Algorithmic generation of random languages argues for syntax as a source of phylogenetic information

Giuseppe Longobardi**, Andrea Ceolin*, Aaron Ecay*, Cristina Guardiano°, Monica Alexandrina Irimia*, Nina Radkevich*, Dimitris Michelioudakis*, Luca Bortolussi*, Andrea Sgarro*

*University of York

°Università di Modena e Reggio Emilia

^Università di Trieste

Language comparison and phylogenetic reconstruction:

- 1) Correspondence problem
- 2) Metric problem
- 3) Probability problem

but in particular...

Language comparison and phylogenetic reconstruction:

4) Globality problem



The classical comparative method and modern lexical/morphophonological methods have addressed problems 1-3 (with some difficulties):

- Correspondence problem: Swadesh-list "meaning" comparison (e.g. Dyen et al. 1992), "root" comparison (e.g. Gray and Atkinson 2003)
- 2) Metric problem: "distances" (e.g. Dyen et al. 1992), "characters" (e.g. Ringe et. al 2002)
- 3) Probability problem (e.g. Ringe 1992, Nichols 1996)

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No solution has been found for the **Globality problem**.

Reason: Lexical and morphological characters are not comparable across established families (e.g. all etymological unrelated characters, all maximum distances).

Solution: Exploring different domains, e.g. Syntax (Guardiano and Longobardi 2005, Longobardi and Guardiano 2009)



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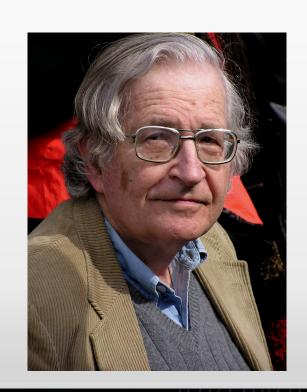
Evidence for syntax as a signal of historical relatedness

Giuseppe Longobardi a,*, Cristina Guardiano b

^aLaboratorio di Linguistica e antropologia cognitiva, DSA, Università di Trieste, Italy
 ^bDipartimento di Scienze del Linguaggio e della Cultura, Università di Modena e Reggio Emilia, Italy
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Problems 1,2 and 4 are solved through the notion of "syntactic parameter" (Chomsky 1981, Baker 2001).

Parameters are species-invariant, ultimately biological, options: the same open choices are presupposed by every language (i.e. by every infant) and environmentally set during the acquisition



• The description of parameters as universals might seem to imply that large amounts of irrelevant information must be encoded by language learners (Berwick & Chomsky 2011, Boeckx 2011)

• However, it is possible to reformulate this description in terms of a Principles&Schemata approach (Longobardi 2014), where there **are** only a small number or parameter schemata preset at S_0 , which learners instantiate as needed, eventually reaching a set of fixed parameters at S_s

- 1) Correspondence problem: parameters are unambiguous
- 2) Metric problem: parameters are discrete (binary values)
- 4) Globality problem: parameters are universal

3) Probability problem



Parametric Comparison Method (PCM) (Guardiano and Longobardi 2005, Longobardi and Guardiano 2009)

Languages are encoded as lists of binary parameters (+,-).

Parametric Comparison Method (PCM) (Guardiano and Longobardi 2005, Longobardi and Guardiano 2009)

Problem: parameters are not **independent**, but there are **implications** which make some parameter values predictable.

Grammaticalized definiteness and enclitic articles

	English	Norwegian	Russian
p10: gramm. Def. (articles)	+	+	-
p14: enclitic articles (+p10)	-	+	?

Grammaticalized definiteness and enclitic articles

	English	Norwegian	Russian
p10: gramm. Def. (articles)	+	+	-
p14: enclitic articles (+p10)	-	+	0

Sample parameters:

65 syntactic parameters from the Nominal Domain (DPs)

Sample languages:

- 21 IE languages (5 Romance, 5 Germanic, 5 Slavic, 3 Indo-Iranian, 2 Celtic, 1 Greek)
- 3 Finno-Ugric languages (Finnish, Estonian, Hungarian)
- 2 Altaic languages (Turkish, Buryat)
- 2 Semitic languages (Semitic, Arabic)
- 2 Basque varieties
- 2 Chinese (Mandarin, Cantonese)
- 1 Wolof

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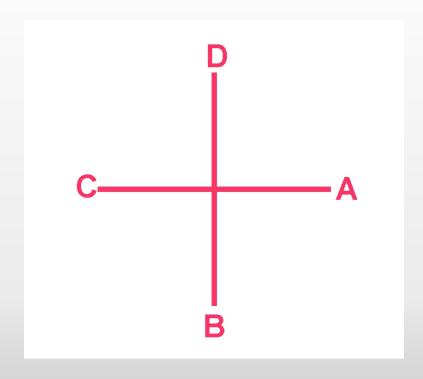
Coding the data: Characters or Distances?

Reasons why character-based approaches are problematic for syntactic comparison:

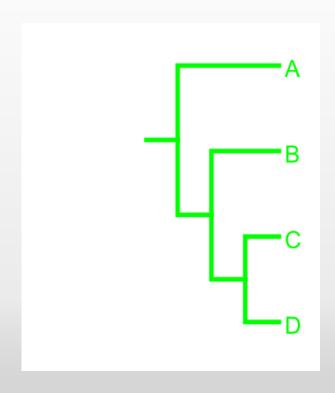
- 1) Homoplasy and borrowing are possible
- 2) Lack of information about directionality of change
- 3) Shared innovations are not always detectable (e.g. implicated values, low number of parameters)

Consider the following example:

PAUP*



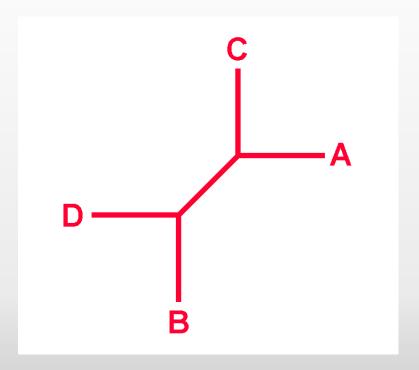
KITSCH or UPGMA

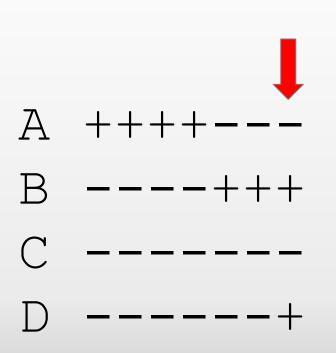


Now consider the following example:

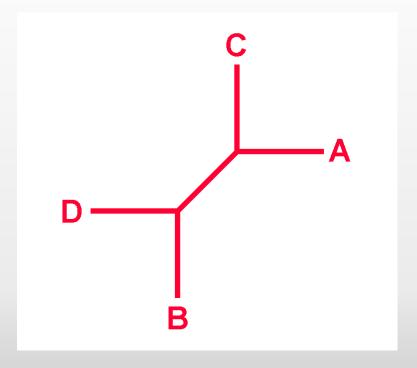
(borrowing, parallel development, resetting, etc. etc.)

PAUP*

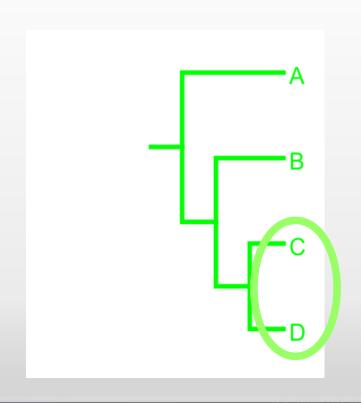




PAUP*

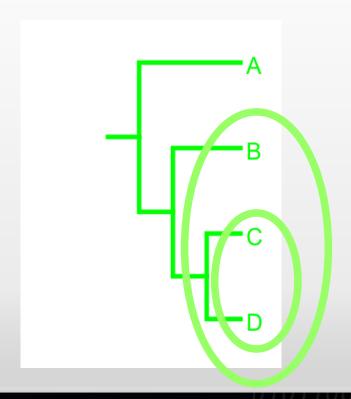


KITSCH or UPGMA



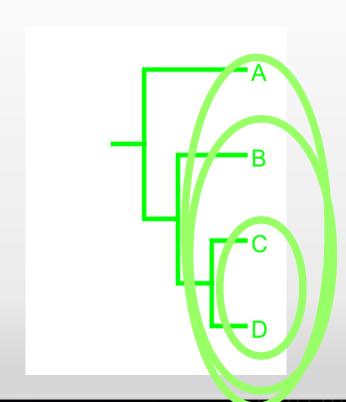
A +++--B ---+++ C ----D ---+

KITSCH or UPGMA



A +++--B ---++ C ----D ---+

KITSCH or UPGMA



Coding the data: Characters or Distances?

Reasons why distances-based programs are better for syntactic comparison:

- 1) More resistant to single borrowing/parallel development effects
- 2) No need of notions like directionality of change/ancestral values/outgroups (when using the molecular clock hypothesis)
- 3) They take into account also parsimony uninformative values (and thus **shared retentions**, like in lexicostatistics)

How to choose a distance measure?

Since we have a lot of '0' values, we cannot rely on a simple Hamming distance.

We can use a **Jaccard-Tanimoto distance** between "comparable" values:

$$\delta(A,B) = d(A,B) / [d(A,B) + i(A,B)]$$

= differences / identities + differences

E.g.: Italian-English: (35 id., 6 diff.) $\delta = 6 / 41 = 0.146$

Are these distances **significant** from a statistical viewpoint?

Comparison of "real" distances versus "randomly generated" distances (Bortolussi et al. 2011).

Bortolussi et al. (2011): Sampling over a uniform distribution of languages

Bortolussi et al. (2011)	L1	L2	L3	L4	Probability of P_= +
P1	+	+	+	-	0.75
P2 (only if +P1)	+	+	-	0	0.67
P3 (only if +P2)	+	_	0	0	0.5
Probability of L_=+	0.25	0.25	0.25	0.25	

Problem: since the sample is made of mostly IE languages, this kind of sampling generates IE-like languages.

A new sampling algorithm: assumption of a uniform distribution of parameters

Our algorithm	L1	L2	L3	L4	Probability of P_= +
P1	+	+	+	- /	0.5
P2 (only if +P1)	+	+	-	0	0.5
P3 (only if +P2)	+	-	0	0	0.5
Probability of L_=+	0.125	0.25	0.25	0.5	

Independent parameters are first assigned a value by chance. Following parameters are checked for implications.

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Pseudo code:

```
given [P1, P2(if and only if +P1), P3....]
set P1 (either + or -, 0.5 chance)
check the implications of P2
if P2 can be set,
set P2 (either + or -, 0.5 chance)
else,
assign 0 to P2 and move to P3
check the implications of P3
if P3 can be set....
...
return the string generated
```

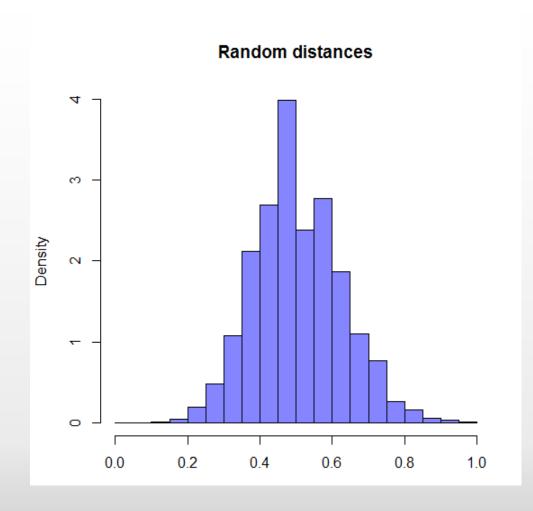
Random sample

1000 random languages

~500.000 random pairs

Mean: 0.510

Median: 0.5



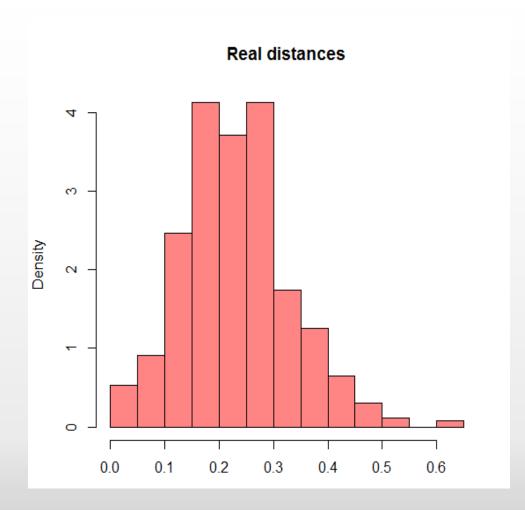
Real sample

33 real languages

528 real pairs

Mean: 0.234

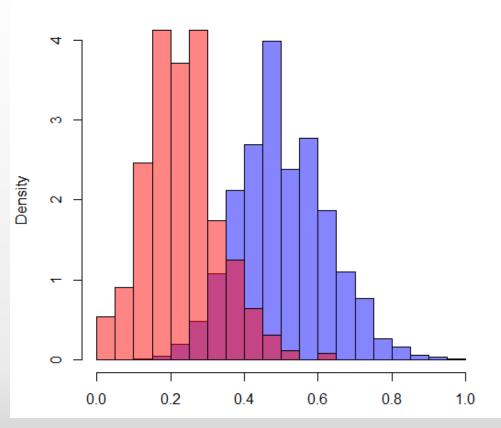
Median: 0.226



Mann-Whitney U test = p<2.2*e⁻¹⁶

The two datasets are unlikely to be drawn from the same distribution

Real vs Random distances

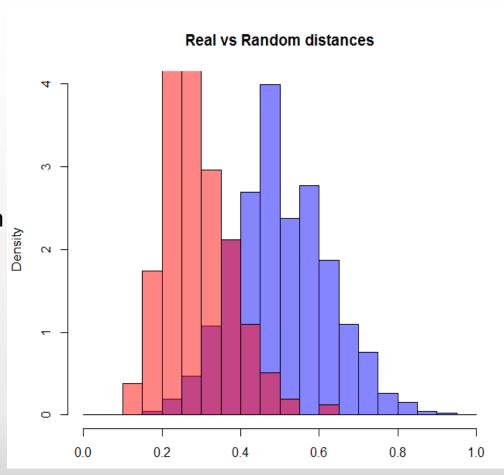


Family-external pairs only

Mann-Whitney U test = p<2.2*e⁻¹⁶

The two datasets are unlikely to be drawn from the same distribution

(Anti-Babelic principle, Guardiano and Longobardi 2005)



Possible explanation?

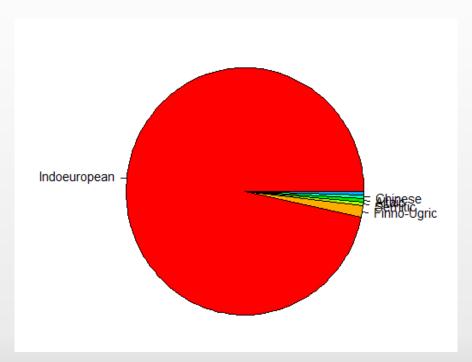
Chance threshold	Distance value	Pairs expected by chance	Pairs under the threshold
P=10 ⁻⁴	0.111	0.05	42
P=10 ⁻³	0.174	0.528	146
P=10 ⁻²	0.250	5.28	310

Possible explanation?

Chance threshold	Distance value	Pairs expected by chance	Pairs under the threshold
P=10 ⁻⁴	0.111	0.05	42
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P=10 ⁻²	0.250	5.28	310

History as the driving force?

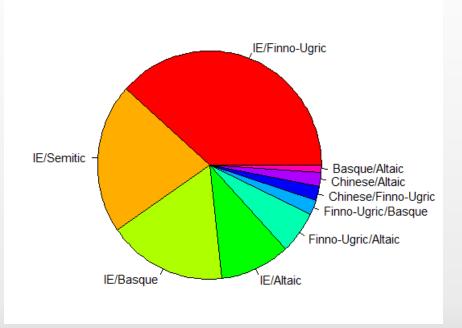
Family-internal pairs (211)



	Under threshold	Total	Percentage
Indoeuropean	204	210	97.14%
Finno-Ugric	3	3	100.00%
Semitic	1	1	100.00%
Basque	1	1	100.00%
Altaic	1	1	100.00%
Chinese	1	1	100.00%

History as the driving force?

Family-external pairs (99)

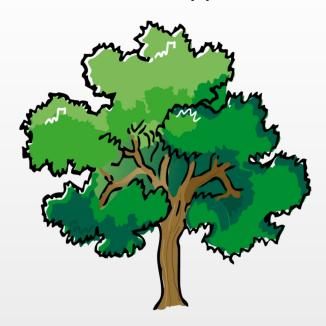


	Under threshold	Total	Percentage
Finno-Ugric/Altaic	6	6	100.00%
IE/Finno-Ugric	38	63	60.32%
IE/Semitic	21	42	50.00%
Chinese/Altaic	2	4	50.00%
IE/Basque	17	42	40.48%
IE/Altaic	10	42	23.81%
Finno-Ugric/Basque	2	6	33.33%
Finno-Ugric/Chinese	2	6	33.33%
Altaic/Basque	1	4	25.00%

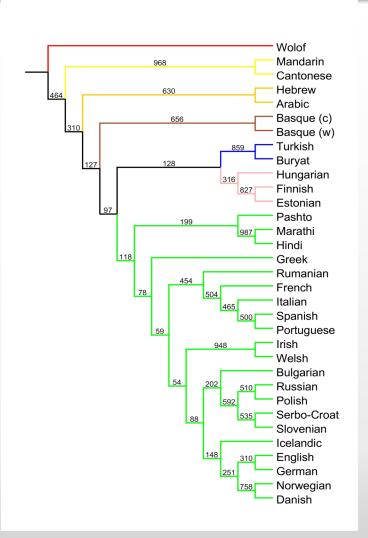
History as the driving force?

	Under the threshold	Total	Percentage
Finno-Ugric/Indo- Iranian	9	9	100.00%
Finno-Ugric/Slavic	14	15	93.33%
Finno-Ugric/Germanic	12	15	80.67%
Finno-Ugric/Greek	1	3	33.33%
Finno-Ugric/Celtic	1	10	10.00%
Finno-Ugric/Romance	1	15	6.67%

Phylogenetic tree (KITSCH, bootstrapped, 1000 resamples)



Supported by genetic evidence (cf. Pagani et al. 2015, in prep.)



Conclusions:

- We provided an algorithm for generating random languages and studying the space of variation modeled taking into account implications between parameters
- Investigating syntax within a generative framework focusing on the intricate system of implications between parameters proved that the parametric approach is able to retrieve a high level of correct historical information
- This is an indirect argument that parametric theories are a realistic approach to syntactic variation at a large cross-linguistic scale



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THANKS!



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