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


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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):

1) 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)
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).
Evidence for syntax as a signal of historical relatedness

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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

<table>
<thead>
<tr>
<th></th>
<th>English</th>
<th>Norwegian</th>
<th>Russian</th>
</tr>
</thead>
<tbody>
<tr>
<td>p10: gramm. Def.</td>
<td>+</td>
<td>+</td>
<td>-</td>
</tr>
<tr>
<td>(articles)</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>p14: enclitic articles (+p10)</td>
<td>-</td>
<td>+</td>
<td>?</td>
</tr>
</tbody>
</table>
Grammaticalized definiteness and enclitic articles

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<td>+</td>
<td>+</td>
<td>-</td>
</tr>
<tr>
<td>p14: enclitic articles (+p10)</td>
<td>-</td>
<td>+</td>
<td>0</td>
</tr>
</tbody>
</table>
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
Workshop on Language Variation and Change and Cultural Evolution: February 12-14, 2015, York, UK
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)
Coding the data: **Characters** or **Distances**?

Consider the following example:

A  +++++---
B  ------------
C  ------------
D  ------------
Coding the data: **Characters** or **Distances**?

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

**PAUP***
Coding the data: **Characters** or **Distances**?

KITSCH or UPGMA

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

Diagram:

A
  /   
B C
  /   
D
Coding the data: **Characters** or **Distances**?

Now consider the following example:

A  +++++-----
B  ----------
C  ----------
D  ----------+  (borrowing, parallel development, resetting, etc. etc.)
Coding the data: **Characters** or **Distances**?

<table>
<thead>
<tr>
<th></th>
<th>A</th>
<th>B</th>
<th>C</th>
<th>D</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>++++--</td>
<td>------</td>
<td>------</td>
<td>------</td>
</tr>
<tr>
<td></td>
<td>------</td>
<td>----++</td>
<td>------</td>
<td>------</td>
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<td></td>
<td>------</td>
<td>------</td>
<td>------</td>
<td>+-----</td>
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</tbody>
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**PAUP***
Coding the data: **Characters** or **Distances**?

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

PAUP*

A  ----+
B  ++++
C  ------
D  +-----
Coding the data: **Characters** or **Distances**?

KITSCH or UPGMA

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<td></td>
<td>++++</td>
<td>----</td>
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<td>-----</td>
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Diagram: A ---- B ---- C ---- D

---
Coding the data: **Characters** or **Distances**?

KITSCH or UPGMA
Coding the data: **Characters** or **Distances**?

KITSCH or UPGMA

A
B
C
D

K

B

C

D
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:

\[
\delta(A,B) = \frac{d(A,B)}{d(A,B) + i(A,B)}
\]

= differences / identities + differences

E.g.: Italian-English: (35 id., 6 diff.) \( \delta = \frac{6}{41} = 0.146 \)
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

<table>
<thead>
<tr>
<th>Bortolussi et al. (2011)</th>
<th>L1</th>
<th>L2</th>
<th>L3</th>
<th>L4</th>
<th>Probability of $P_\text{=}+$</th>
</tr>
</thead>
<tbody>
<tr>
<td>P1</td>
<td>+</td>
<td>+</td>
<td>+</td>
<td>-</td>
<td>0.75</td>
</tr>
<tr>
<td>P2 (only if +P1)</td>
<td>+</td>
<td>+</td>
<td>-</td>
<td>0</td>
<td>0.67</td>
</tr>
<tr>
<td>P3 (only if +P2)</td>
<td>+</td>
<td>-</td>
<td>0</td>
<td>0</td>
<td>0.5</td>
</tr>
<tr>
<td>Probability of $L_\text{=}+$</td>
<td>0.25</td>
<td>0.25</td>
<td>0.25</td>
<td>0.25</td>
<td></td>
</tr>
</tbody>
</table>

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

<table>
<thead>
<tr>
<th>Our algorithm</th>
<th>L1</th>
<th>L2</th>
<th>L3</th>
<th>L4</th>
<th>Probability of P_ = +</th>
</tr>
</thead>
<tbody>
<tr>
<td>P1</td>
<td>+</td>
<td>+</td>
<td>+</td>
<td>-</td>
<td>0.5</td>
</tr>
<tr>
<td>P2 (only if +P1)</td>
<td>+</td>
<td>+</td>
<td>-</td>
<td>0</td>
<td>0.5</td>
</tr>
<tr>
<td>P3 (only if +P2)</td>
<td>+</td>
<td>-</td>
<td>0</td>
<td>0</td>
<td>0.5</td>
</tr>
<tr>
<td>Probability of L_ =+</td>
<td>0.125</td>
<td>0.25</td>
<td>0.25</td>
<td>0.5</td>
<td></td>
</tr>
</tbody>
</table>

Independent parameters are first assigned a value by chance. Following parameters are checked for implications.
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 = $p < 2.2 \times 10^{-16}$

The two datasets are unlikely to be drawn from the same distribution.
Family-external pairs only

Mann-Whitney $U$ test = $p < 2.2 \times 10^{-16}$

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

(Anti-Babelic principle, Guardiano and Longobardi 2005)
Possible explanation?

<table>
<thead>
<tr>
<th>Chance threshold</th>
<th>Distance value</th>
<th>Pairs expected by chance</th>
<th>Pairs under the threshold</th>
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<tbody>
<tr>
<td>P=10^{-4}</td>
<td>0.111</td>
<td>0.05</td>
<td>42</td>
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<tr>
<td>P=10^{-3}</td>
<td>0.174</td>
<td>0.528</td>
<td>146</td>
</tr>
<tr>
<td>P=10^{-2}</td>
<td>0.250</td>
<td>5.28</td>
<td>310</td>
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<td>5.28</td>
<td>310</td>
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History as the driving force?

Family-internal pairs (211)

<table>
<thead>
<tr>
<th>Language</th>
<th>Under threshold</th>
<th>Total</th>
<th>Percentage</th>
</tr>
</thead>
<tbody>
<tr>
<td>Indoeuropean</td>
<td>204</td>
<td>210</td>
<td><strong>97.14%</strong></td>
</tr>
<tr>
<td>Finno-Ugric</td>
<td>3</td>
<td>3</td>
<td><strong>100.00%</strong></td>
</tr>
<tr>
<td>Semitic</td>
<td>1</td>
<td>1</td>
<td><strong>100.00%</strong></td>
</tr>
<tr>
<td>Basque</td>
<td>1</td>
<td>1</td>
<td><strong>100.00%</strong></td>
</tr>
<tr>
<td>Altaic</td>
<td>1</td>
<td>1</td>
<td><strong>100.00%</strong></td>
</tr>
<tr>
<td>Chinese</td>
<td>1</td>
<td>1</td>
<td><strong>100.00%</strong></td>
</tr>
</tbody>
</table>
History as the driving force?

Family-external pairs (99)

<table>
<thead>
<tr>
<th>Language Pair</th>
<th>Under threshold</th>
<th>Total</th>
<th>Percentage</th>
</tr>
</thead>
<tbody>
<tr>
<td>Finno-Ugric/Altaic</td>
<td>6</td>
<td>6</td>
<td>100.00%</td>
</tr>
<tr>
<td>IE/Finno-Ugric</td>
<td>38</td>
<td>63</td>
<td>60.32%</td>
</tr>
<tr>
<td>IE/Semitic</td>
<td>21</td>
<td>42</td>
<td>50.00%</td>
</tr>
<tr>
<td>Chinese/Altaic</td>
<td>2</td>
<td>4</td>
<td>50.00%</td>
</tr>
<tr>
<td>IE/Basque</td>
<td>17</td>
<td>42</td>
<td>40.48%</td>
</tr>
<tr>
<td>IE/Altaic</td>
<td>10</td>
<td>42</td>
<td>23.81%</td>
</tr>
<tr>
<td>Finno-Ugric/Basque</td>
<td>2</td>
<td>6</td>
<td>33.33%</td>
</tr>
<tr>
<td>Finno-Ugric/Chinese</td>
<td>2</td>
<td>6</td>
<td>33.33%</td>
</tr>
<tr>
<td>Altaic/Basque</td>
<td>1</td>
<td>4</td>
<td>25.00%</td>
</tr>
</tbody>
</table>
History as the driving force?

<table>
<thead>
<tr>
<th>Language Combination</th>
<th>Under the threshold</th>
<th>Total</th>
<th>Percentage</th>
</tr>
</thead>
<tbody>
<tr>
<td>Finno-Ugric/Indo-Iranian</td>
<td>9</td>
<td>9</td>
<td>100.00%</td>
</tr>
<tr>
<td>Finno-Ugric/Slavic</td>
<td>14</td>
<td>15</td>
<td>93.33%</td>
</tr>
<tr>
<td>Finno-Ugric/Germanic</td>
<td>12</td>
<td>15</td>
<td>80.67%</td>
</tr>
<tr>
<td>Finno-Ugric/Greek</td>
<td>1</td>
<td>3</td>
<td>33.33%</td>
</tr>
<tr>
<td>Finno-Ugric/Celtic</td>
<td>1</td>
<td>10</td>
<td>10.00%</td>
</tr>
<tr>
<td>Finno-Ugric/Romance</td>
<td>1</td>
<td>15</td>
<td>6.67%</td>
</tr>
</tbody>
</table>
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.
THANKS!

Selected references:


