Formal syntax and deep history Supplementary Material

Andrea Ceolin, Cristina Guardiano, Monica Alexandrina-Irimia, Giuseppe Longobardi*

*** Correspondence:**

Corresponding Author giuseppe.longobardi@york.ac.uk

Keywords: phylogeny, formal syntax, parameters, language reconstruction, biolinguistics

1. Online Repository

The source code to replicate all the figures and the experiments presented in the paper and in the Supplementary Material is found in the following online repository (along with other relevant data and information):<https://github.com/AndreaCeolin/FormalSyntax>

2. Languages

The 69 languages of the dataset, along with their associated Glottolog [\(https://glottolog.org/glottolog/language\)](https://glottolog.org/glottolog/language) and ISO 639-3 codes, the family and subfamily they belong to, their location and geographic coordinates, are listed in **Supplementary Table 1**.

Supplementary Table 1. The languages of the dataset. For the languages marked with '*' we encoded two diastratic varieties.

3. The syntactic dataset

Supplementary Figure 1 contains the 94 binary nominal parameters used for the experiments presented in the paper, set in 69 languages spanning across up to 13 traditionally irreducible Eurasian families.

The table should be read as follows:

1st column: progressive number of the parameters (p1, p2, p3, ...)

2nd column: acronym of the parameter

3rd column: name of the parameter

4th column: implicational constraints specifying the conditions for setting the parameter

A detailed list of questions used to determine the state of the parameters and instructions to map them to **Supplementary Figure 1** can be found in:

Crisma, P., C. Guardiano and G. Longobardi (2020), Syntactic parameters and language learnability. *Studi e Saggi Linguistici* 58, 99-130. doi: 10.4454/ssl.v58i2.265

Supplementary Figure 1. 94 binary nominal parameters set in 69 languages.

4. Possible languages

We calculated the number of possible languages generated from the first 30 parameters of Table A using an algorithm first presented in Bortolussi et al. (2011). This is a breadth-first search algorithm that keeps track of the number of 'possible strings', namely, those strings which do not violate the implicational rules. The algorithm takes as input two strings of length=1, one with the value "+" and one with the value "-".Then, from each string it creates three different strings of length=2, adding one of the three possible values ("+", "-" and "0"), so that at the first iteration we have "+/+", "+/-", " $+/0$ " and "-/+", "-/-", and "-/0", for a total of six possible strings. Before the next iteration, only the strings which are compatible with the implicational structures are kept, while the others are discarded. The procedure is then repeated, so that at each iteration only the strings which are compatible are kept.

We limited the analysis to the first 30 parameters because the algorithm has exponential complexity, and therefore, as every subset of strings needs to be triplicated at each iteration, the algorithm will take much more time to process every string at each following iteration (see the online repository for the Python script that we used). Through the algorithm, we calculated that the first 30 parameters used here generate only 152,448 possible languages $({\sim}2^{17})$ instead of 2^{30} . These figures suggest that calculations of the probability of relatedness based on grammatical structure but neglecting the pervasive effect of such predictable information could be seriously undermined. We expect the rate of possible languages to increase at an even lower rate when more parameters are added to the search space, because they will be potentially constrained by higher numbers of previous parameters.

5. Heatmap - Syntactic Distances

Instructions to visualize the heatmap in **Figure 1** in the text.

- 1. Go to the page <https://software.broadinstitute.org/morpheus/>
- 2. Upload to the page the file *jaccard_distances.txt* from the GitHub repository (link: [https://github.com/AndreaCeolin/FormalSyntax/blob/master/jaccard_distances.txt\)](https://github.com/AndreaCeolin/FormalSyntax/blob/master/jaccard_distances.txt) and click the "OK" button to visualize the heatmap
- 3. In the "Tools" menu, select the option "Hierarchical clustering", and then the following options: a. Metric > Matrix values (from a precomputed distance matrix)
	- b. Linkage method > average
	- c. Cluster > Rows and columns
	- Click the "OK" button.
- 4. To visualize the same color distribution as **Figure 1**, follow the instructions below:
	- a. In the "View" menu, select "Options"
	- b. In the "Color Scheme" window:
		- i. Uncheck the "Relative color scheme" choice
		- ii. "Maximum" > 0.857
		- iii. "Add color stop"
		- iv. "Selected color" > yellow
		- v. "Selected value" > 0.430

Supplementary Table 2 lists the maximal clusters of cells in **Figure 1** which do not contain any yellow/red cell. The symbol δ refers to the Jaccard distance between two languages, the symbol μ

to the average distance among the languages belonging to a given aggregation/cluster, obtained as the mean of all the pairwise distances between the languages of that aggregation.

Supplementary Table 3 lists the subgroups which can be identified within each of the cluster in **Supplementary Table 2**, along with the distance range and mean within each subfamily.

Supplementary Table 2. Clusters of cells which do not contain any yellow/red cell in **Figure 1**.

Supplementary Table 3. Distances and means within the subfamilies identifiable in **Figure 1**.

Other observations:

- a. Only one pair formed by a member of **Cluster 1** (IE) and a language outside of it has δ<0.26 (i.e. lower than the μ of the cluster), i.e. Ma-Ta (0.25); two pairs have δ =0.26 (Ma-Te and Hi-Te). Overall, there are 185 white/blue cells (δ *<* 0.429) involving a member of **Cluster 1** and a language outside of it. Most such pairs contain one Indo-Iranian language and one Dravidian, NE Caucasian, Uralic or Altaic language.
- b. All the members of **Cluster 2** display many similarities with other languages of the sample: overall, 93 pairs involving either of the two Dravidian languages and one Indo-European, Uralic or Altaic language, and 90 pairs involving either of the two NE Caucasian languages and one Indo-European, Uralic or Altaic language are either white or light blue, with δ ranging from 0.25 to 0.42.
- c. Almost all the languages belonging to **Cluster 3A** display similarities with many other languages outside of it (124 blue/white cells), notably Indo-Iranian, Dravidian, NE Caucasian, Altaic, Yukaghir and (to a smaller extent) Malagasy and Basque, with δ ranging from 0.19 to 0.42.

- d. As far as **Cluster 4A** is concerned, there are 163 blue/white cells involving one of its members with a language outside of the cluster, and most of them involve Indo-Iranian, Dravidian, NE Caucasian, Uralic and, marginally, Malagasy and other IE languages. Buryat and Yukaghir are the outliers of the cluster: yet, no aggregation of blue/white cells containing either of the two languages displays a μ/δ smaller than those they hold with the rest of Cluster 4A (see **Supplementary Table 4**).
- e. The languages sharing non-yellow/red cells with Malagasy (an isolate in the Heatmap) are: Mari 2 (δ=0.39), Udmurt 2 (δ=0.42), Uzbek, Kazakh, Kirghiz, Turkish (δ=0.40).
- f. The languages sharing non-yellow/red cells with **Cluster 5** (Basque) are: Mari_2 (δ[Basque_Western]*=*0.41, δ[Basque_Central]=0.40), Marathi (δ[Basque_Western]=0.39) and Pashto (δ [Basque Western]=0.41).
- g. Sinitic languages (**Cluster 6**) do not share any white/blue cell with other languages of the sample, with the exception of Hindi ($\delta = 0.38$).
- h. There are two languages which share non-yellow/red cells with **Cluster 7**, i.e., Greek and Cypriot Greek (δ = 0.42 with Japanese, and δ = 0.36 with Korean).

Supplementary Table 4. Relations between Buryat/Yukaghir and closest languages.

6. PCoAs

The PCoAs have been produced using the software PAST [\(https://www.nhm.uio.no/english/research/infrastructure/past/\)](https://www.nhm.uio.no/english/research/infrastructure/past/). After the distance matrix is loaded, the following option should be selected: *Multivariate -> Ordination -> PCoA*.

In the scatter plot, the attribute *Row Labels* must be selected to display the name of the languages. The PCoA in **Supplementary Figure 2** was obtained from the parametric Jaccard distances between the 30 non-Indo-European languages of our sample.

In **Supplementary Figure 2**, the first coordinate, which accounts for about 58% of the variance, separates Uralic, Dravidian, NE Caucasian, Altaic, and Yukaghir (left area) from the others.

- a. Left area: the second coordinate (accounting for 17% of the variance) separates Altaic (with Buryat falling precisely on the horizontal axis) and Yukaghir (bottom quadrant) from the rest. In the top quadrant, Uralic, Dravidian and NE Caucasian are not clearly separated: this reflects the high amount of similarities among these languages observed in the Heatmap.
- b. Right quadrant: the second coordinate separates the languages of the Far-East (bottom quadrant) from the rest. Japanese and Korean, which appear very close to one another in the Heatmap, in this representation are quite separated.

As it appears in the graph, distances, especially in the left quadrant, are quite compressed: hence, the internal distribution of the pairs does not emerge clearly. In order to observe it in more detail, we visualized the two groups identified by the first coordinate as two separate graphs, shown in **Supplementary Figure 3** and **Supplementary Figure 4.**

The distribution of the pairs in **Supplementary Figure 3** further emphasizes the neat separation between Sinitic and Japanese-Korean.

In **Supplementary Figure 4**:

- a. Dravidian and NE Caucasian are a separate cloud (top right quadrant).
- b. The top left quadrant shows two major clouds:
	- i. all Altaic languages but Buryat
	- ii. Buryat (that expectedly appears as an outlier of the group) and Yukaghir (that, again, is attracted by the Altaic group)
- c. Uralic forms a relatively compact cloud in the bottom area of the graph, with Estonian and Finnish in an outlying position, as seen in the Heatmap.

Finally, **Supplementary Figure 5** contains the 39 IE languages of our sample. Their distribution partitions the known subfamilies with a discrete resolution and without historical errors. The first coordinate, which accounts for 46% of the variance, separates Romance from the other subfamilies. In the left area, the horizontal axis (which accounts for 18% of the variance) identifies: a. Germanic and Slavic, which form two separate clouds in the bottom-left quadrant

b. Celtic, Greek and Indo-Iranian (more scattered)

Coordinate 1 - 58%

Supplementary Figure 2. PCoA of the 30 non-Indo-European languages.

Coordinate 1 - 61%

Supplementary Figure 3. PCoA of 7 non-Indo-European languages.

Coordinate 1-42%

Supplementary Figure 4 - PCoA of 18 non-Indo-European languages.

Coordinate 1 - 46%

Supplementary Figure 5 - PCoA of the 39 Indo-European languages.

7. Phylogenetic analysis - UPGMA

The UPGMA tree (**Figure 3** in the main text) has been generated using a modified bootstrapping procedure.

The bootstrapping technique resamples the whole dataset by selecting each character with equal probability and recreating a matrix of the same length. The content of the new matrix is different from the original matrix, because some characters might be absent and some others might be present multiple times as a consequence of the sampling procedure. This allows one to estimate the robustness of the dataset by repeating the same analysis on different samples of the dataset.

Since the Jaccard distance between two languages excludes all parameters that are set to '0' in either one of them, a standard bootstrapping procedure runs the risk of making a pair of languages not comparable, because in some replicas the number of identities plus differences can reduce to zero, and then yield a zero denominator for the Jaccard formula. For this reason, we decided to adopt a moderated bootstrap procedure, by creating 1000 datasets in which only six parameters are resampled. Since the minimum number of comparable parameters between any two languages in the dataset is seven, a resampling of six parameters will assure that the two strings are comparable by means of the Jaccard distance.

The UPGMA tree presented in the text is a consensus tree resulting from applying UPGMA to the 1000 replicas of the dataset.

The first two splits of **Figure 3** identify the following nodes:

- a. The languages spoken in East Asia, with Japanese and Korean falling under one and the same node
- b. Basque
- A further split separates two major clusters, internally articulated as follows:
- 1. a. Malagasy
	- b. Uralic, articulated into the following groups:
		- Balto-Finnic
		- Ugric
		- Volgaic-Permic, with a low bootstrapping score, which shows that the two subfamilies are often mixed when replicating the experiment
- 2. a. Altaic+Yukaghir, with the following internal articulation
	- Yukaghir is the outlier
	- Buryat
	- Tungusic
	- Turkic: Kazakh and Kirghiz are clustered together, followed in succession by Turkish, Yakut and Uzbek (NE Turkic). Note the low bootstrapping score of the Kazakh and Kirghiz node, which means that by replicating the experiment they might end up clustering with Turkish first.
	- b. i. NE-Caucasian and Dravidian
		- ii. Indo-European, articulated into the following major subfamilies:
			- Indo-Iranian. Pashto is the outlier. The two Indo-Aryan languages are together
			- Romance. Romanian is the outlier. The Ibero-Romance unit (Spanish and Portuguese) is recognized. The dialects of Italy, and Italian, are under the same node, with the following internal articulation: Northern Gallo-Italic dialects (Casalasco, Parma and Reggio_Emilia); Extreme-southern dialects (Salentino, Calabrese_Southern and Siciliano); Upper-southern dialects (Teramano, Barese, Campano and Calabrese_Northern) and Italian
			- Celtic
			- Greek. Greek clusters with Greek_Cypriot; Greek_Calabria_1 is the outlier of this group, reflecting its documented conservative nature (Guardiano et al. 2016, Guardiano and Stavrou 2014, 2019)
			- Slavic. Bulgarian occurs as the outlier. Polish and Russian fall together
			- Germanic. Three out of four traditional West-Germanic languages (Continental West Germanic) are under one and the same node (Afrikaans, Dutch and German). English falls within the North-Germanic cluster (Icelandic, Danish, Faroese, Norwegian)
- 8. Phylogenetic analysis - Hamming distances

We created a UPGMA tree (**Supplementary Figure 6**) from a matrix of Hamming distances, using the same procedure as for **Figure 3**. The tree retrieves most of the nodes observed in **Figure 3,** with three major differences:

- a. Pashto and Romanian go together
- b. the nodes containing the two Basque varieties, the two Sinitic languages and Japanese/Korean are not the outliers (they are closer to the Indo-European node)
- c. West-Germanic and a North-Germanic node are identified

Supplementary Figure 6. UPGMA tree calculated using Hamming distances.

9. Phylogenetic analysis – BEAST 2

In order to determine the best model for the BEAST tree (Bouckaert et al. 2019), we used the software Tracer [\(https://beast.community/tracer\)](https://beast.community/tracer) to compare the posterior likelihood of several models. The analysis is summarized in **Supplementary Figure 7.** The best model that we determined is a Gamma Site Model with Substitution Rate = 1, a Mutation Death Model with death $p = 0.1$, a Relaxed Clock (Logarithmic) with clock rate $= 1$, and a uniform Yule model for the birth rate. The Monte Carlo Markov Chain produced 10,000,000 trees, 25% of which were used for the burn-in and discarded for the purpose of the calculation of the consensus tree. The tree is a consensus tree of 7,500 different trees sampled through the 7,500,000 trees (with a sample stored every 1000 generated trees) produced by Monte Carlo sampling.

Supplementary Figure 7. Tracer analysis for different BEAST models used to generate a tree from the syntactic dataset.

The constrained BEAST tree (**Figure 4** in the text) identifies the following splits:

- a. The languages spoken in East Asia, with Japanese and Korean falling under one and the same node
- b. Malagasy and Basque
- c. Uralic, articulated into the following groups:
	- Balto-Finnic (Estonian and Finnish)

- Ugric (Hungarian and Khanty)
- Volgaic-Permic (Mari and Udmurt), with a low posterior probability, which means that the two subfamilies can appear mixed in some replications of the experiments
- d. A node that splits into the following:
	- Dravidian (Tamil and Telugu) + NE Caucasian (Archi and Lak)
	- Altaic+Yukaghir, with the following internal articulation:
		- Buryat
		- Yukaghir
		- Tungusic (Even, Evenki)

- Turkic: Kazakh and Kirghiz are clustered together, followed in succession by Turkish, Yakut and Uzbek. All these nodes have low posterior probability, which means that the internal articulation of the family is not defined, and therefore is not stable across different replications

- e. Indo-European, articulated into the following major subfamilies:
	- Indo-Iranian. Pashto is the outlier of the two Indo-Aryan languages (Hindi, Marathi)
	- Romance. Romanian is the outlier. French is the outlier of a node that also includes the Northern Gallo-Italic dialects (Casalasco, Parma and Reggio_Emilia). Salentino is the outlier of a node that has the following splits: Italian and Upper southern dialects of Italy (Calabrese_Northern, Teramano, Barese, Campano); Ibero-Romance and the Extreme southern dialects of Italy (Calabrese Southern, Siciliano Mussomeli, Siciliano Ragusa), with the exception of Salentino)
	- Celtic (Irish and Welsh) + Greek (with the same subarticulation as in UPGMA)
	- Slavic (with the same subarticulation as in UPGMA)
	- Germanic, split into West- vs. North-Germanic (contrary to UPGMA, both nodes are correctly identified)

Supplementary Figure 8 displays an unconstrained tree generated using BEAST. Here, Finnish and Estonian do not cluster with the other Uralic languages, but are the outliers of a group containing Uralic, NE Caucasian and Dravidian, Turkic, Tungusic, Buryat and Yukaghir. In other replications, Balto-Finnic appears as an outlier of the Indo-European languages, or even inside this family. A tree without Finnish and Estonian is displayed in **Supplementary Figure 9.**

Supplementary Figure 8. Unconstrained BEAST tree.

Supplementary Figure 9. BEAST tree without Finnish and Estonian.

10. Network analysis - NeighborNet

For the network analysis, we used the software SplitsTree (Huson and Bryant 2006) and the algorithm NeighborNet. The network (**Supplementary Figure 10**) identifies all the major aggregations already identified in the other experiments. The two graphs containing the Δ-scores (**Supplementary Figure 11**) and the Q-residuals (**Supplementary Figure 12**) have been produced using matplotlib in Python3. **Supplementary Table 5** lists the ten highest Δ-scores and Qresiduals for our dataset.

Δ -scores		Q-residuals	
Mandarin	0.387	Mandarin	0.125
Cantonese	0.387	Cantonese	0.125
Korean	0.371	Japanese	0.107
Japanese	0.369	Korean	0.098
Pashto	0.367	Hungarian	0.097
Basque_Central	0.365	Lak	0.092
Tamil	0.350	Archi	0.092
Basque Western	0.349	Basque_Central	0.089
Hungarian	0.336	Basque_Western	0.085
Malagasy	0.336	Tamil	0.081

Supplementary Table 5. The ten highest Δ-scores and Q-residuals for our dataset.

Supplementary Figure 10. NeighborNet network obtained using SplitsTree on the syntactic dataset.

Supplementary Figure 11. Δ-scores derived from the network in **Supplementary Figure 10**.

Supplementary Figure 12. Q-residuals derived from the network in **Supplementary Figure 10**.

11. Phonemic data - the Ruhlen Database

The Tracer analysis for the tree generated from Ruhlen's dataset is summarized in **Supplementary Figure 13.** The best model that we determined is a Gamma Site Model with Substitution Rate = 1, a Mutation Death Model with death $p = 0.1$, a Relaxed Clock (Logarithmic) with clock rate $= 1$ with clock rate = 1, and a uniform Yule model for the birth rate. The Monte Carlo Markov Chain produced 10,000,000 trees, 25% of which were used for the burn-in and discarded for the purpose of the calculation of the consensus tree. The tree is a consensus tree of 7,500 different trees sampled through the 7,500,000 trees (with a sample stored every 1000 generated trees) produced by Monte Carlo sampling.

Supplementary Figure 13. Tracer analysis for different BEAST models used to generate a tree from the subset of the Ruhlen dataset overlapping with our languages.

12. Ultralocality

The Network of **Supplementary Figure 14** has been generated from the Romance languages of the sample. Here, the languages of Italy are separated from the rest of Romance, and their internal classification is largely the expected one: the Lausberg dialect (Calabrese_Northern) is an isolate bridging the other Upper southern dialects (Campano, Barese and Teramano) and Italian; the Northern Gallo-Italic group (Teggio_Emilia, Parma and Casalasco) is singled out; the Extreme southern dialects (Siciliano and Calabrese Southern) are together, with Salentino as the outlier; the position of the Extreme southern group suggests some relation with Ibero-Romance.

In the Heatmap in **Supplementary Figure 15,** white and blue cells mark distances ranging from 0 to 0.142, yellow and red cells mark distances ranging from 0.143 to 0.286.

Instructions to visualize the heatmap:

- 1. Go to the following page:<https://software.broadinstitute.org/morpheus/>
- 2. Upload to the page the file *jaccard_distances.txt* from the GitHub repository (link: [https://github.com/AndreaCeolin/FormalSyntax/blob/master/Romance/jaccard_distances_rom](https://github.com/AndreaCeolin/FormalSyntax/blob/master/Romance/jaccard_distances_romance.txt) [ance.txt](https://github.com/AndreaCeolin/FormalSyntax/blob/master/Romance/jaccard_distances_romance.txt)), and click the "OK" button to visualize the heatmap.
- 3. In the "Tools" menu, select the option "Hierarchical clustering", and then the following: a. Metric > Matrix values (from a precomputed distance matrix)
	- b. Linkage method > average

- c. Cluster $>$ Rows and columns
- Click the "OK" button.
- 4. To visualize the same color distribution as Fig.1, follow the instructions below:
	- a. In the "View" menu, select "Options"
	- b. In the "Color Scheme" window:
		- i. Uncheck the "Relative color scheme" choice
		- ii. "Maximum" > 0.286
		- iii. "Add color stop"
		- iv. "Selected color" > yellow
		- v. "Selected value" > 0.143

Supplementary Table 6 lists the maximal clusters of cells in **Supplementary Figure 15** which do not contain any yellow/red cell. The symbol δ refers to the Jaccard distance between two languages, the symbol μ to the average distance among the languages belonging to a given aggregation/cluster, obtained as the mean of all the pairwise distances between the languages of that aggregation.

Supplementary Table 6. Clusters suggested by the distribution of the distances in the Heatmap in **Supplementary Figure 15**.

The white/blue cells outside of the clusters in **Supplementary Table 6** correspond to the pairs listed in **Supplementary Table 7**.

3 - Parma	2 - Barese (0.13), Campano (0.13), Teramano (0.08), Italian (0.12)		
4 - Portuguese	1 - Siciliano_Ragusa (0.12), Siciliano_Mussomeli (0.12), Calabrese_Southern (0.12)		
	2 - Italian (0.11)		
4 - Spanish	2 - Italian (0.14)		
(isolate) Romanian	2 - Italian (0.14)		

Supplementary Table 7. White/blue cells in **Supplementary Figure 15** outside of the clusters listed in **Supplementary Table 6**.

In the PCoA in **Supplementary Figure 16,** the vertical axis (43% of the variance) separates Ibero-Romance and the dialects of central/southern Italy from the rest of Romance, with the exception of Teramano; Barese and Campano fall precisely on the vertical axis. The horizontal axis (36% of the variance) separates the dialects of Italy from the other Romance languages, with two exceptions: Calabrese_Southern (that appears right below the axis), and Casalasco (the Northern Gallo-Italic dialect closest to French).

Supplementary Figure 14. Network of the Romance languages.

Coordinate 1 - 43%

Supplementary Figure 16. PCoA of the Romance languages.