



**LANGELIN - LANguages Genes LINeages**  
**ERC Advanced Grant n. 295733**

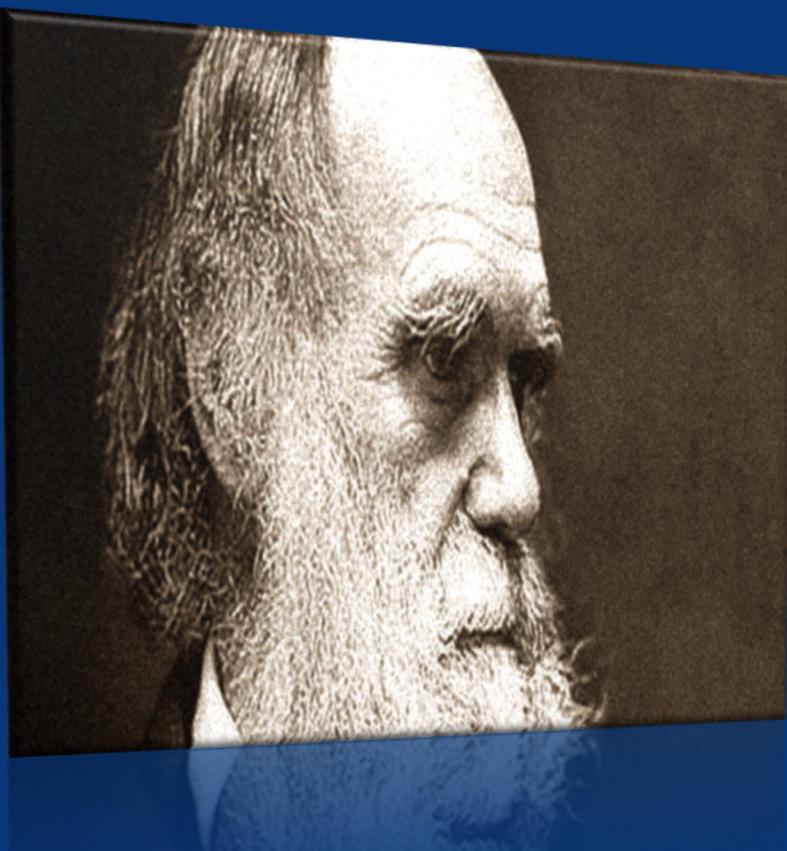


Funded by  
the European Union

## **Across language families: Genome mirrors linguistic variation within Europe**

**Giuseppe Longobardi, Cristina Guardiano, Andrea Ceolin,  
Silvia Ghirotto, Guido Barbujani**





## Darwin's last challenge



*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, were to be included, such an arrangement would be the only possible one*

# Genes mirror geography within Europe

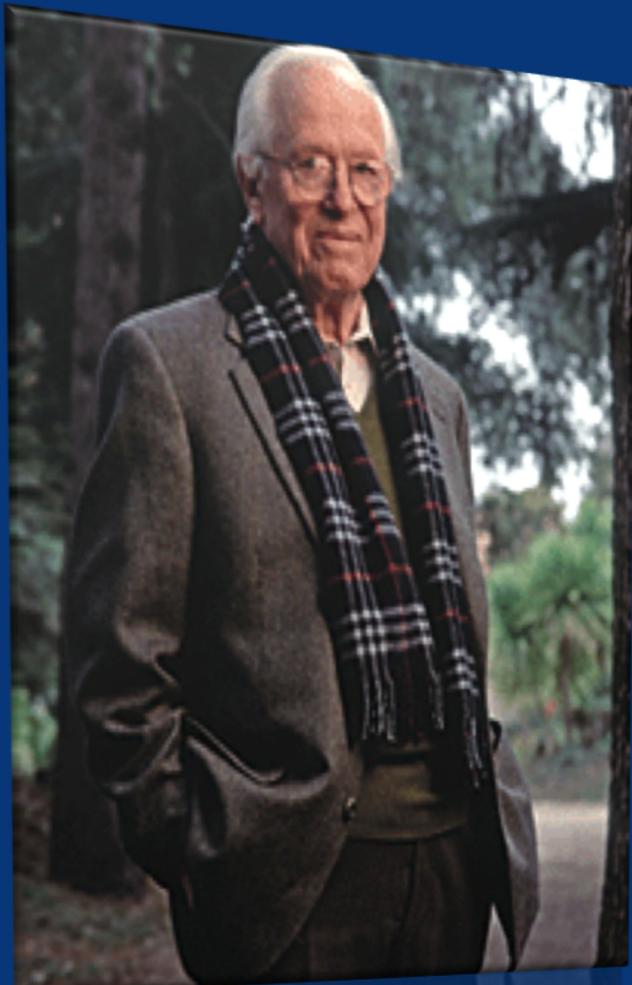
See associated Correspondence: [Detours, Nature 455, 861 \(October 2008\)](#)

John Novembre<sup>1,2</sup>, Toby Johnson<sup>4,5,6</sup>, Katarzyna Bryc<sup>7</sup>, Zoltán Kutalik<sup>4,6</sup>, Adam R. Boyko<sup>7</sup>, Adam Auton<sup>7</sup>, Amit Indap<sup>7</sup>, Karen S. King<sup>8</sup>, Sven Bergmann<sup>4,6</sup>, Matthew R. Nelson<sup>8</sup>, Matthew Stephens<sup>2,3</sup> & Carlos D. Bustamante<sup>7</sup>

*...among Europeans,  
we find a close correspondence between genetic and  
geographic distances ...*

*...a geographical map of Europe  
arises naturally as an efficient two-dimensional  
summary  
of genetic variation in Europeans*

Cavalli Sforza, Menozzi, and Piazza (1994)  
*The History and Geography of Human Genes*



*We believe that the  
major breakthrough  
in the study of human variation has  
been  
the introduction of genetic markers,  
which are strictly inherited and  
basically immune to the problem of  
rapid changes induced  
by the environment*

# Population Genetics as a Model

- **Biology**

Reduction of human ***genetic variation*** to the complex effects of a **finite** and **universal** set of **discrete biological** options  
(genetic polymorphisms)

- **Linguistics**

Reduction of the whole space of possible ***grammatical variation*** to the complex effects of a **finite** and **universal** set of **discrete biological** options (parameters, i.e. syntactic polymorphisms)

объектов (параметров, т.е. синтаксических полиморфизмов)

# Parametric Comparison Method

Longobardi (2003),  
Guardiano and Longobardi  
(2005),  
Longobardi and Guardiano  
(2009),  
Longobardi, Guardiano, et  
al. (2013)

## Parameter values

may appropriately act as *comparanda*  
for historical reconstruction

It becomes possible:

- ◆ to precisely calculate the syntactic distance between any two languages
- ◆ to assess the probabilistic value of such distances

# IE parameters: Longobardi et al (2013)

	TABLE A		Sic	Cal	It	Sal	Sp	Fr	Ptg	Rm	Gri	BoG	Grk	E	D	Da	Ice	Nor	Big	SC	Slo	Po	Rus	Ir	Wel	Far	Ma	Hi	
1	± gramm. person	FGP	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	1	
2	± gramm. number	+FGP	FGN	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	2	
3	± gramm. gender	+FGN	FGG	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	3		
4	± NP over D	+FGP	NOD	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	4		
5	± feature spread to N	+FGN	FSN	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	5		
6	± numb. on N (BNs)	+FSN	FNN	+	+	+	+	+	-	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	6		
7	± gramm. partial def	DGP	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	-	-	-	-	-	-	-	7		
8	± gramm. def	+DGP	DGR	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	0	0	0	0	0	+	0	0	8	
9	± strong person	+FGP, +DGR, -NOD	NSD	+	+	+	+	+	+	+	+	+	+	+	+	-	-	-	+	0	0	0	0	-	-	0	0	9	
10	± free null partitive Q	+FNN	DPQ	-	-	-	-	0	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	10		
11	± gramm. dist. art.	-FSN or -FNN or +DGR	DDA	-	-	-	-	-	-	-	-	-	-	-	-	-	-	0	0	0	0	0	-	0	0	11			
12	± def-checking N	+DGR	DCN	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	0	0	0	12			
13	± def spread to N	+DCN, -NSD	DSN	0	0	0	0	0	0	0	0	0	0	0	0	-	-	0	0	0	0	0	0	0	0	13			
14	± def over relatives	+DGR	DOR	-	-	-	-	-	-	-	-	-	-	-	-	-	-	0	0	0	0	0	-	0	0	14			
15	± D-controlled infl. on N	+FSN	DIN	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	15			
16	± plural spread from cardinals	+FSN	CPS	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	16			
17	± gramm. boundedness	CGB	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	17			
18	± strong article	+DGR, +FNN, -CGB	CGR	+	+	+	+	+	0	+	+	+	+	+	+	+	+	-	0	0	0	0	-	-	0	0	18		
19	± bounded-checking N	+CGB	CCN	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	+	-	19		
20	± null-N-licensing art	-FSN or -FNN or -DCN, +NOD or +NSD	DNN	-	-	-	+	-	0	-	-	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	20		
21	± structured APs	AST	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	21		
22	± feature spread to struct. APs	+FSN, +AST	FFS	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	-	-	+	22		
23	± feature spread to pred. APs	+FGN	FSP	+	+	+	+	+	+	+	+	+	+	+	+	-	-	+	+	+	+	+	+	-	-	+	23		
24	± D-controlled infl. on A	-NSD, +FFS	ADI	0	0	0	0	0	0	0	0	0	0	0	0	+	+	+	0	0	0	0	-	0	0	0	24		
25	± DP over relatives	ADR	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	-	25		
26	± relative extrap.	-ADR	AER	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	+	26		
27	± free reduced rel	+AST	ARR	+	+	+	+	+	+	+	+	+	+	+	+	-	-	-	-	-	-	-	-	-	-	+	27		
28	± N-raising with obl. pied-piping	+AST	NPP	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	28			
29	± free Gen	GFR	GUN	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	29		
30	± uniform Gen	+GFR	GUN	-	-	-	-	-	-	0	0	0	0	0	-	-	-	-	0	0	0	0	-	-	-	30			
31	± DP over free Gen	+GFR, +ADR	GPR	+	+	+	+	+	+	0	0	0	0	+	+	+	+	+	0	0	0	0	+	+	0	0	31		
32	± GenO	=+GUN	GFO	-	+	-	-	-	-	+	+	+	+	+	-	-	-	-	-	-	-	-	-	-	-	32			
33	± Gen-feature spread to N	GFS	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	33			
34	± D checking poss.	+DGR, +NSD or =+CGR	PDC	-	-	-	-	+	+	?	-	-	-	0	0	0	+	0	-	0	0	0	0	+	+	0	0	34	
35	± adjectival poss.	APO	+	+	+	+	+	+	+	+	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	35			
36	± post-affix poss.	DCN	PAP	0	0	0	0	0	0	0	+	0	0	0	-	+	+	0	0	0	0	0	0	0	0	36			
37	± clitic poss.	PCL	-	-	-	-	-	-	-	-	+	+	+	-	-	-	-	-	-	-	-	-	-	-	-	37			
38	± N-feat. spr. to pron. poss.	+FFS or -AST, +PAP or +PCL	PHS	0	0	0	0	0	0	0	+	-	-	0	0	0	+	+	-	0	0	0	0	0	0	0	38		
39	± N-feature spread to free Gen	+FFS, +GFR, =-PHS	GSP	-	-	-	-	-	0	0	0	0	0	-	-	-	-	0	0	0	0	0	-	0	0	+	39		
40	± adjectival Gen	+APO	AGE	-	-	-	-	-	0	0	0	0	0	-	0	0	0	+	+	+	-	+	0	0	0	0	40		
41	± Poss <sup>o</sup> -checking N	-GFS	GCN	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	41		
42	± Loc. Checking Dem	=+CGR, -FSN or +FNN	TLC	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	+	0	+	+	+	+	+	+	42		
43	± Split Locality	=-TLC	TSL	-	-	-	-	+	-	+	-	+	-	-	-	-	-	-	-	-	-	-	-	-	0	0	-	43	
44	± D Checking Dem	=-TLC, -FSN or +DGR	TDC	+	+	+	+	+	+	+	+	+	?	-	+	+	+	+	+	0	0	0	0	0	0	0	0	44	
45	± N over cardinals	NOC	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	45		
46	± N over ordinals	-NO	NOO	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	+	46		
47	± N over M <sub>1</sub> As	-NO <sub>1</sub> , -NPP	NM <sub>1</sub>	+	+	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	+	47		
48	± N over M <sub>2</sub> As	-NM <sub>1</sub>	NM <sub>2</sub>	0	0	+	0	+	+	+	0	0	-	-	-	-	-	-	-	-	-	-	-	-	0	0	-	48	
49	± N over As	-NM <sub>2</sub>	NOA	0	0	0	0	0	0	0	0	0	-	-	-	-	-	-	-	-	-	-	-	-	0	0	-	49	
50	± N over GenO	=-GFO, -NOA or -AST	NGO	0	0	0	0	0	0	0	0	0	0	0	+	0	+	0	+	0	0	+	+	+	0	0	0	50	
51	± N over ext. arg.	-NGO or (-GFO, -NOA or -AST)	NOE	0	0	0	0	0	0	0	0	0	0	0	-	0	-	0	-	+	0	0	0	0	0	+	51		
52	± free MOD	-NOA	AFM	0	0	0	0	0	0	0	0	0	0	0	+	-	-	-	-	-	-	-	-	0	0	-	52		
53	± class MOD	-AFM	ACM	0	0	0	0	0	0	0	0	0	0	0	0	-	-	-	-	-	-	-	-	-	+	0	0	-	53
54	± def on APs	+DGP, +postnom. APs	DOA	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	0	0	0	0	0	-	-	0	0	54	
55	± gramm. AP marker	+postnom. APs	DMO	-	-	-	-	-	-	-	-	-	-	-	-	-	-	0	0	0	0	0	-	-	-	+	0	0	55
56	± Cons. Pr.	(-NM <sub>1</sub> , +A-Cpl) or (+NPP or =-NM <sub>2</sub> , +Cpl-A)	ACP	0	0	+	0	+	+	+	+	0	0	-	+	+	+	+	-	-	-	-	-	0	0	-	0	56	

# The structure of linguistic distances

## A problem: internal implications

### GRAMMAR:

PCM = designed to control for the non-independence of characters.

- Explicit hypotheses about implications among syntactic parameters.
- $D_{SYN}$  : normalized Hamming (or Jaccard) distance =  $d/(i+d)$

# IE cognates: Bouckaert et al. (2012)

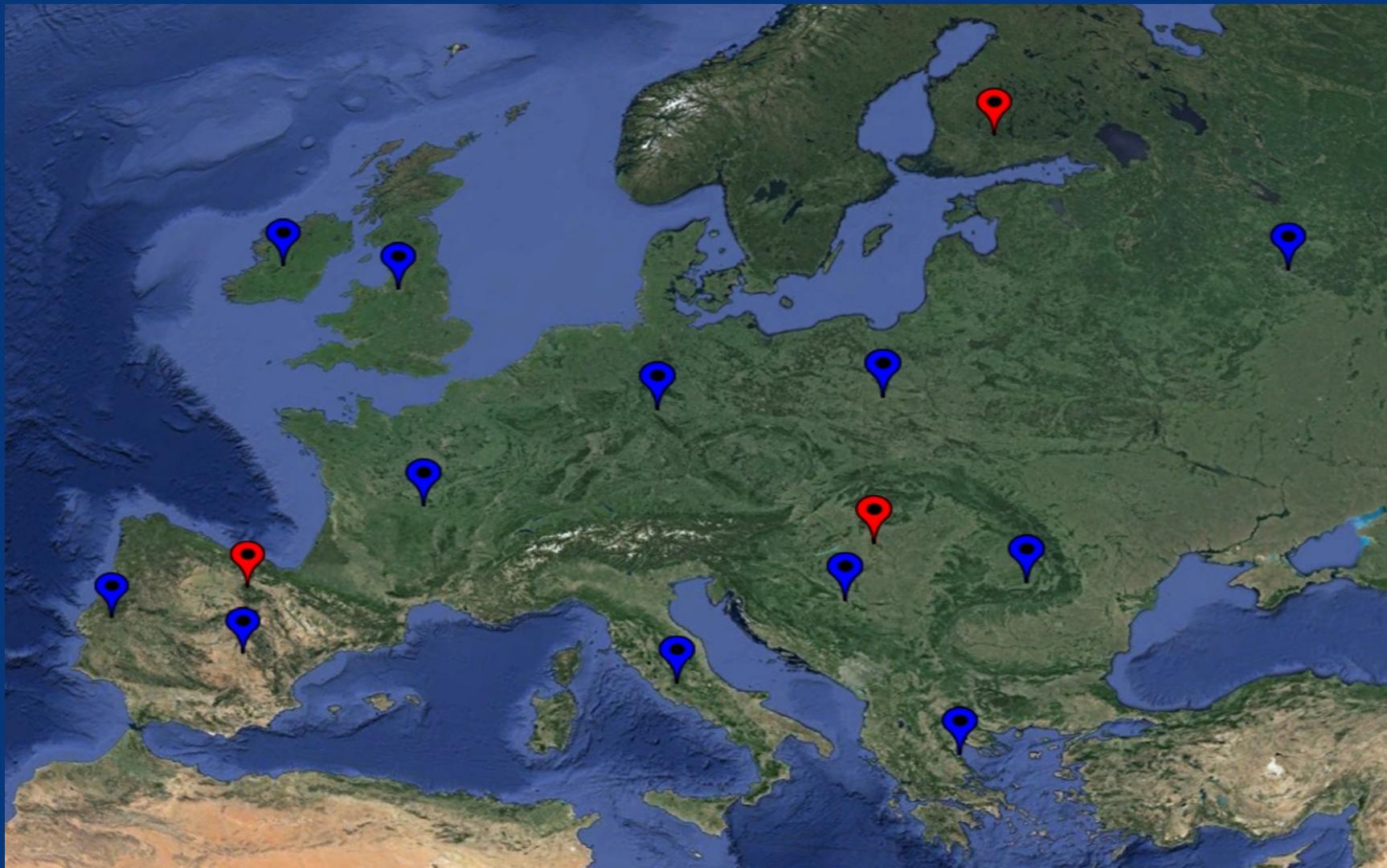
- Expansion/revision of Dyen et al.'s (1992) list of IE cognate words
- Lists actual roots for each meaning (no 1:1 correspondence between meaning and word)
  - Codes for **synonymy**
- Richer device for quantitative experiments on IE lexical diversification

# LEXICAL DISTANCES

	English	German	
<i>fish</i>	+ (fish)	+ (Fisch)	<b>1 identity</b>
<i>breathe</i>	+ (breathe)	-	<b>1 difference</b>
	-	+	<b>1 difference</b>
		(atmen)	

- $D_{LEX} : d/(i+d) = 2/3$
- $D_{LEX} : \text{differences} = 0.5 = 1/2$

# Europe across language families

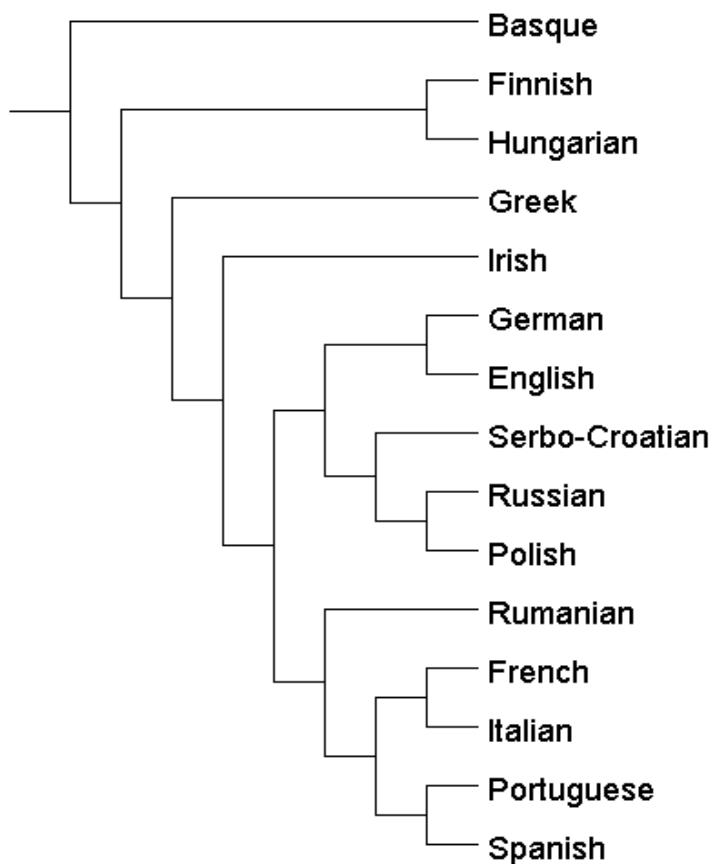


# Syntactic and Lexical distances

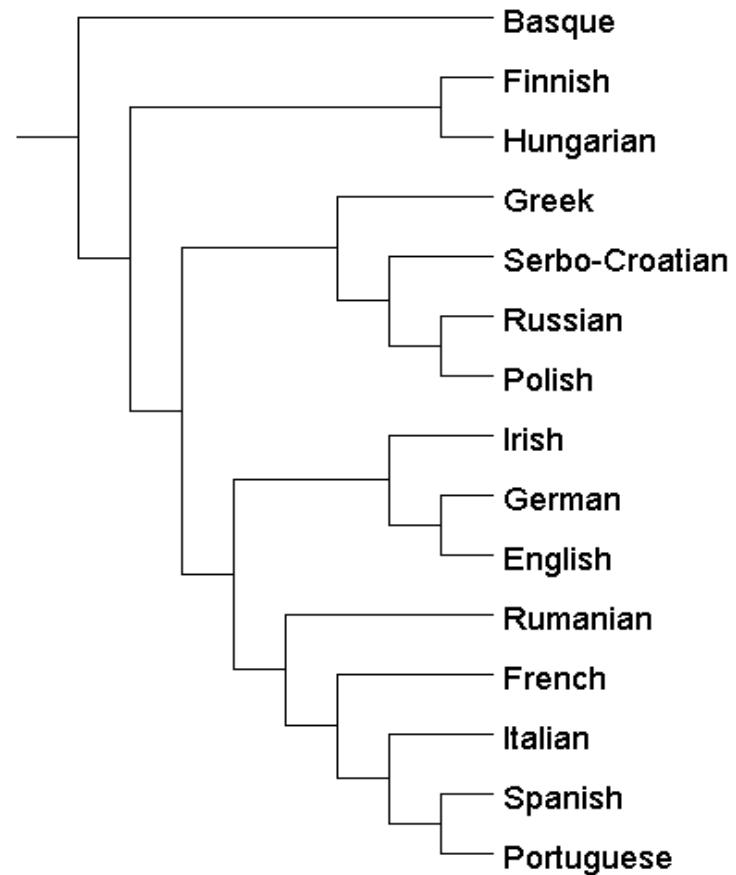
	E	Fr	D	Grk	Ir	It	Po	Ptg	Rm	Rus	SC	Sp
E	0	0.1842	0.0732	0.3	0.1111	0.15	0.2424	0.15	0.2105	0.2424	0.2188	0.175
Fr	0.7193	0	0.1579	0.2895	0.1944	0.0476	0.2333	0.0488	0.1622	0.2667	0.2759	0.0714
D	0.38847	0.73272	0	0.2564	0.1111	0.125	0.1471	0.125	0.25	0.1765	0.1471	0.15
Grk	0.82439	0.82432	0.81124	0	0.2571	0.225	0.1818	0.2564	0.2	0.1818	0.1875	0.25
Ir	0.81074	0.81176	0.81221	0.86456	0	0.2105	0.2143	0.1892	0.2571	0.2143	0.2222	0.1842
It	0.73012	0.23111	0.72889	0.81345	0.80543	0	0.1935	0.0233	0.1026	0.2258	0.2333	0.0682
Po	0.72816	0.77629	0.74944	0.84649	0.83066	0.77489	0	0.1935	0.2333	0.0278	0.0571	0.2258
Ptg	0.76233	0.3431	0.75884	0.83903	0.84615	0.31313	0.78049	0	0.1053	0.2258	0.2333	0.0233
Rm	0.75799	0.44186	0.75476	0.82609	0.84052	0.39468	0.79835	0.44788	0	0.2333	0.2414	0.1026
Rus	0.7201	0.75234	0.74766	0.83562	0.81862	0.75676	0.31519	0.76371	0.77302	0	0.0286	0.2581
SC	0.73298	0.77458	0.76978	0.82028	0.83092	0.76498	0.33488	0.77778	0.78462	0.309	0	0.2667
Sp	0.75	0.30193	0.75589	0.82809	0.82895	0.27122	0.775	0.22505	0.44664	0.76139	0.77728	0

$$r = 0.850$$
$$p = 0.001$$

# Lexical distances



# Syntactic distances



# Genetic Data

## ARTICLE

### The Population Reference Sample, POPRES: A Resource for Population, Disease, and Pharmacological Genetics Research

Matthew R. Nelson,<sup>1,\*</sup> Katarzyna Bryc,<sup>2</sup> Karen S. King,<sup>1</sup> Amit Indap,<sup>2</sup> Adam R. Boyko,<sup>2</sup> John Novembre,<sup>3,4</sup> Linda P. Briley,<sup>1</sup> Yuka Maruyama,<sup>1</sup> Dawn M. Waterworth,<sup>5</sup> Gérard Waerber,<sup>6</sup> Peter Vollenweider,<sup>6</sup> Jorge R. Oksenberg,<sup>7</sup> Stephen L. Hauser,<sup>7</sup> Heide A. Stirnadel,<sup>8</sup> Jaspal S. Koerner,<sup>9</sup> John C. Chambers,<sup>10</sup> Brendan Jones,<sup>1</sup> Vincent Mooser,<sup>5</sup> Carlos D. Bustamante,<sup>2</sup> Allen D. Roses,<sup>1</sup> Daniel K. Burns,<sup>1</sup> Margaret G. Ehm,<sup>1</sup> and Eric H. Lai,<sup>1</sup>

5,886 subjects genotyped at 500,568 loci using the Affymetrix 500K single nucleotide polymorphism (SNP) chip.

Basque

OPEN  ACCESS Fully available online

PLOS GENETICS

### Genomic Ancestry of North Africans Supports Back-to-Africa Migrations

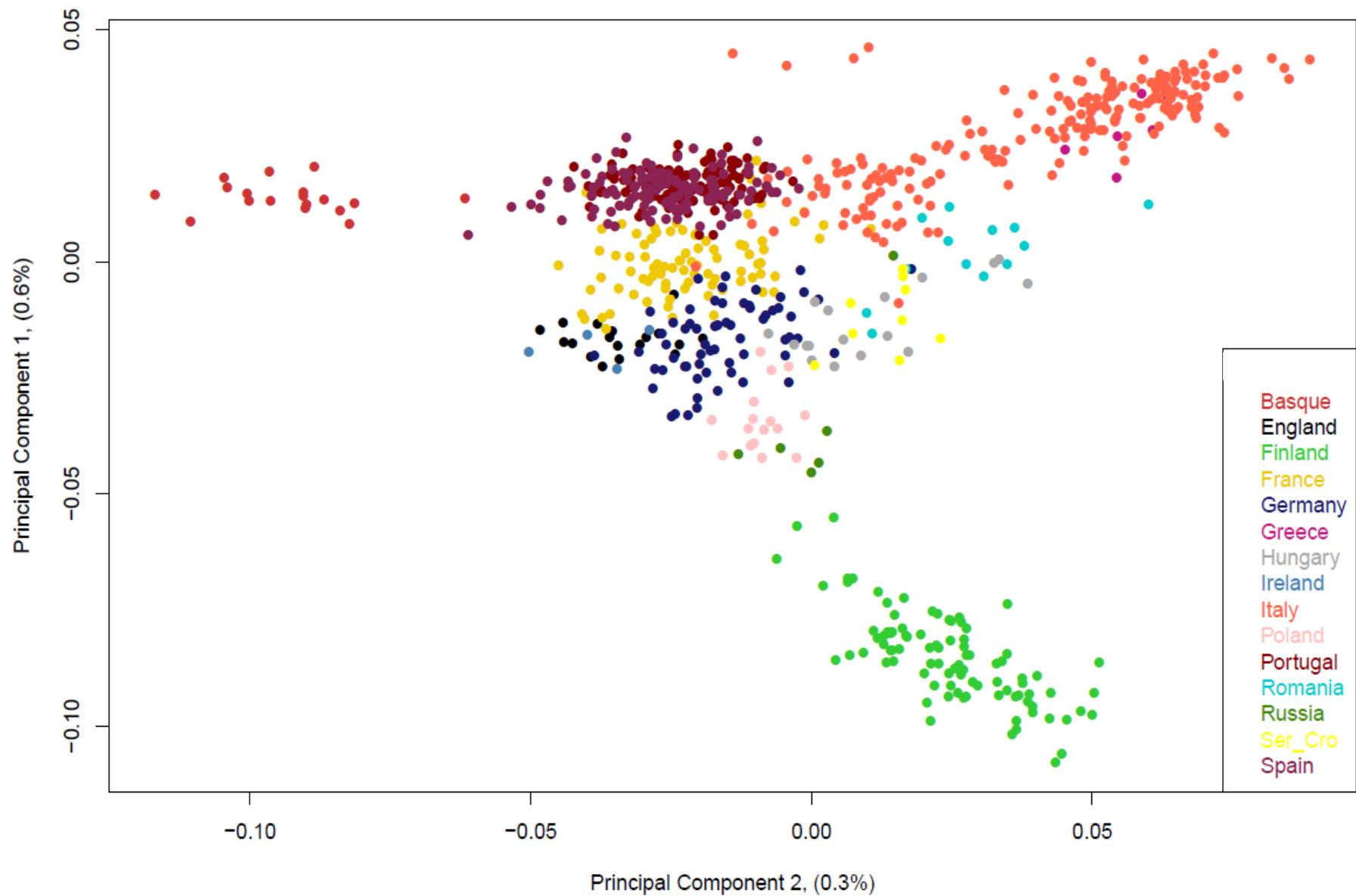
Brenna M. Henn,<sup>1,9</sup> Laura R. Botigué,<sup>2,3</sup> Simon Gravel,<sup>1</sup> Wei Wang,<sup>2</sup> Abra Brisbin,<sup>2</sup> Jake K. Byrnes,<sup>3</sup> Karima Fadhlouli-Zid,<sup>4</sup> Pierre A. Zalloua,<sup>5</sup> Andres Moreno-Estrada,<sup>1</sup> Jaume Bertranpetti,<sup>2</sup> Carlos D. Bustamante,<sup>1,\*</sup> David Comas,<sup>2,6</sup>

<sup>1</sup> Department of Genetics, Stanford University, Stanford, California, United States of America, <sup>2</sup> Institute of Evolutionary Biology (CSC-UPF), Universitat Pompeu Fabra, Barcelona, Spain, <sup>3</sup> Department of Biological Statistics and Computational Biology, Cornell University, Ithaca, New York, United States of America, <sup>4</sup> Laboratory of Genetics, Immunology, and Human Pathology, University Tunis El Manar, Tunis, Tunisia, <sup>5</sup> The Lebanese American University, Beirut, Lebanon

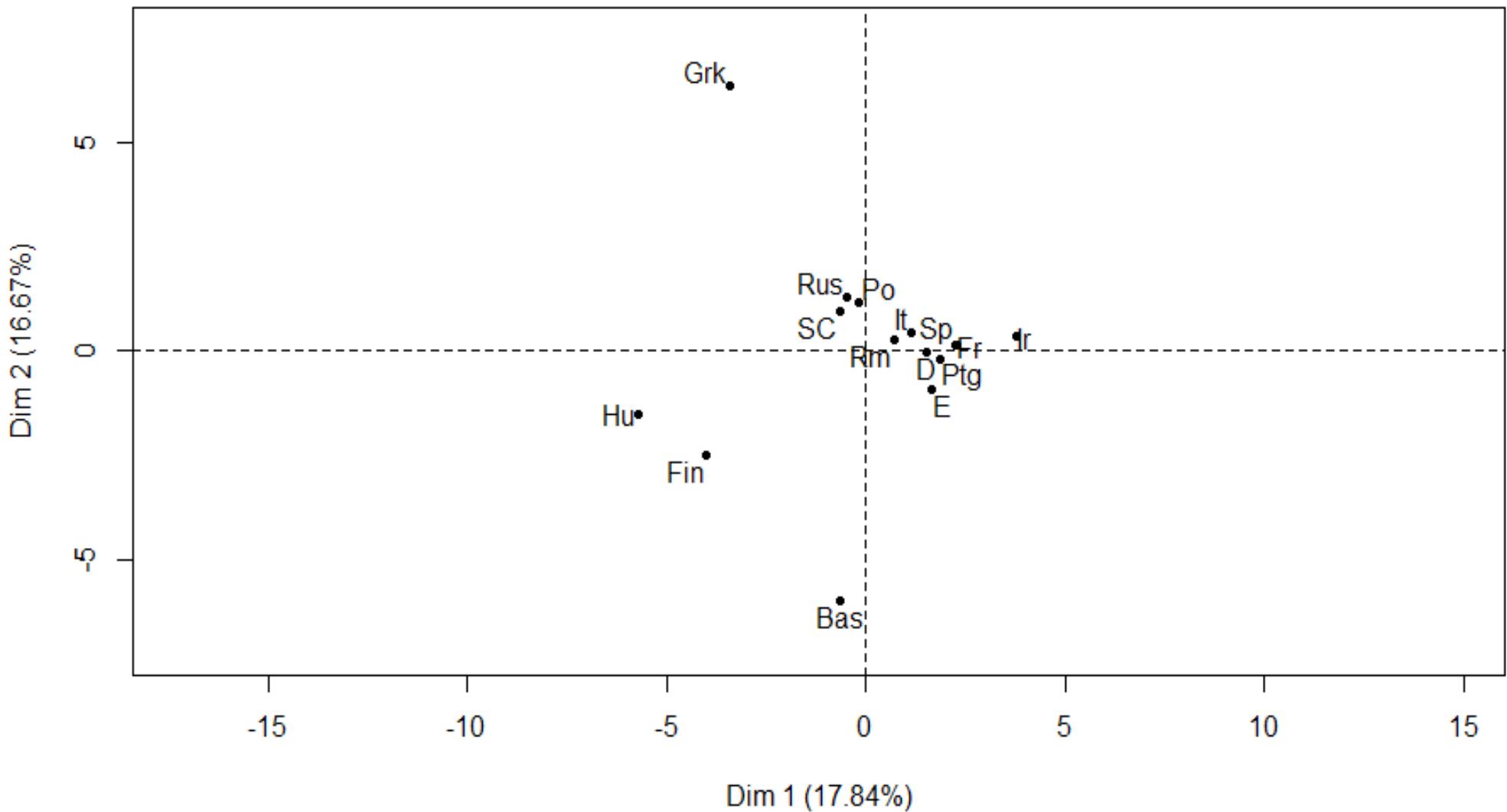


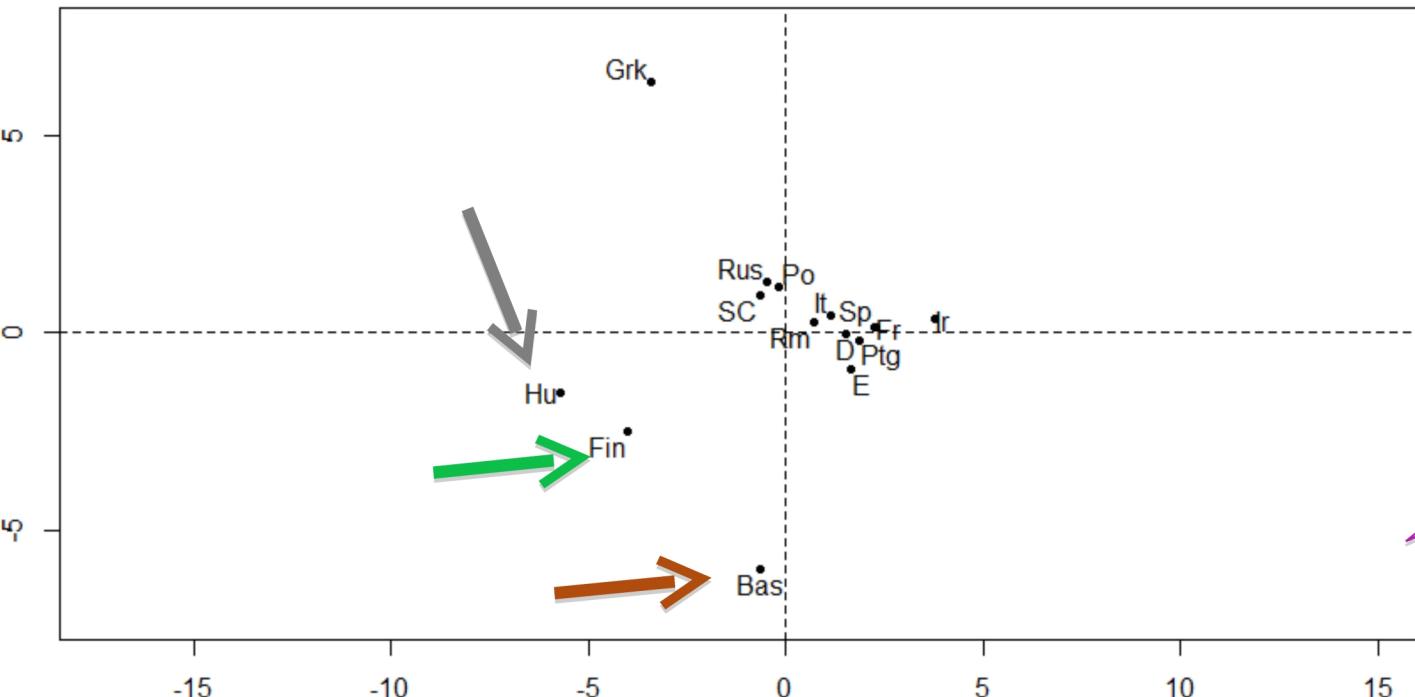
Finnish





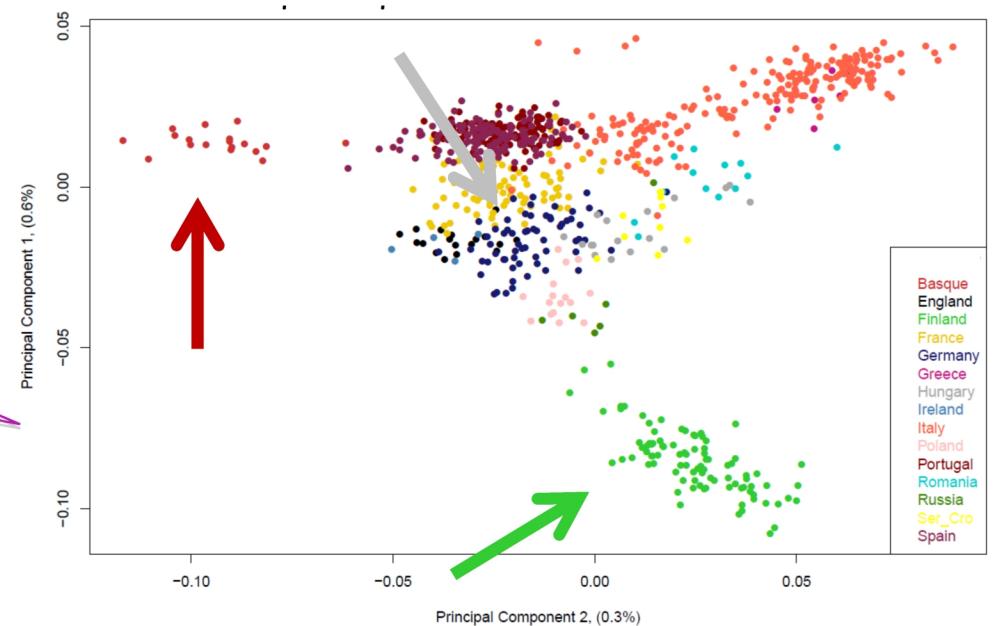
## Individuals factor map (PCA)



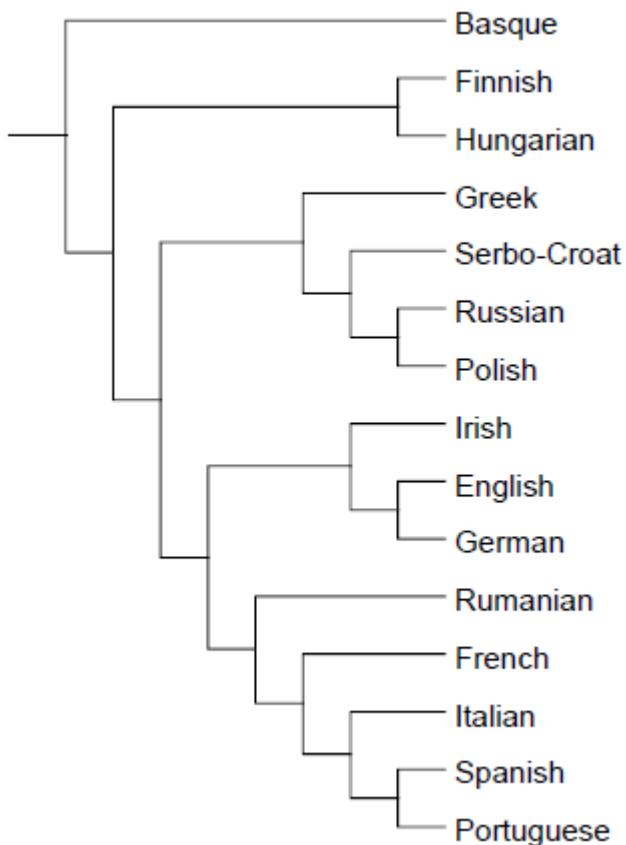


Syntactic distances

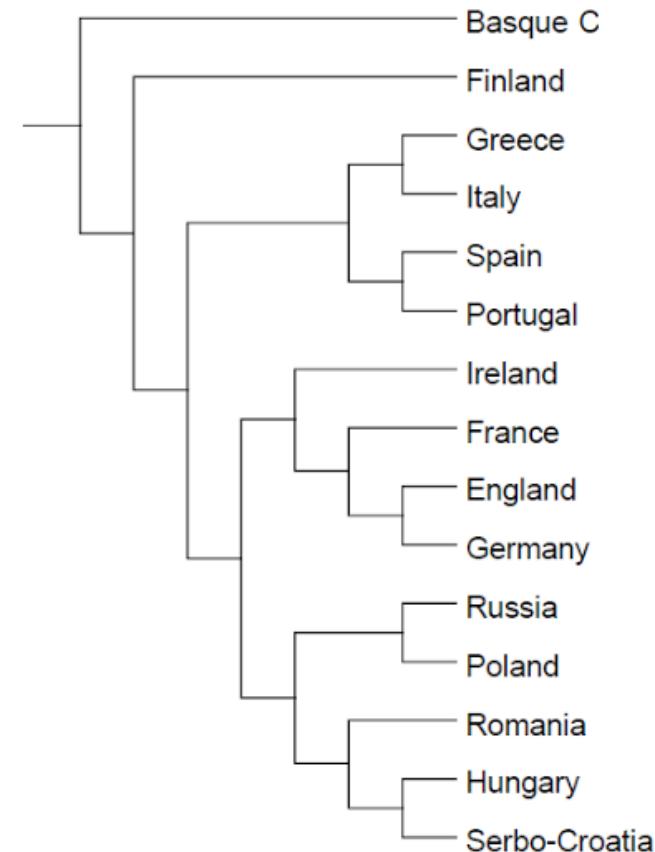
Genetic distances



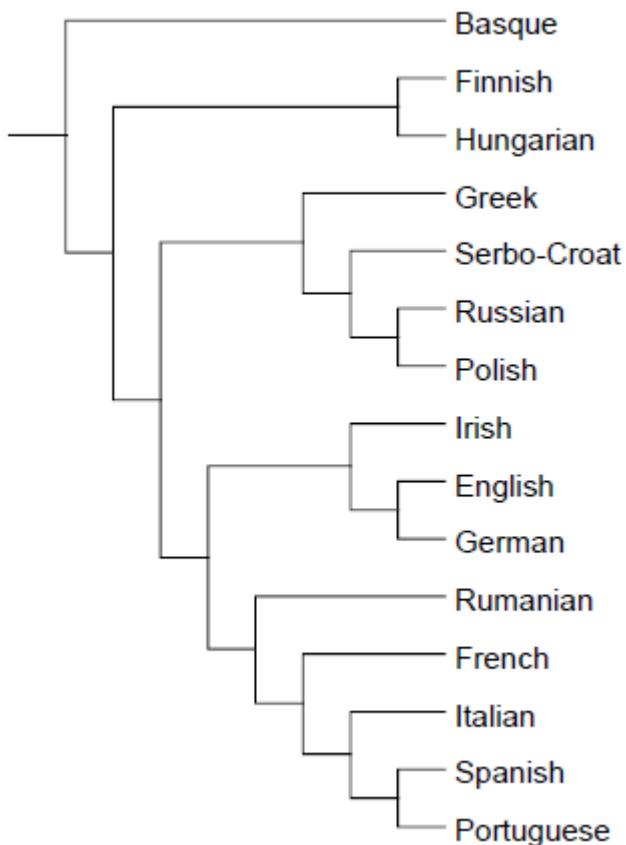
# Syntactic distances



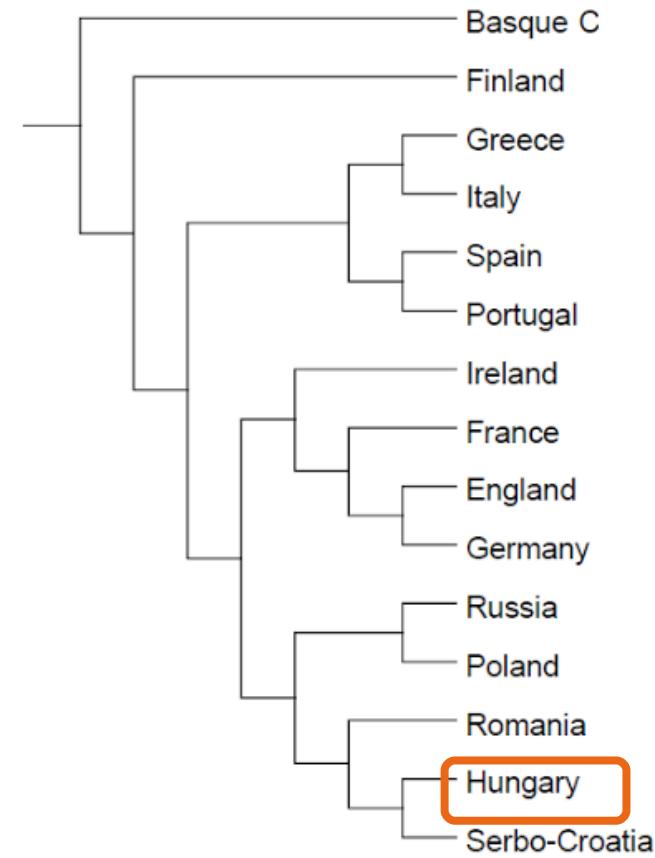
# Genetic distances

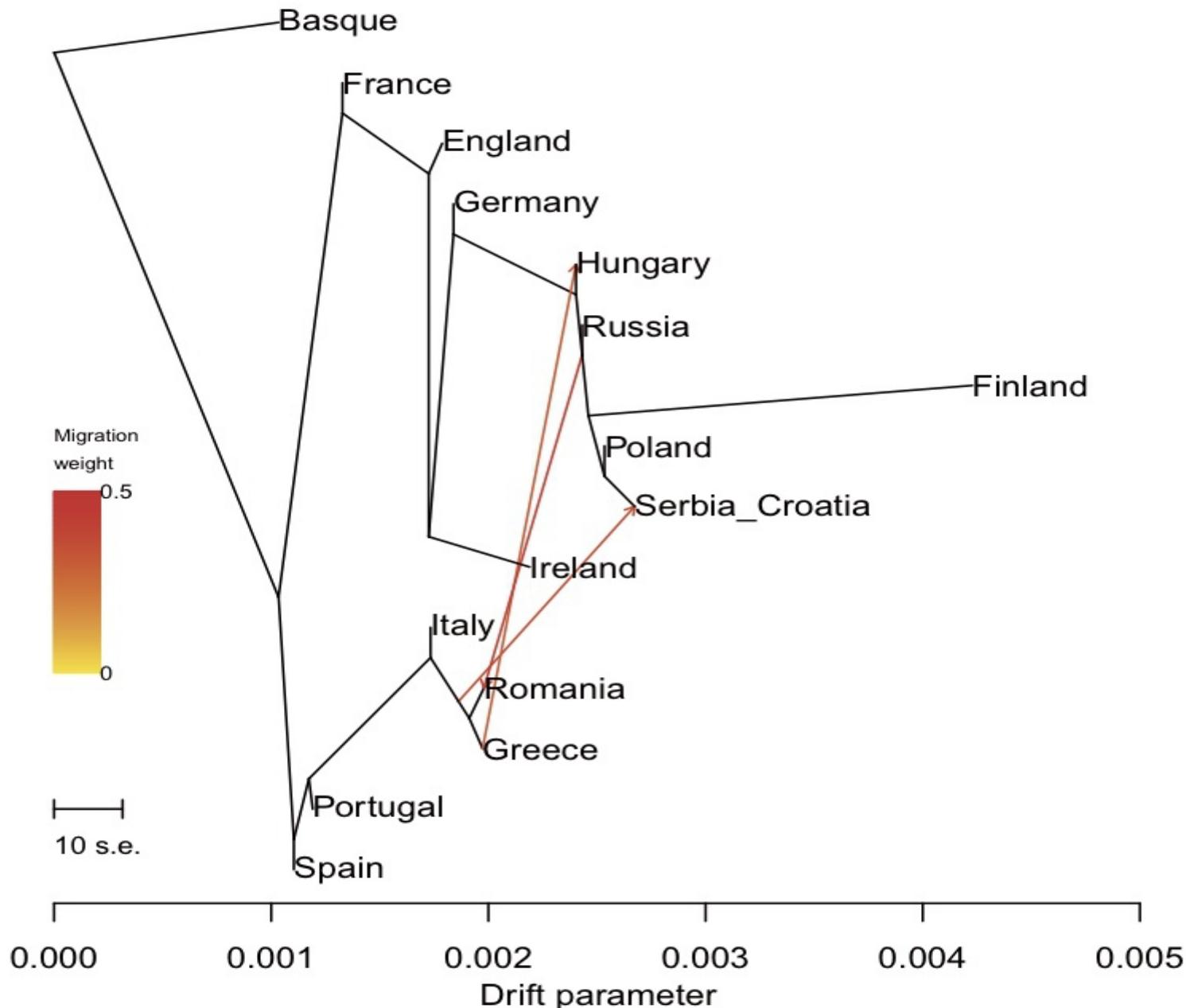


# Syntactic distances



# Genetic distances

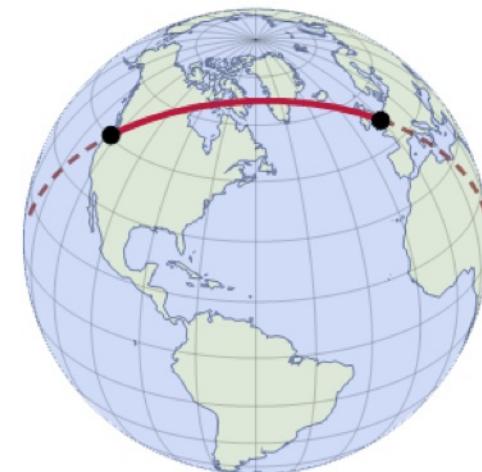


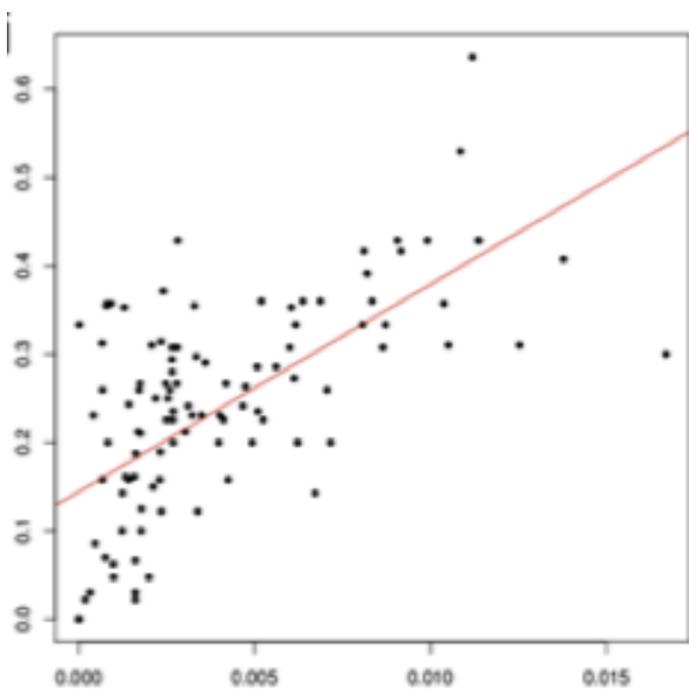
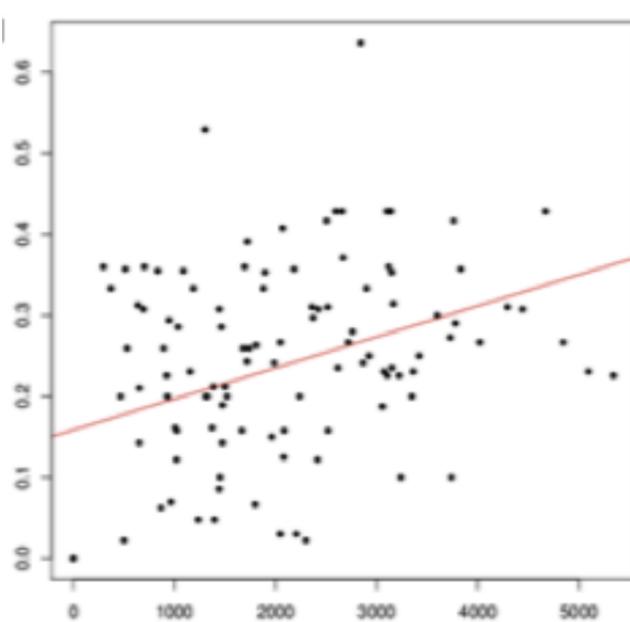
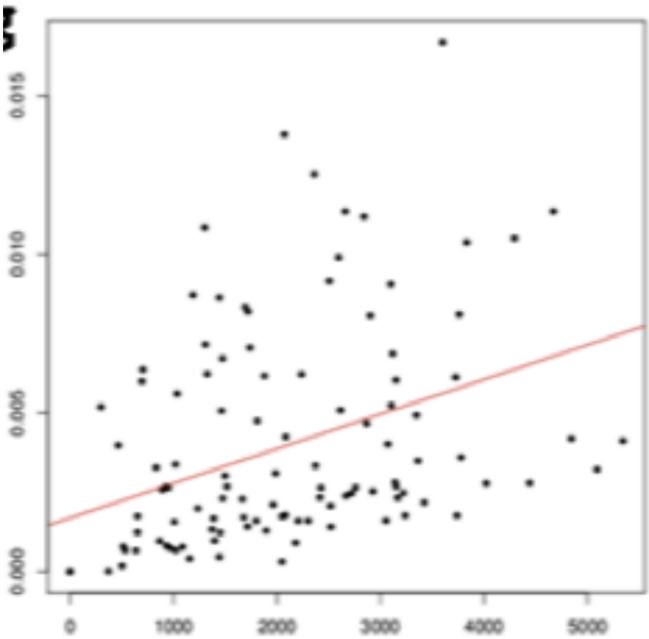


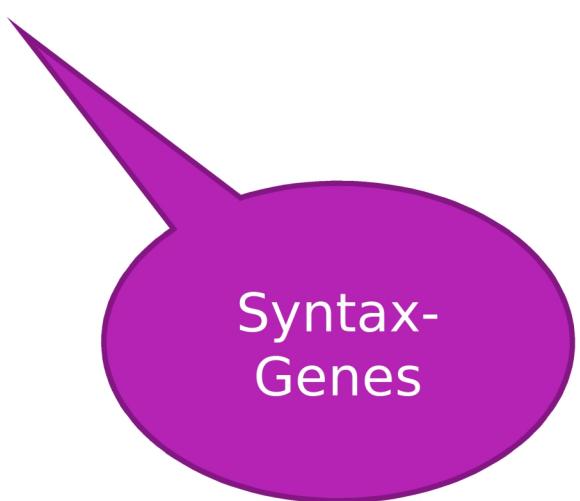
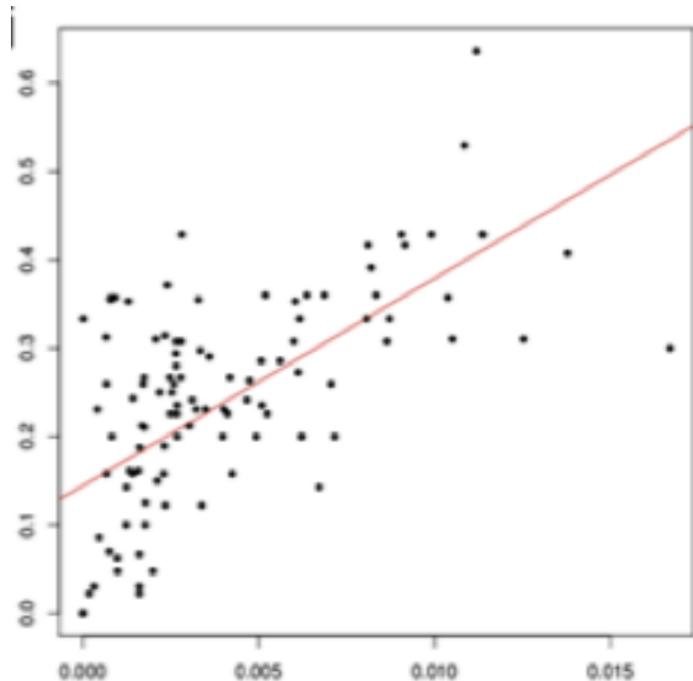
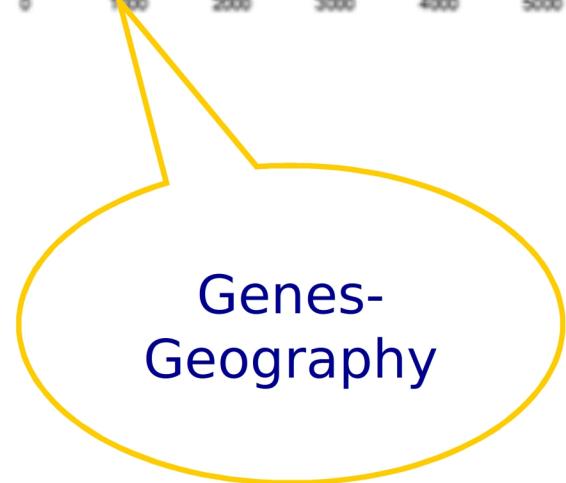
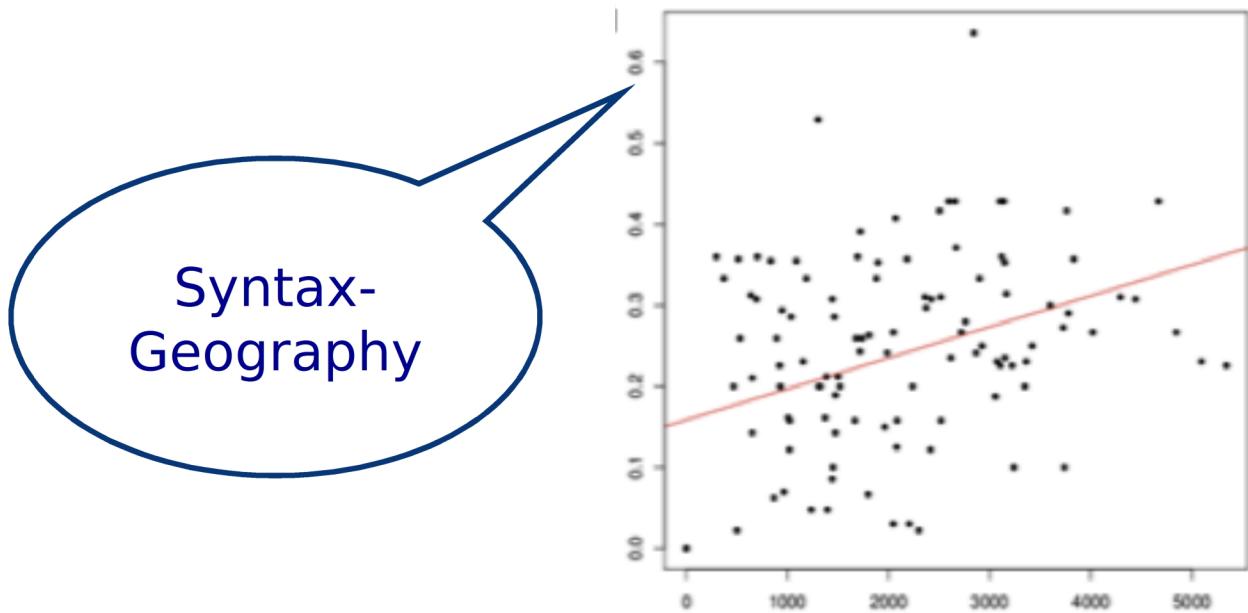
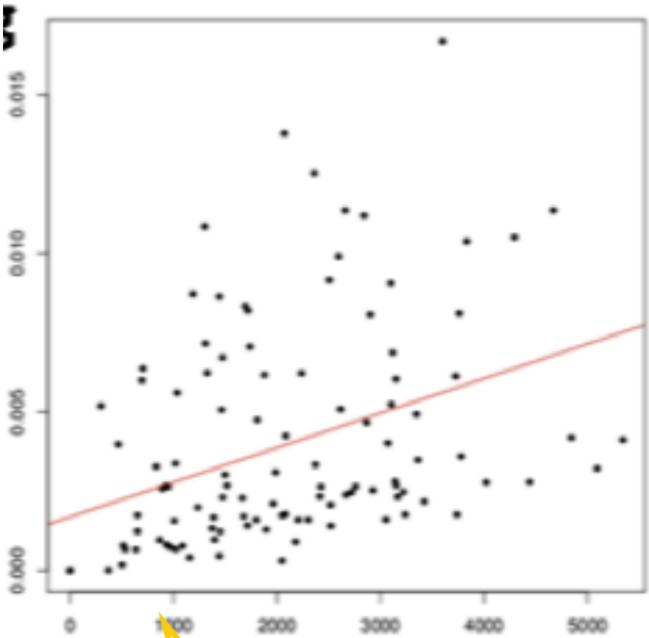
## Geographic distances

Great Circle Distances (the shortest distance between two points on the surface of a sphere)

	<b>Basque</b>	<b>England</b>	<b>Finland</b>	<b>France</b>	<b>Germany</b>	<b>Greece</b>	<b>Hungary</b>	<b>Ireland</b>	<b>Italy</b>	<b>Poland</b>	<b>Portugal</b>	<b>Romania</b>	<b>Russia</b>	<b>Ser_Cro</b>	<b>Spain</b>
<b>Basque</b>	0														
<b>England</b>	1187.32	0													
<b>Finland</b>	3598.33	3116.53	0												
<b>France</b>	703.27	930.48	2900.12	0											
<b>Germany</b>	1720.55	1441.89	1879.06	1021.06	0										
<b>Greece</b>	2842.08	3148.58	2070.09	2370.7	1808.53	0									
<b>Hungary</b>	2504.1	2515.3	1472.55	1894.75	1086.01	833.19	0								
<b>Ireland</b>	1301.76	652.09	3760.08	1386.19	2081.45	3726.67	3140.04	0							
<b>Italy</b>	1692.39	2083.82	2359.24	1234.44	1019.94	1155.1	948.34	2614.46	0						
<b>Poland</b>	2659.05	2423.91	1035.1	1986.03	1007.66	1309.18	514.5	3072.68	1325.44	0					
<b>Portugal</b>	693.88	1665.57	4292.19	1395.39	2414.33	3420.15	3164.26	1498.94	2299.75	3346.22	0				
<b>Romania</b>	3099.24	3151.21	1442.74	2518.15	1715.71	652.92	637.63	3777.63	1450.7	892.46	3738.87	0			
<b>Russia</b>	4669.32	4440.39	1463.4	4020.28	3053.41	2236.19	2181.1	5092.48	3103.42	2046.74	5340.66	1678.13	0		
<b>Ser_Cro</b>	2594.25	2759.21	1739.13	2048.29	1372.57	466.32	370.15	3361.71	924.19	868.04	3220.66	531.06	2204.72	0	
<b>Spain</b>	298.17	1473.97	3830.7	965.2	1962.6	2924.66	2666.35	1517.52	1798.83	2864.87	501.42	3237.63	4845.04	2719.27	0





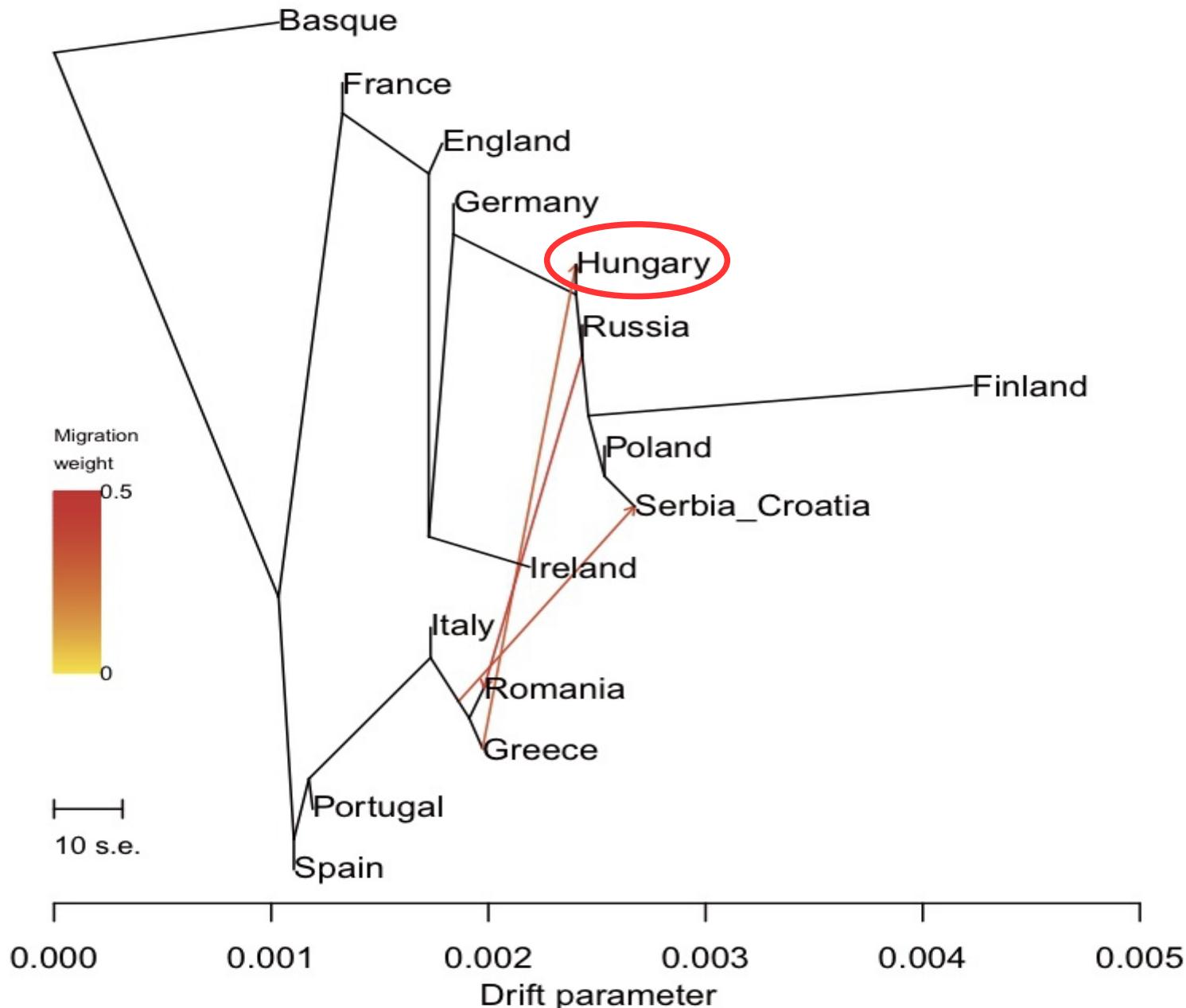


Syntax-  
Geography

Genes-  
Geography

Syntax-  
Genes

Distance matrices	<i>r</i>	<i>P</i>
$d_{\text{GEN}} d_{\text{GEO}}$ Genetic - Geographic	0.299	0.030
$d_{\text{SYN}} d_{\text{LEX}}$ Syntactic - Lexical	0.850	0.001
$d_{\text{SYN}} d_{\text{GEO}}$ Syntactic - Geographic	0.240	0.039
$d_{\text{LEX}} d_{\text{GEO}}$ Lexical - Geographic	0.084	0.264
$d_{\text{SYN}} d_{\text{GEN}}$ Syntactic - Genetic	0.599	0.001
$d_{\text{LEX}} d_{\text{GEN}}$ Lexical - Genetic	0.537	0.001
$d_{\text{GEN}} d_{\text{GEO}} (d_{\text{SYN}})$ Genetic - Geographic (Syntax held constant)	0.200	0.114
$d_{\text{GEN}} d_{\text{GEO}} (d_{\text{LEX}})$ Genetic - Geographic (Lexicon held constant)	0.302	0.035
$d_{\text{SYN}} d_{\text{GEO}} (d_{\text{GEN}})$ Syntactic - Geographic (Genetics held constant)	0.079	0.264
$d_{\text{LEX}} d_{\text{GEO}} (d_{\text{GEN}})$ Lexical - Geographic (Genetics held constant)	-0.095	0.736
$d_{\text{SYN}} d_{\text{GEN}} (d_{\text{GEO}})$ Syntactic - Genetic (Geography held constant)	0.570	0.002
$d_{\text{LEX}} d_{\text{GEN}} (d_{\text{GEO}})$ Lexical - Genetic (Geography held constant)	0.538	0.001



## Europe's diversity without Hungary

G. Tömöry, B. Csányi, E. Bogácsi-Szabó, T. Kalmár, A. Czibula, A. Csosz, K. Priskin, B. Mende, P. Langó, C. S. Downes, and I. Raskó. (2007) **Comparison of maternal lineage and biogeographic analyses of ancient and modern Hungarian populations.** *American Journal of Physical Anthropology* 134:354-368

Ancient DNA in Hungary shows a **predominance of European mitochondrial haplotypes** in burials attributed to the **lower classes**, and a **high incidence of Asian haplotypes in high-status individuals** of the tenth century, which points to the **Asian immigrants** as representing a **social elite**, rather than the bulk of the population

Distance matrices	<i>r</i>	<i>P</i>
$d_{GEN} d_{GEO}$ Genetic - Geographic	0.275	0.048
$d_{SYN} d_{LEX}$ Syntactic - Lexical	0.850	0.001
$d_{SYN} d_{GEO}$ Syntactic - Geographic	0.291	0.026
$d_{LEX} d_{GEO}$ Lexical - Geographic	0.152	0.144
$d_{SYN} d_{GEN}$ Syntactic - Genetic	0.740	0.001
$d_{LEX} d_{GEN}$ Lexical - Genetic	0.687	0.001
$d_{GEN} d_{GEO} (d_{SYN})$ Genetic - Geographic (Syntax held constant)	0.093	0.254
$d_{GEN} d_{GEO} (d_{LEX})$ Genetic - Geographic (Lexicon held constant)	0.238	0.083
$d_{SYN} d_{GEO} (d_{GEN})$ Syntactic - Geographic (Genetics held constant)	0.135	0.178
$d_{LEX} d_{GEO} (d_{GEN})$ Lexical - Geographic (Genetics held constant)	-0.053	0.615
$d_{SYN} d_{GEN} (d_{GEO})$ Syntactic - Genetic (Geography held constant)	0.717	0.001
$d_{LEX} d_{GEN} (d_{GEO})$ Lexical - Genetic (Geography held constant)	0.679	0.001

# CONCLUSIONS

- A few dozen high quality syntactic features single out the 3 linguistic components of modern Europe **without any appeal to words and meaning**
- Combined with genetic information, they are able to tell us of the **secondary character** of one fraction of one of these components (Ugric)
- The demonstration that syntax **distributes along with independent space/time-bound variables** is FULLY COMPATIBLE with its being cast within a universal grammar framework

THANKS!  
Grazie!