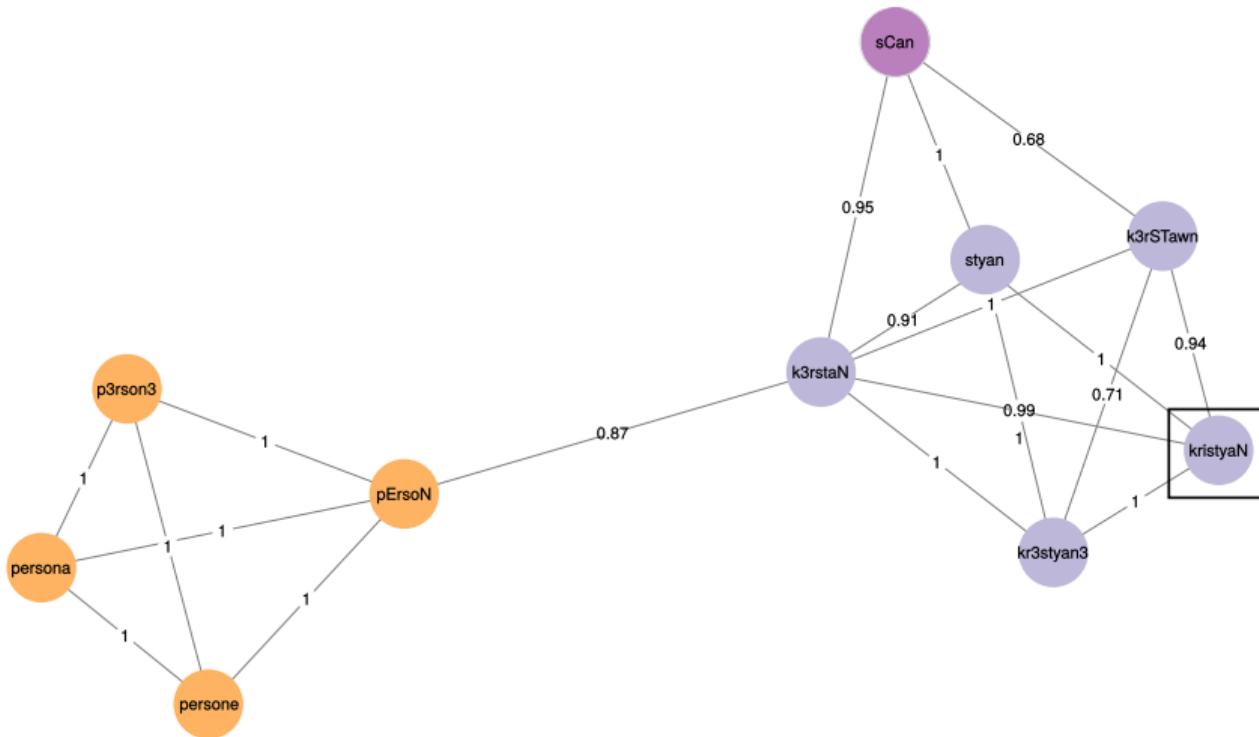
Clustering via Label Propagation



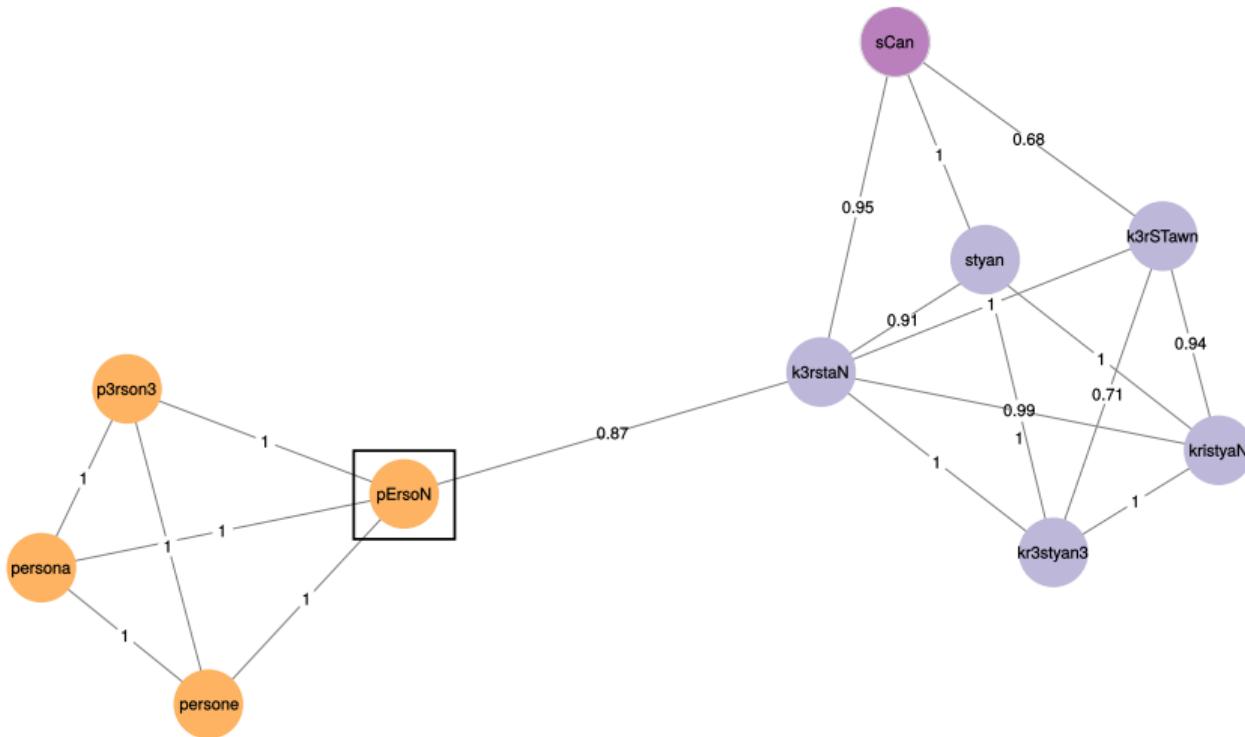
Clustering via Label Propagation



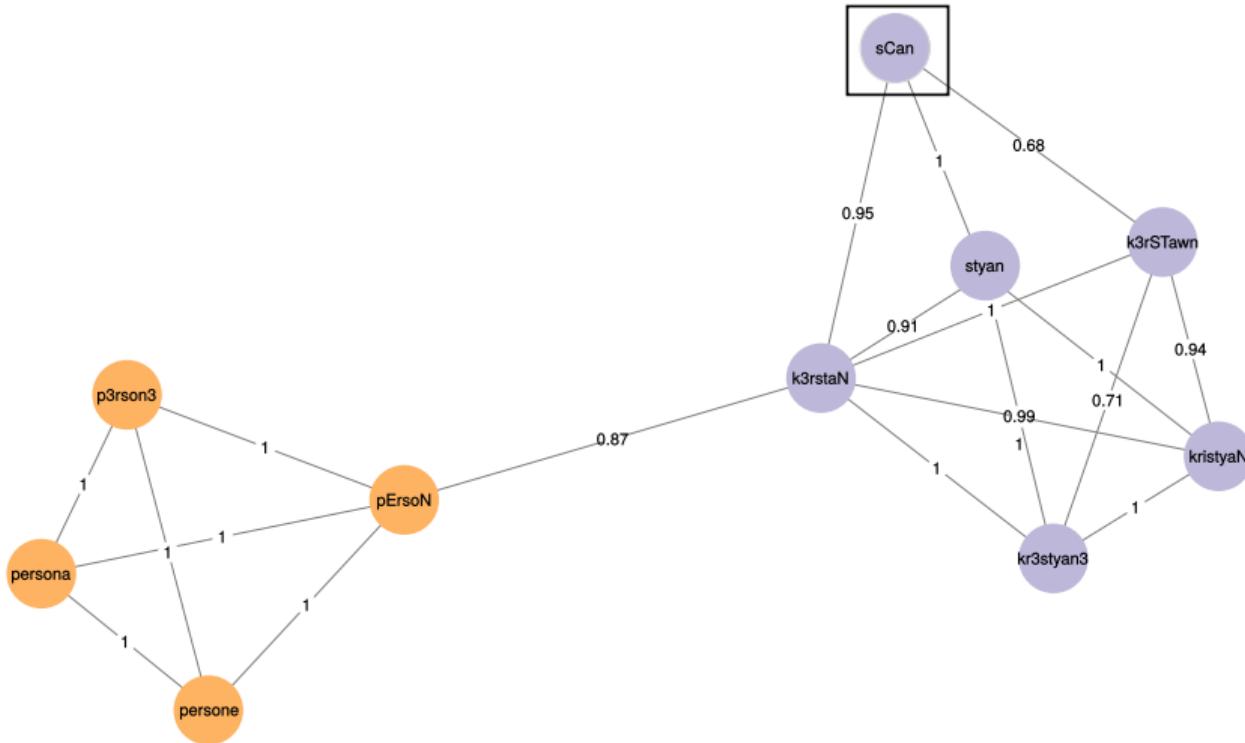
Clustering via Label Propagation



Clustering via Label Propagation



Clustering via Label Propagation



Cognate clustering

doculect	word	class label
ALBANIAN	vet3	0
ALBANIAN_TOSK	vEt3	0
ARAGONESE	ombre	1
ITALIAN_GROSSETO_TUSCAN	omo	2
ROMANIAN_MEGLENO	wom	2
VLACH	omu	2
ASTURIAN	persona	3
BALEAR_CATALAN	p3rson3	3
CATALAN	p3rson3	3
FRIULIAN	pErson	3
ITALIAN	persona	3
SPANISH	persona	3
VALENCIAN	persone	3
CORSICAN	nimu	4
DALMATIAN	om	5
EMILIANO_CARPIGIANO	om	5
ROMANIAN_2	om	5
TURIA_AROMANIAN	om	5
EMILIANO_FERRARESE	styan	6
LIGURIAN_STELLA	kristyaN	6
NEAPOLITAN_CALABRESE	kr3styan3	6
ROMAGNOL_RAVENNATE	sCan	6
ROMANSH_GRISHUN	k3rSTawn	6
ROMANSH_SURMIRAN	k3rstaN	6
GALICIAN	ome	7
GASCON	omi	7
PIEMONTESE_VERCELLESE	omaN	8
ROMANSH_VALLADER	uman	8
ALBANIAN_GHEG	5eri	9
SARDINIAN_CAMPIDANESE	omini	9
SARDINIAN_LOGUDARESE	omine	9

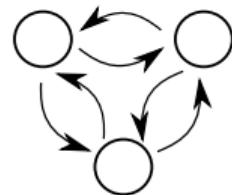
Cognate clustering

concept	doculect	glot_fam	transcription
eye	DORASQUE	Chibchan	oko
eye	NORTHERN_LOW_SAXON	Indo-European	ok
eye	NORTH_FRISIAN_AMRUM	Indo-European	uk
eye	STELLINGWERFS	Indo-European	ok
eye	ASSAMESE	Indo-European	soku
eye	CHAKMA_UnnamedInSource	Indo-European	sog
eye	DALMATIAN	Indo-European	vaklo
eye	FRIULIAN	Indo-European	voli
eye	ITALIAN	Indo-European	okkyo
eye	ITALIAN_GROSSETO_TUSCAN	Indo-European	okyo
eye	JUDEO_ESPAGNOL	Indo-European	oxo
eye	LATIN	Indo-European	okulus
eye	NEAPOLITAN_CALABRESE	Indo-European	woky3
eye	ROMANIAN_2	Indo-European	oky
eye	ROMANIAN_MEGLENO	Indo-European	wokLu
eye	SARDINIAN	Indo-European	ogu
eye	SARDINIAN_CAMPIDANESE	Indo-European	oxu
eye	SARDINIAN_LOGUDARESE	Indo-European	okru
eye	SICILIAN_UnnamedInSource	Indo-European	okiu
eye	SPANISH	Indo-European	oho
eye	TURIA_AROMANIAN	Indo-European	okLu
eye	VLACH	Indo-European	okllu
eye	BELARUSIAN	Indo-European	voka
eye	BOSNIAN	Indo-European	oko
eye	BULGARIAN	Indo-European	oko
eye	CROATIAN	Indo-European	oko
eye	CZECH	Indo-European	oko
eye	KASHUBIAN	Indo-European	wokwo
eye	LOWER_SORBIAN	Indo-European	voko
eye	LOWER_SORBIAN_2	Indo-European	woko
eye	MACEDONIAN	Indo-European	oko
eye	OLD_CHURCH_SLAVONIC	Indo-European	oko
eye	POLISH	Indo-European	oko
eye	SERBOCROATIAN	Indo-European	oko
eye	SLOVAK	Indo-European	oko
eye	SLOVENIAN	Indo-European	oko
eye	UKRAINIAN	Indo-European	oko
eye	UPPER_SORBIAN	Indo-European	voCko
eye	UPPER_SORBIAN	Indo-European	voko
eye	BAINOUK_GUNYAAMOLO	Atlantic-Congo	g3li
eye	USINO	Nuclear_Trans_New_Guinea	ogo

Phylogenetic inference

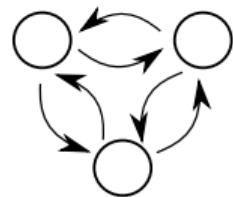
Modeling language change

Markov process



Modeling language change

Markov process

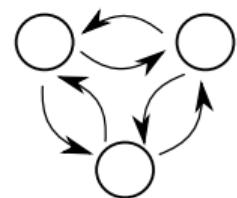


Phylogeny



Modeling language change

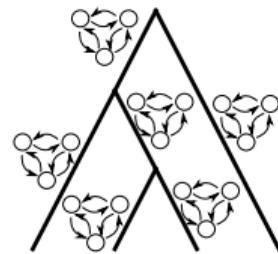
Markov process



Phylogeny

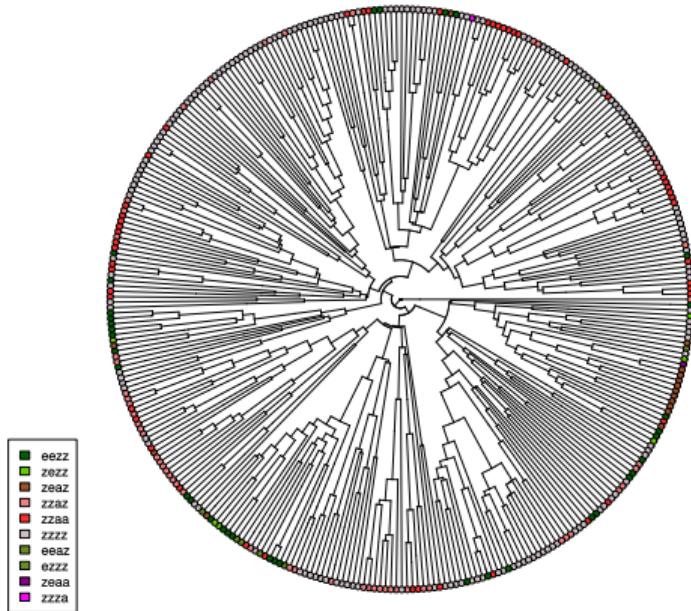


Branching process



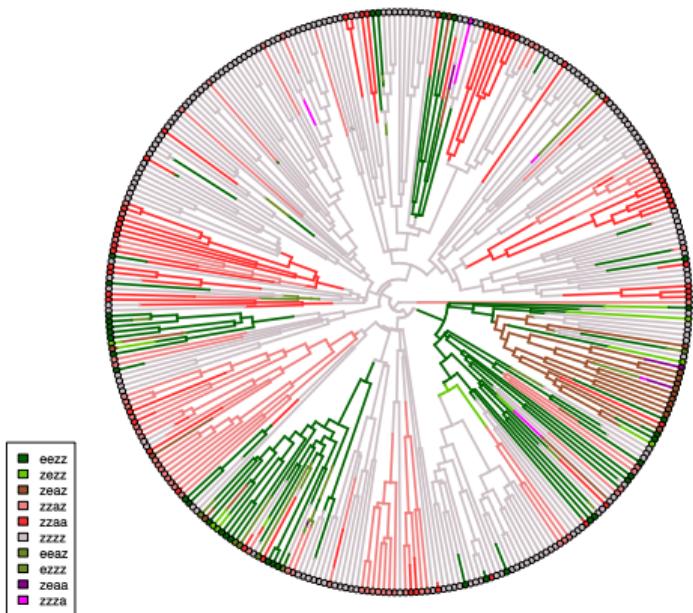
Estimating rates of change

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



Estimating rates of change

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



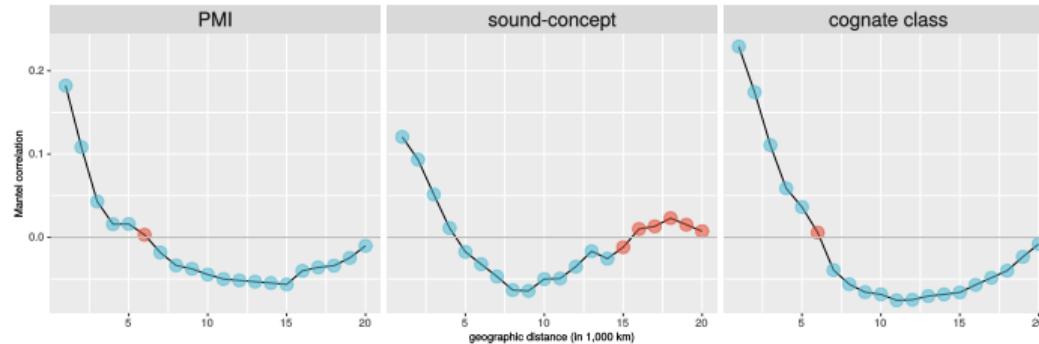
ASJP word lists → character matrix

1 Automatically inferred cognate classes

- each cluster cc defines one character
- doculect l has value 1 if its word list contains an element of cc , undefined if the slot of the corresponding concept is undefined, and 0 else

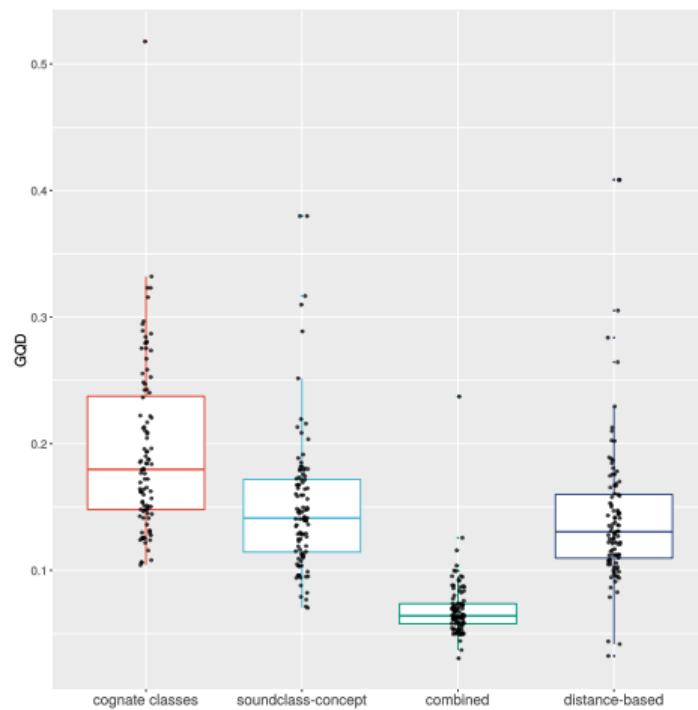
2 Soundclass-concept characters

- each combination (c, s) of an ASJP concept c and an ASJP sound class s is a character
- doculect l has value 1 if one of its entries for c contains s , 0 if not, and undefined if there is no entry for c



Character matrix → trees

- validation
 - correlation with geographic distance
 - phylogenetic inference (Maximum Likelihood) + comparison to Glottolog expert tree on 100 random sample of ASJP doculects, containing between 20 and 400 doculects
 - using Stamatakis' **RAXML** (which is great)
- partitioned character-based inference seems to work best



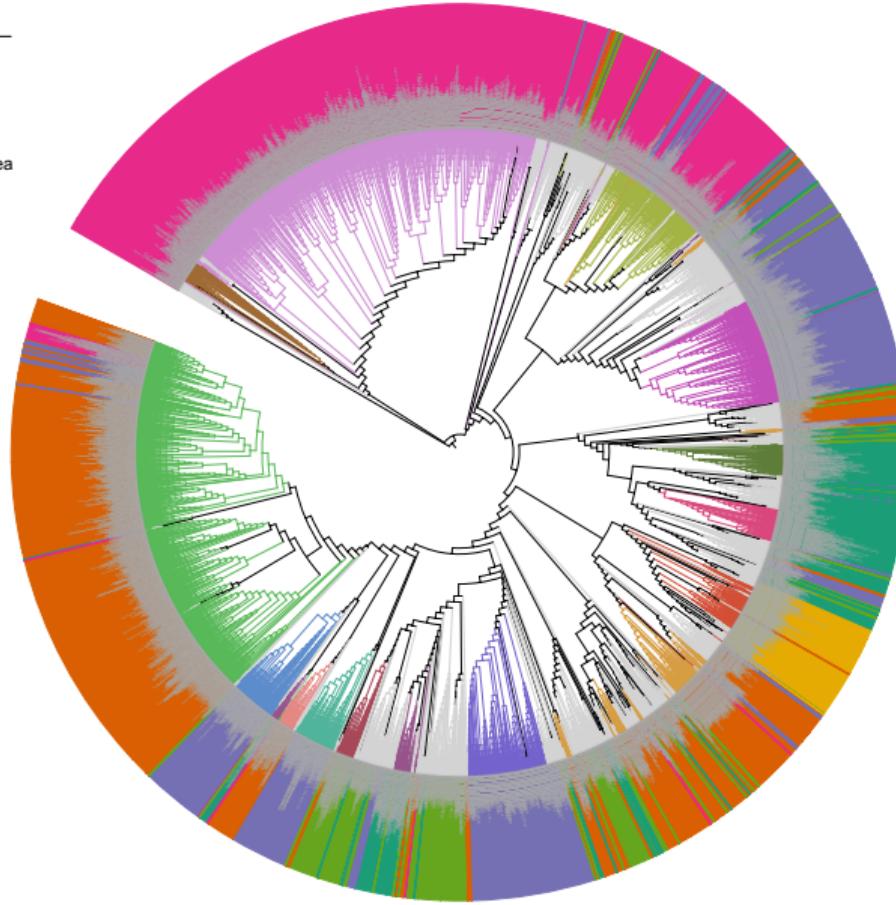
The world tree

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

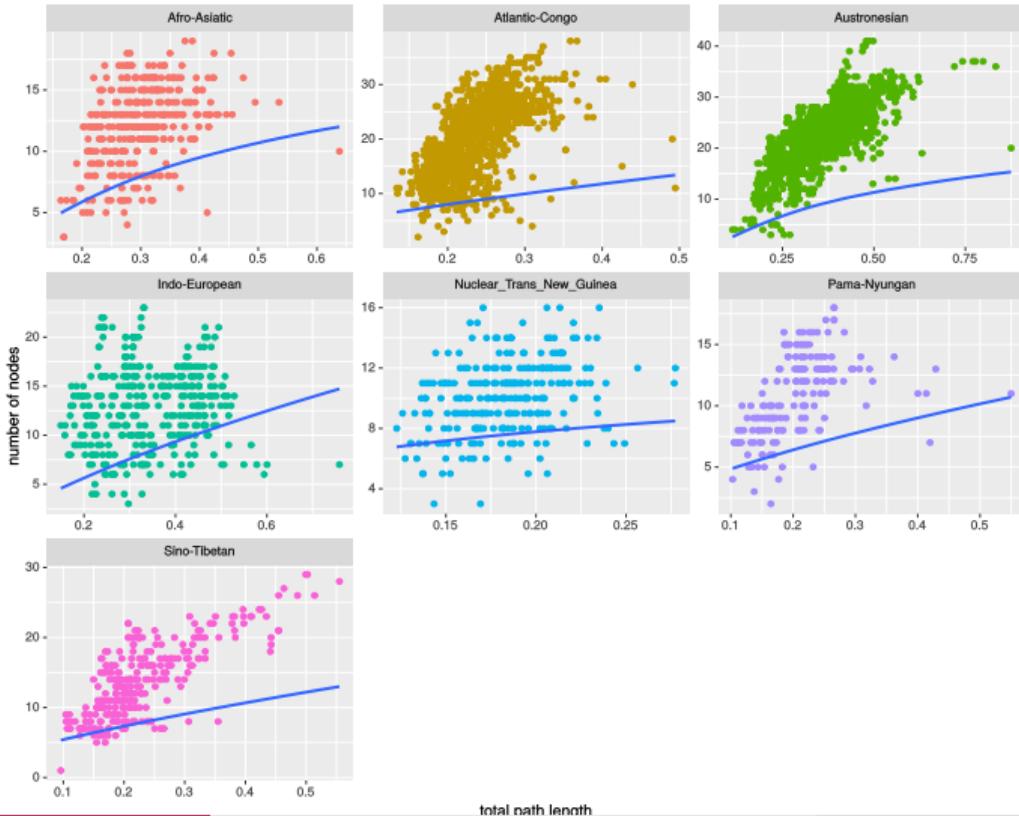
Macro-Area

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

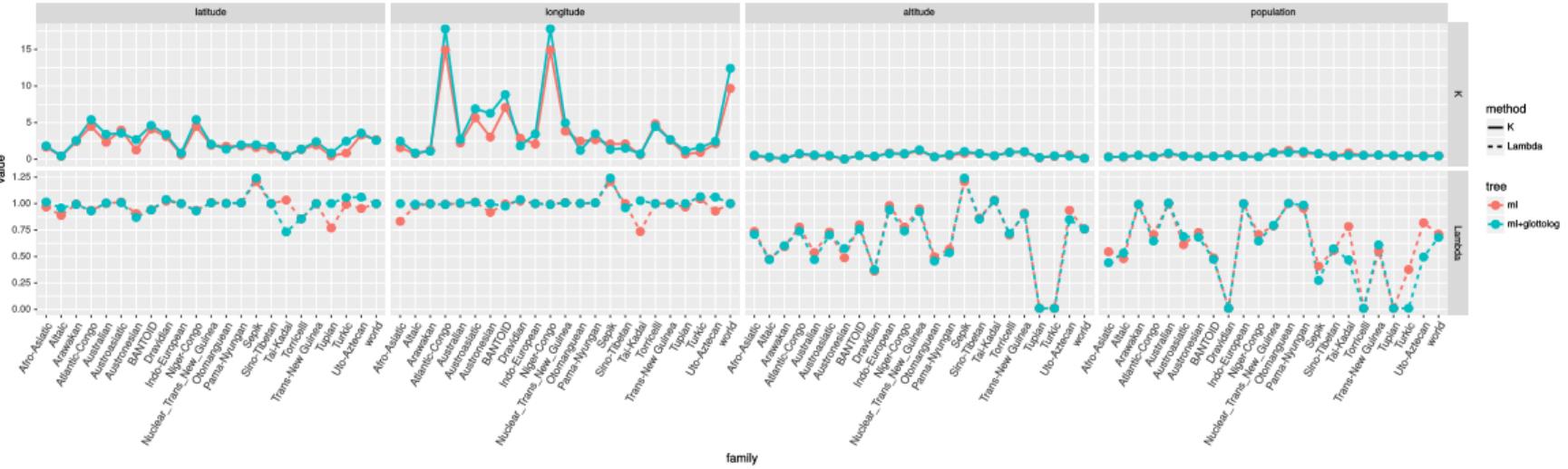


Applications

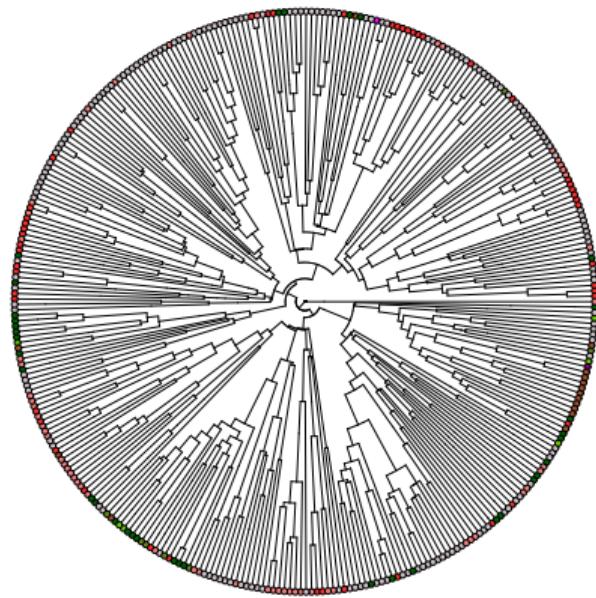
Punctuated language evolution



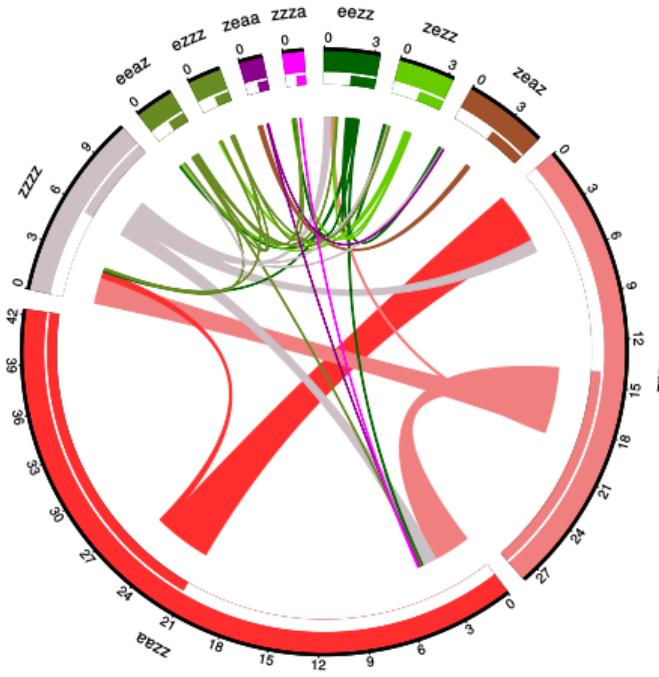
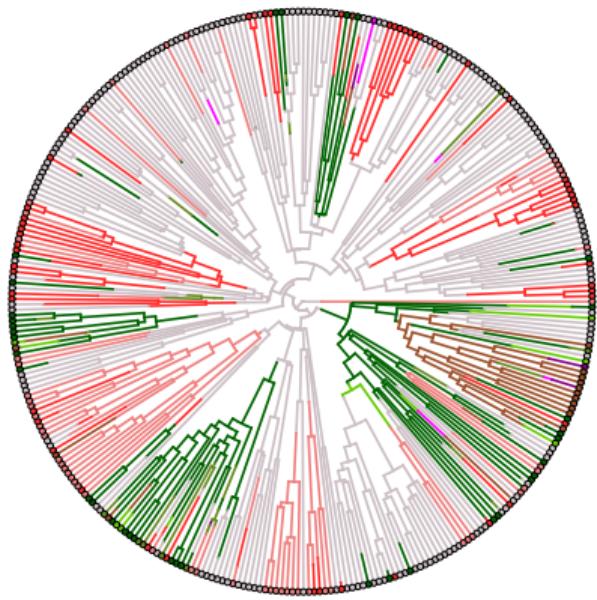
Phylogenetic signal



Estimating Markov processes

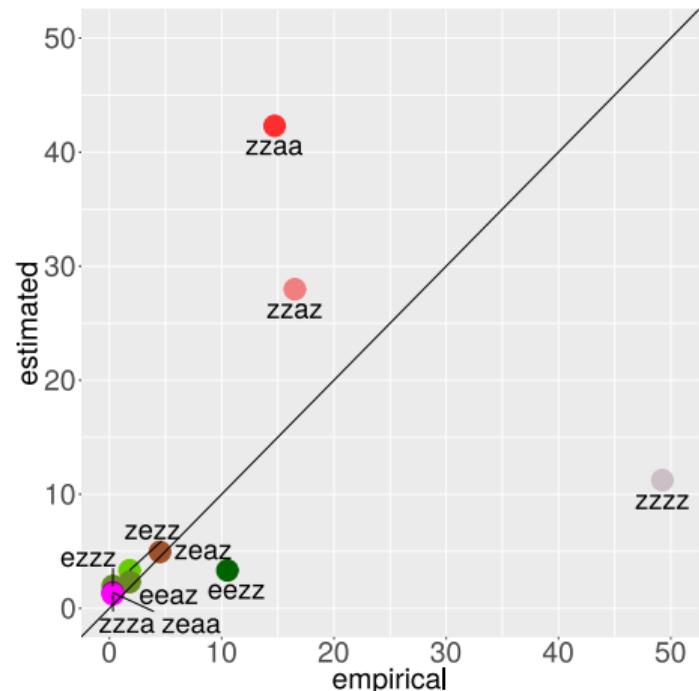


Estimating Markov processes

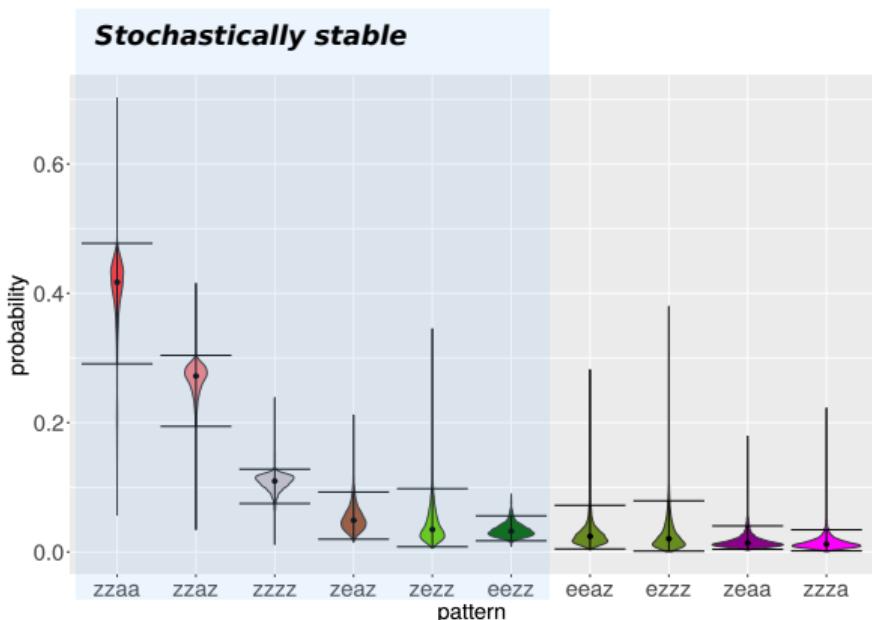


Equilibrium probabilities

Empirical vs. estimated percentages

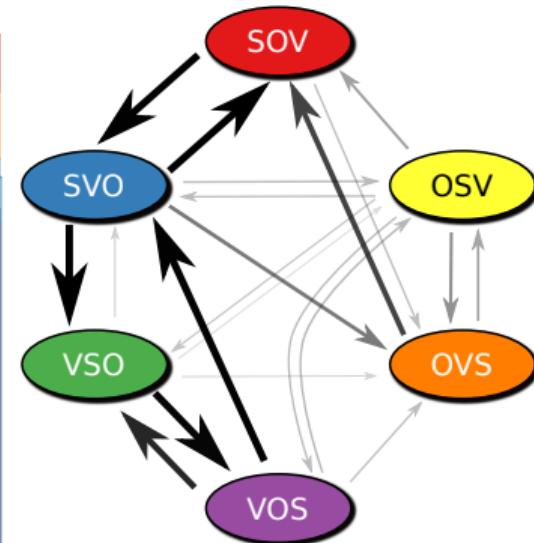
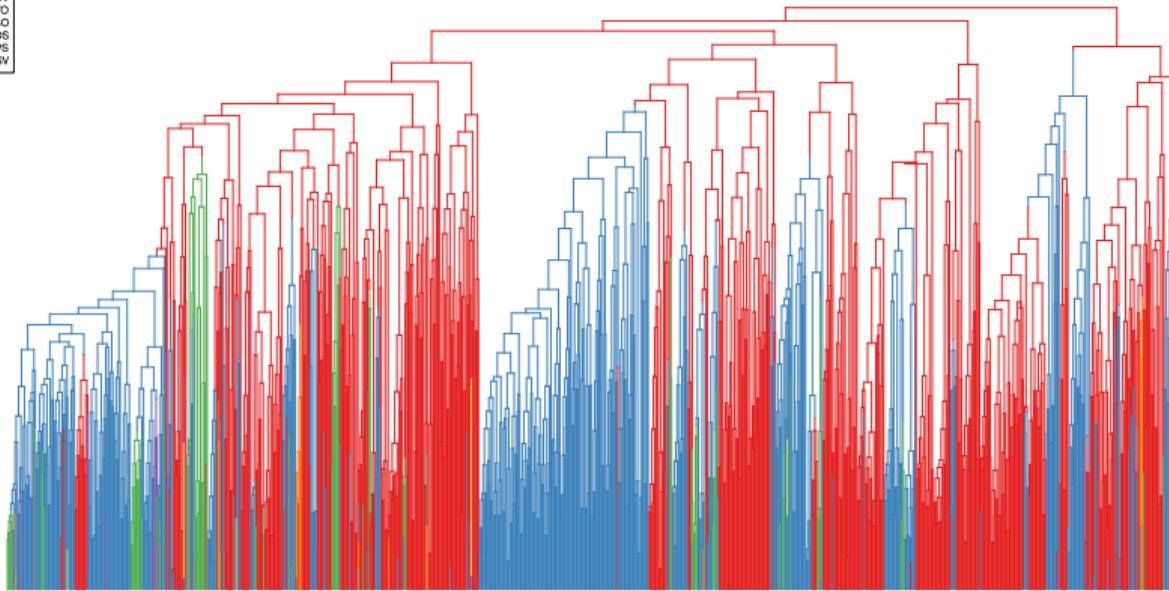


Posterior distribution

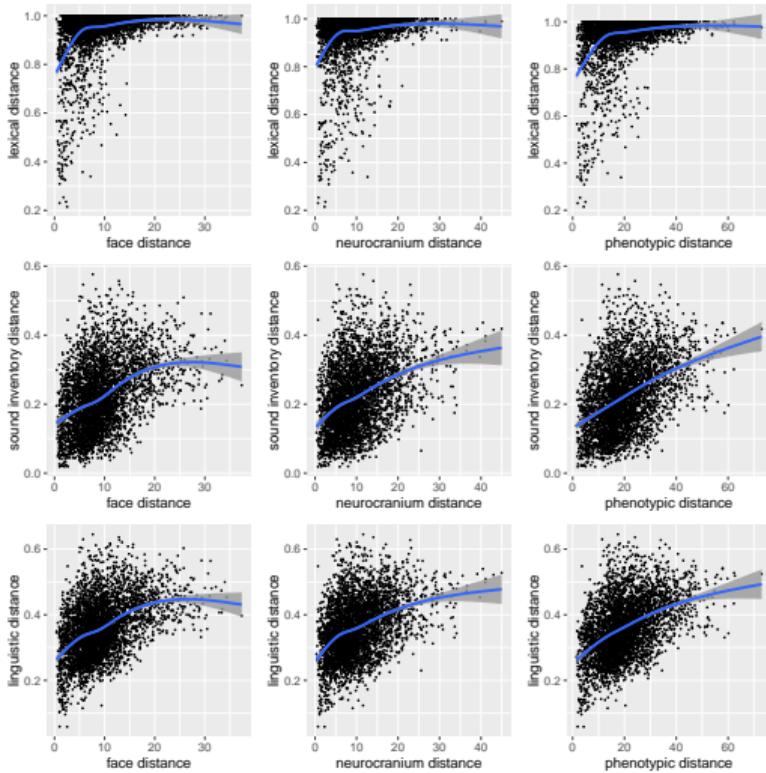


Clines of typological change

■ SOV
■ SVO
■ VSO
■ VOS
■ OVS
■ OSV



Correlation between linguistic and phenotypic distances



Conclusion

- two areas where this might be useful:
 - prehistory/anthropology: identifying deep patterns of common ancestry and contact
 - historical linguistics and typology: statistical model for phylogenetically controlled inference
- data and code are available on arXiv/OSF: Jäger (2018)

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