Further evidence for punctuated language evolution

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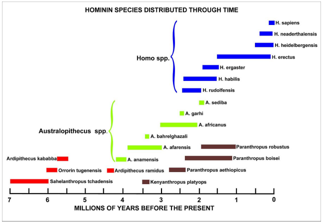
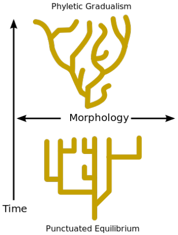
Punctuated equilibrium

Gould and Eldredge (1977):

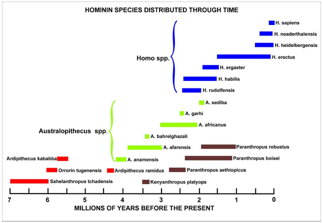
- surprising lack of **intermediate stages** in fossil record
- possible explanation:
    - evolutionary change occurs primarily during speciation phases
    - when a species is in equilibrium, it neither changes nor speciates

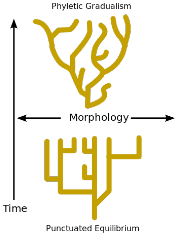




Punctuated equilibrium

- Possible causal mechanism
  - large population sizes *stabilizes* species
  - mutations, even beneficial ones, rarely reach fixation
  - speciation leads to small populations (bottlenecks) → accelerated evolution
- both the existence of the phenomenon and the causal explanation are still contentious in biology





Punctuated language evolution

- Dixon (1997):
  - same logic applies to language change as well
  - rapid tree-like diversification (as in history of IE languages) are the exception in human history
  - Australia prior to European conquest, with an equilibrium between diversification and contact — and hence no tree-like structure — are the rule
- rejected by most historical linguists, especially by experts on Australian languages

Quantitative approaches 1

- Pagel et al. (2006)
  - amount of evolutionary change is reflected in path lengths of phylogenetic tree (without molecular clock)
  - if punctuational hypothesis is true, there should be positive correlation between length of a path (tip to root) and number of nodes on that path
  - correlation is tested via phylogenetic regression (PGLS)

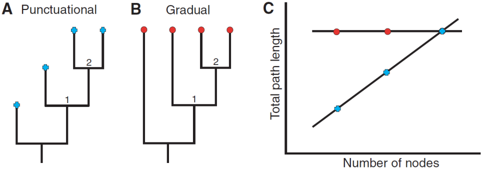
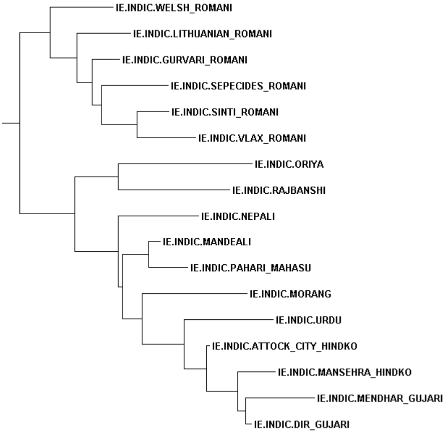


Fig. 1. Signatures of punctuational and gradual evolution on phylogenetic trees. (**A**) Punctuational evolution presumes a burst of evolution associated with each node of the tree. Path lengths, measured as the sum of branches along a path from the root to the tips of the tree, are proportional to the number of nodes along that path (C). Branches are assumed to be in units of nucleotide substitutions. (**B**) Gradual evolution presumes that change is independent of speciation events. Path lengths do not correlate with the number of nodes along a path (C). (**C**) Punctuational evolution predicts a positive relationship between path length and the number of nodes, whereas gradual evolution does not.

Quantitative approaches 1

Typical shape of a tree instantiating punctual evolution



Quantitative approaches 1

- Atkinson et al. (2008):
  - apply this logic to Bayesian trees, based on manual cognacy data, from Austronesian, Bantu, Indo-European and Polynesian

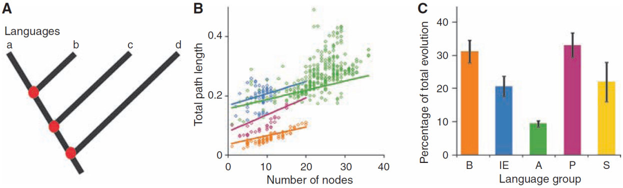


Fig. 1. Inferring punctuational language evolution. (**A**) Tree of four languages. If language-splitting events (red nodes) cause bursts of change, the paths from the root to a and b should be longest, followed by c then d (*8*); here, they are all equal. (**B**) Root-to-tip path length plotted against number of nodes along each path for punctuational trees in Bantu (orange), Indo-European (blue), Austronesian (green), and Polynesian (purple). Fitted lines show the relationship between path length and nodes after controlling for phylogeny (*8*). A positive slope is indicative of punctuational evolution. Path lengths for each data set were scaled to account for the number of characters examined. (**C**) Histogram showing the percentage of lexical evolution attributable to punctuational bursts at language-splitting events (mean ± SD) for Bantu (B, orange), Indo-European (IE, blue), Austronesian (A, green), and Polynesian (P, purple) (*8*). For comparison, the percentage of molecular evolution attributable to punctuational effects in biological species is also shown (S, yellow) (*4*).

Desiderata

- Results only for small number of large and well-studied language families
- Based on manual cognate judgments → possible source of implicit bias
- Addressed in Holman and Wichmann (2016) using a different technical approach
- Next part of this talk:
    - Use Atkinson et al.'s method
    - Applied to phylogenies from 6,000+ ASJP doculects,
    - using automatically obtained characters for phylogenetic inference

The Automated Similarity Judgment Program

- Collaborative data collection project around Cecil Brown, Eric Holman, Søren Wichmann and others
- covers more about 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

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

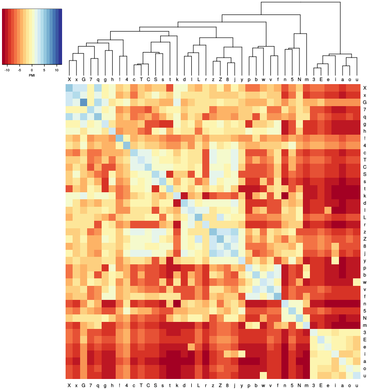
concept	Latin	English
nose	nasus	nos
tooth	dens	tu8
tongue	liNgw∼E	t3N
knee	genu	ni
hand	manus	hEnd
breast	pektus, mama	brest
liver	yekur	liv3r
drink	bibere	drink
see	widere	si
hear	audire	hir
die	mori	dEi
come	wenire	k3m
sun	sol	s3n
star	stela	star
water	akw∼a	wat3r
stone	lapis	ston
fire	iNnis	fEir

PMI string similarity

- *Pointwise Mutual Information* (PMI) between two sound classes a and b:

$$\mathrm{PMI}(a,b) \doteq \log \frac{P(a,b \text{ are homologous})}{P(a)P(b)}$$

- automatically trained from ASJP data (Jäger, 2013)
- PMI similarity between two strings: aggregate PMI score for optimal pairwise alignment of those strings



Calibrated PMI similarity

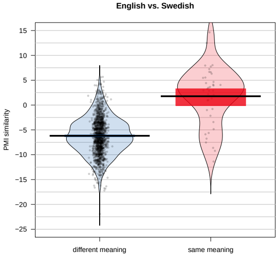
English / Swedish

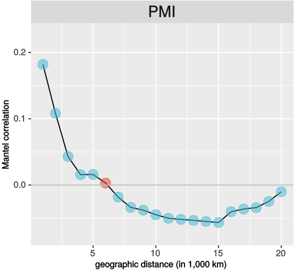
	Ei	**yu**	**wi**	**w3n**	**tu**	**fiS**	...
yog	**−7.77**	0.75	−7.68	−7.90	−8.57	−10.50	
du	−7.62	**0.33**	−5.71	−7.41	2.66	−8.57	
vi	−2.72	−2.83	**4.04**	−1.34	−6.45	0.70	
et	−5.47	−7.87	−5.47	**−6.43**	−1.83	−4.70	
tvo	−7.91	−4.27	−3.64	−4.57	**0.39**	−6.98	
fisk	−7.45	−11.2	−3.07	−9.97	−8.66	**7.58**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

- 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**: $-\log($probability that random word pairs are more similar than $s)$
- **language similarity:** average word similarity for all concepts





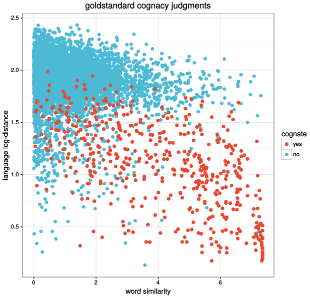
Cognate clustering

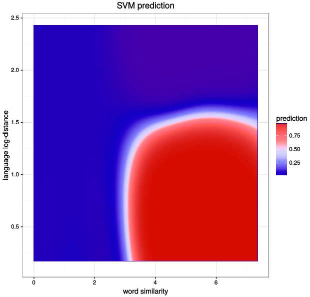
- clustering of ASJP strings into *automatically inferred cognate classes* (Jäger and Sofroniev, 2016; Jäger et al., 2017) (take “cognate” with a grain of salt)
- supervised learning, based on expert cognacy judgments as goldstandard
- sources (only the 40 ASJP concepts were used)

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	Běijīng 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	Zhivlov (2011)	769	39	21	Uralic	68
total		10,106	40	318	13	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



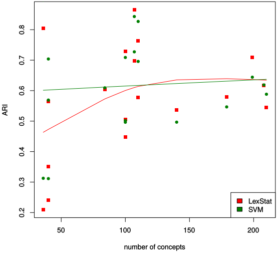


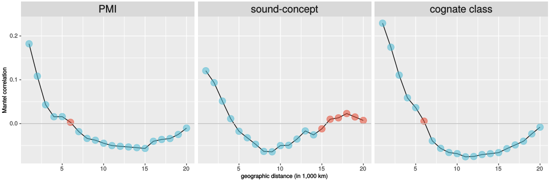
Cognate clustering

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	okklu
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

ASJP word lists → character matrix

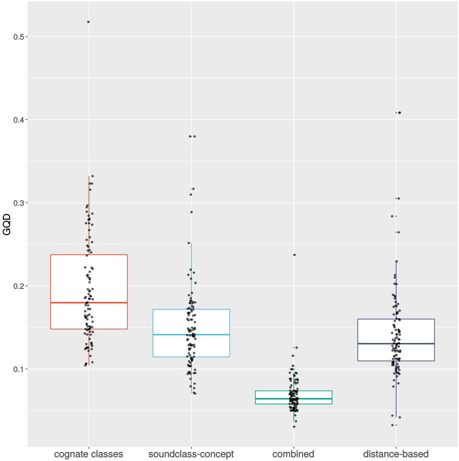
1. **Automatically inferred cognate classes**
   - each cluster cc defines one character
   - doculect l has value 1 if its word list contains an element of cc, undefined if the slot of the corresponding concept is undefined, and 0 else
2. **Soundclass-concept characters**
   - each combination (c, s) 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





ASJP word lists → character matrix

- 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
- partitioned character-based inference seems to work best



The node density artifact

- character-based phylogenetic inference tends to under-estimate branch lengths (measured in expected number of mutations) (Webster et al., 2003; Venditti et al., 2006)
- intuitive reason:
  - multiple changes of the same character remain undetected
- effect is stronger on long than on short branches
- leads to spurious correlation between estimated root-to-tip distance and number of intervening nodes
- most pronounced for Maximum Parsimony, but Bayesian and Maximum-Likelihood inference also affected

Detecting the node density artifact

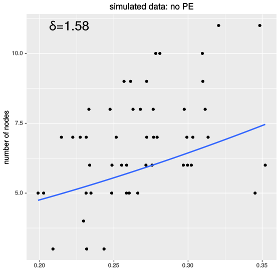
Webster et al. (2003); Venditti et al. (2006):

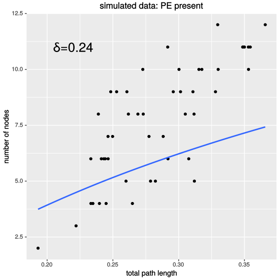
- if the relationship is due to the node density artifact, it has a characteristic curved tendency
- model:

$$\begin{aligned} y &= a + bx^{\delta} + \epsilon \\ x &: \text{total path length} \\ y &: \text{number of nodes} \end{aligned}$$

- a, b, δ fitted via phylogenetic generalized least square
- if $b > 0$ and $\delta > 1$, the correlation is due to the node density artifact

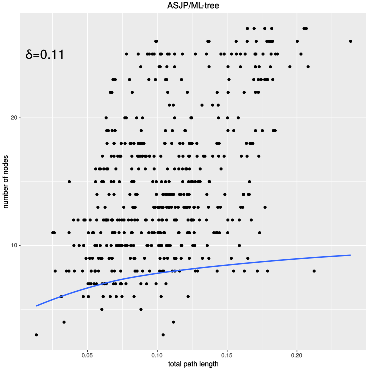
(simulated data: courtesy of Søren Wichmann)





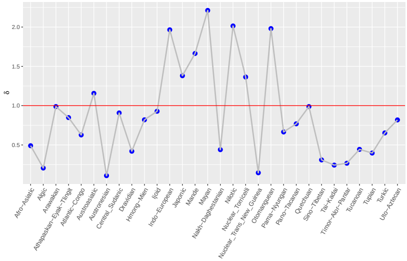
Application to ASJP data

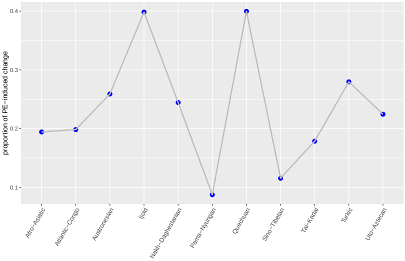
- 500 randomly selected doculects from ASJP
- Maximum-Likelihood tree/partitioned analysis (cognate-class and sound-concept characters)
- Glottolog expert tree as constraint tree
- results:
  - $\delta = 0.11 \rightarrow$ no node density effect
  - $b > 0$: $p = 1.4 \times 10^{-9}$
  - 20.4% of all change due to punctuation



Family-wise analysis

- separate model for each Glottolog family with ≥ 30 doculects in ASJP
- 30 families in total
- if there are more than 500 doculects, 500 doculects randomly selected
- ML tree with Glottolog expert tree constraints
- $\delta < 1$ for 22 families
- significant $b > 1$ ($\alpha = 0.05$, corrected for multiple testing via Holm-Bonferroni method): 11 families

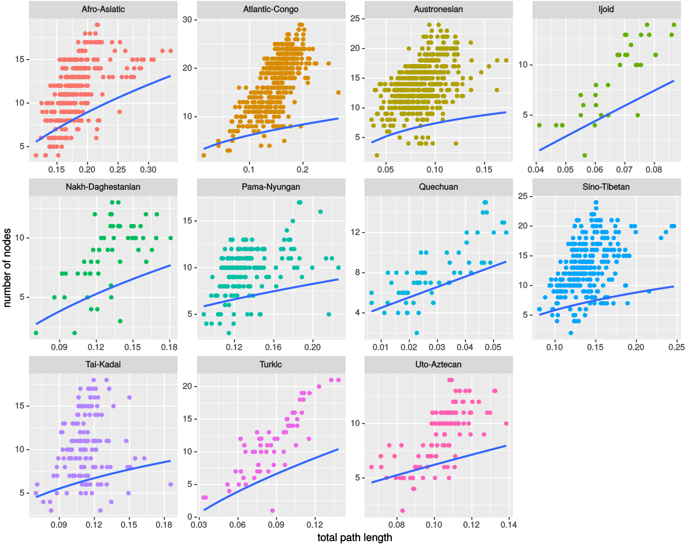




Family-wise analysis

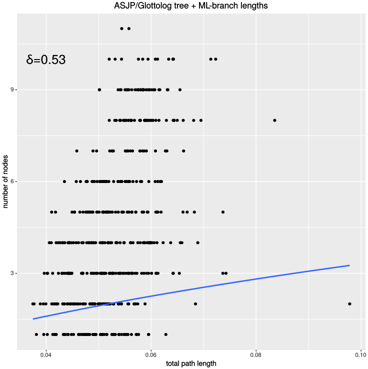
	δ	b	p	percentage
Austronesian	0.11	0.0034	0.0	25.9
Afro-Asiatic	0.49	0.0042	1.1-14	19.4
Atlantic-Congo	0.63	0.0035	9.1-12	19.8
Sino-Tibetan	0.31	0.0024	2.0-06	11.6
Ijoid	0.93	0.0029	1.5-05	39.8
Turkic	0.65	0.0031	1.7-05	28.0
Uto-Aztecan	0.82	0.0027	1.3-04	22.4
Tai-Kadai	0.24	0.0025	2.1-04	17.9
Nakh-Daghestanian	0.44	0.0048	2.3-04	24.4
Quechuan	0.99	0.0018	4.9-04	40.0
Pama-Nyungan	0.67	0.0023	2.9-03	8.7
Nuclear_Trans_New_Guinea	0.15	0.0019	1.7-02	7.0
Central_Sudanic	0.91	0.0041	1.7-02	22.6
Timor-Alor-Pantar	0.27	0.0030	4.9-02	17.7
Arawakan	0.99	0.0016	7.9-02	6.7
Athapaskan-Eyak-Tlingit	0.85	0.0042	1.1-01	18.9
Dravidian	0.42	0.0025	1.1-01	15.2
Hmong-Mien	0.82	0.0030	1.4-01	17.4
Tupian	0.40	0.0010	2.5-01	4.9
Pano-Tacanan	0.77	0.0011	5.2-01	5.5
Tucanoan	0.44	0.0003	9.1-01	2.1
Algic	0.21	-0.0001	9.7-01	-0.3
Indo-European	1.97	0.0017	3.8-12	12.7
Mayan	2.21	0.0024	5.2-08	28.8
Otomanguean	1.98	0.0042	2.7-05	20.2
Nilotic	2.01	0.0032	3.0-04	20.6
Austroasiatic	1.16	0.0018	4.5-04	10.7
Japonic	1.38	0.0050	3.2-03	47.6
Mande	1.66	0.0019	1.8-02	12.0
Nuclear_Torricelli	1.36	0.0020	8.7-02	7.8

Family-wise analysis



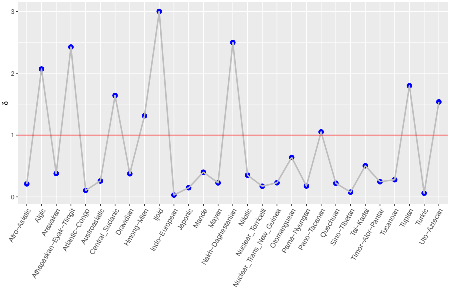
Polytomies

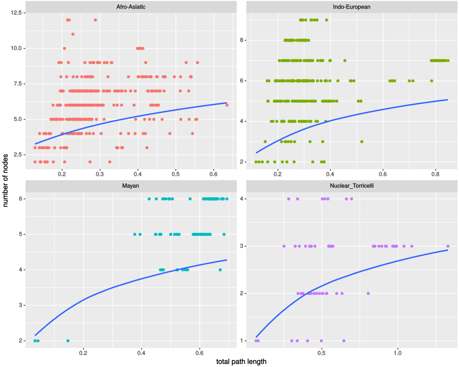
- phylogenetic inference always produces binary-branching trees
- language diversification possibly involve genuine polytomies → ML-tree might overestimate number of nodes
- second test:
  - use topology of Glottolog expert tree
  - ML-optimization of branch lengths
- $\delta = 0.53 \rightarrow$ no node density effect
- $b > 0$: $p = 3 \times 10^{-5}$



Polytomies — family-wise

- $\delta < 1$ for 20 families
- significant $b > 0$ only for four families





Polytomies — family-wise

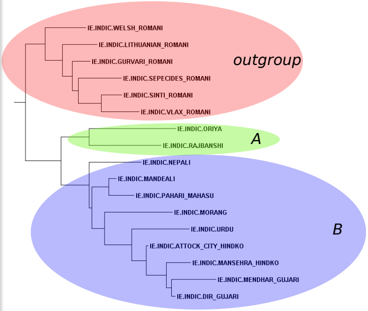
	δ	b	p
Afro-Asiatic	0.21	0.0108	5.7-07
Indo-European	0.03	0.0134	8.8-06
Mayan	0.23	0.0560	1.4-05
Nuclear_Torricelli	0.17	0.1100	1.9-04
Tai-Kadai	0.50	0.0144	3.3-03
Atlantic-Congo	0.11	0.0036	7.6-03
Pama-Nyungan	0.18	0.0016	2.1-02
Nuclear_Trans_New_Guinea	0.23	0.0036	2.8-02
Austroasiatic	0.26	0.0097	4.4-02
Sino-Tibetan	0.08	0.0047	6.2-02
Quechuan	0.22	0.0243	1.4-01
Japonic	0.15	0.0339	1.7-01
Arawakan	0.38	0.0111	2.9-01
Otomanguean	0.64	0.0066	3.1-01
Turkic	0.06	0.0098	3.4-01
Tucanoan	0.28	-0.0235	4.1-01
Nilotic	0.35	0.0072	5.9-01
Dravidian	0.37	0.0056	6.7-01
Mande	0.40	0.0015	6.7-01
Timor-Alor-Pantar	0.25	0.0591	7.9-01
Nakh-Daghestanian	2.50	0.1239	4.4-05
Uto-Aztecan	1.54	0.0149	3.8-03
Athapaskan-Eyak-Tlingit	2.42	-0.0406	1.2-02
Central_Sudanic	1.64	0.0295	2.2-02
Hmong-Mien	1.31	0.0602	8.6-02
Tupian	1.80	-0.0045	1.2-01
Pano-Tacanan	1.05	0.0474	1.3-01
Algic	2.07	-0.0079	1.8-01
Ijoid	3.00	0.2448	3.3-01

Quantative approaches 2

- Holman and Wichmann (2016):
  - alternative, non-parametric approach
  - various data sources (cognacy data, ASJP/LDND)

basic idea (cf. graphics to the right)

- B is larger than A
- therefore members of B underwent, on average, more diversification events than members of A
- A and B have same distance (in years) from members of outgroup
- if punctuational hypothesis is true, average distance in amount of change between A and outgroup should be smaller than between B and outgroup

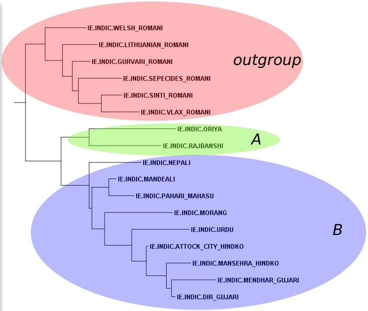


Quantative approaches 2

- Holman and Wichmann (2016):
  - alternative, non-parametric approach
  - various data sources (cognacy data, ASJP/LDND)

basic idea (cf. graphics to the right)

- if d(A,outgroup)<d(B,outgroup), this triplet is counted as evidence for puncuation, and vice versa
- Null hypothesis (no punctuational change): probability of a triplet to be evidence for punctuation is 50%
- tested on maximal collection of *independent usable triplets* in a given phylogeny



Independent usable triplets

- a triplet is a local subtree of the shape *((A,B),outgroup)*
- a triplet is *usable* if A and B contain an unequal number of tips
- a group of *independent usable triplets* is a group of usable triplets where no element is contained in another element

Independent usable triplets

Algorithm for maximal collectio of independent usable triplets

- the *ratio* of a branching node is the size of its largest daughter, divided by the size of its smallest daughter
- traverse through the tree tip-to-root
- let N the the current node and $C(N)$ be N's *candidate set*
- If N is a tip, $C(N) = \emptyset$, else
- $CC(N) \doteq \bigcup\{C(N')|N'$ is a daughter of $N\}$
- If N's ratio > 1 and
  - $CC(N) = \emptyset$ or
  - $CC(N) = \{x\}$ and N's ratio $>$ x's ratio:
- $C(N) = \{N\}$, else
- $C(N) = CC(N)$
- $C(\mathrm{root})$ is the maximal collection of independent usable triplets

Results

- Holman and Wichmann (2016): significant evidence for punctional evolution if amount of change is operationalized as
  - path lengths in an automatically inferred phylogeny
  - difference in cognate class inventory
- no significant effect for LDND

My results

- “average distance” defined as **median** distance
- PMI-distance and Levenshtein-derived distances
- 5,522 ASJP17-doculects (no ancient, pidgins, creoles, artificial and reconstructed languages)
- Glottolog and ML-inferred topology
- binomial test

Topology	Distance	positive triplets	total triplets	proportion	p-value
Glottolog	PMI	284	512	0.55	$0.007**$
Glottolog	LDPV	273	512	0.53	0.072
ML	PMI	513	960	0.53	$0.018*$
ML	LDPV	516	960	0.54	$0.011**$

- not a single individual family give significant evidence for PE (if we control for multiple testing)

Conclusion

- automatically extracted characters give similar results to manually collected ones
- further evidence for punctuated language evolution across the world
- open questions:
  - How much of the effect is due to node denisity artifact?
  - What impact have incomplete lineage sorting, borrowing, hard polytomies on branch length estimation?
  - Is punctuated evolution confined to lexical change?

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