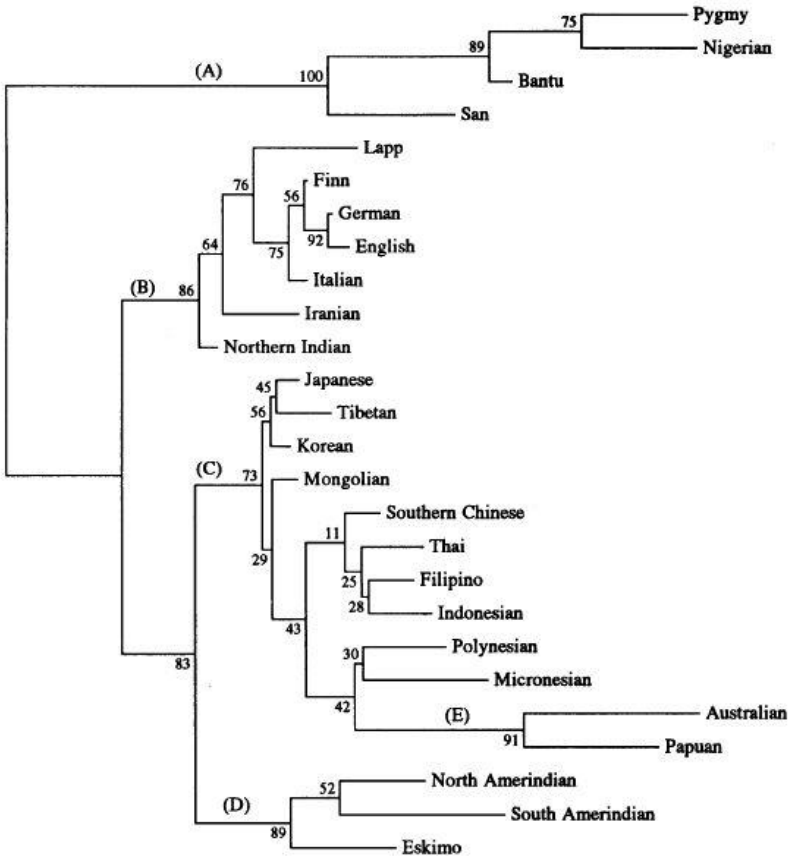
1,2,3, language!



Andrew Berdahl, Lucas Lacasa
SFI – CSSS '09

The idea

DATASET: numbers 1 to 10 in over 5,000 languages
http://zompist.com/numbers.shtml

- **Mapping between alphabet and DNA-like codons**
  - **Alphabet-based (Hamming-like)**
  - **Phonetic-based**
  - **Feature-based**

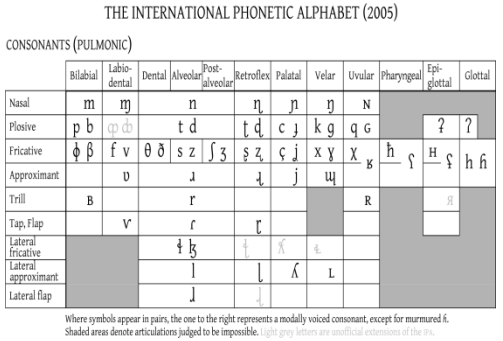
- **Use of evolutionary biology measures to quantify the distance between 2 strings**
  - **Global sequence allignment methods**

- **Generate the distance matrix between languages and its associated phylogenetic tree**

- **Compare with state of the art results**
  - **Are we able to deduce the language phylogenetic tree from "so few data"?**
  - **Importance of numbers within a language: fundamental quantity?**
  - **Relation to culture-based concepts (trading, etc)**

- **Relate with invasion-like spreading of culture**

Alphabet mapping: criteria



- Each letter maps into a 3-nucleotide string from {A,T,C,G}
- Phonetic and feature-based properties are encoded in the mapping
- We finally have a new alphabet: each of the 26 letters is a 3-nucleotide string
- We concatenate the numbers in a single string
- We make global sequence allignment

The mapping recipe

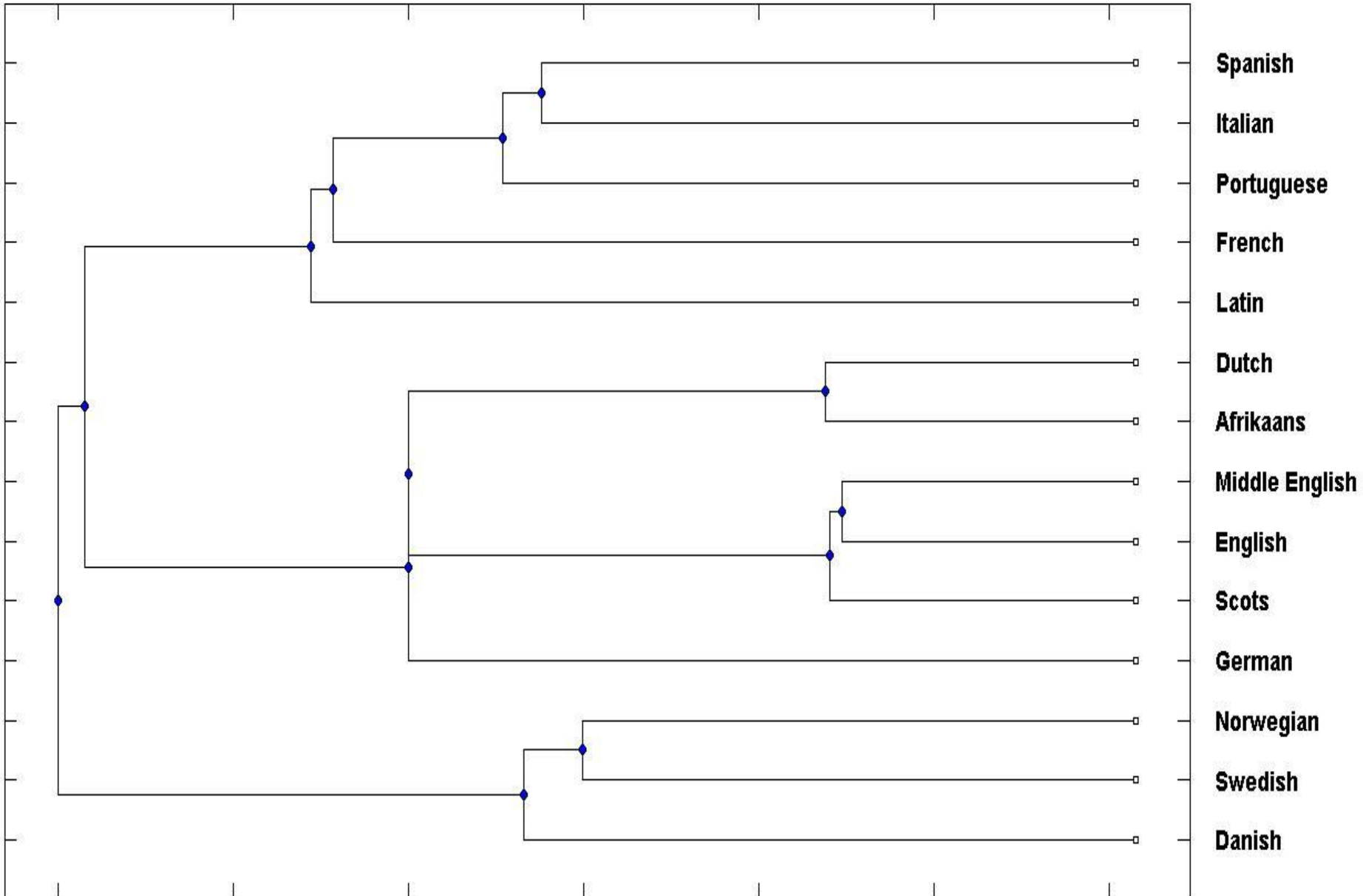
A	AAA
E	ACA
I	AGA
O	ATA
U	ATC
Y	AGG

B	CGT
P	CGA
V	CGG
F	CAG
W	AGG

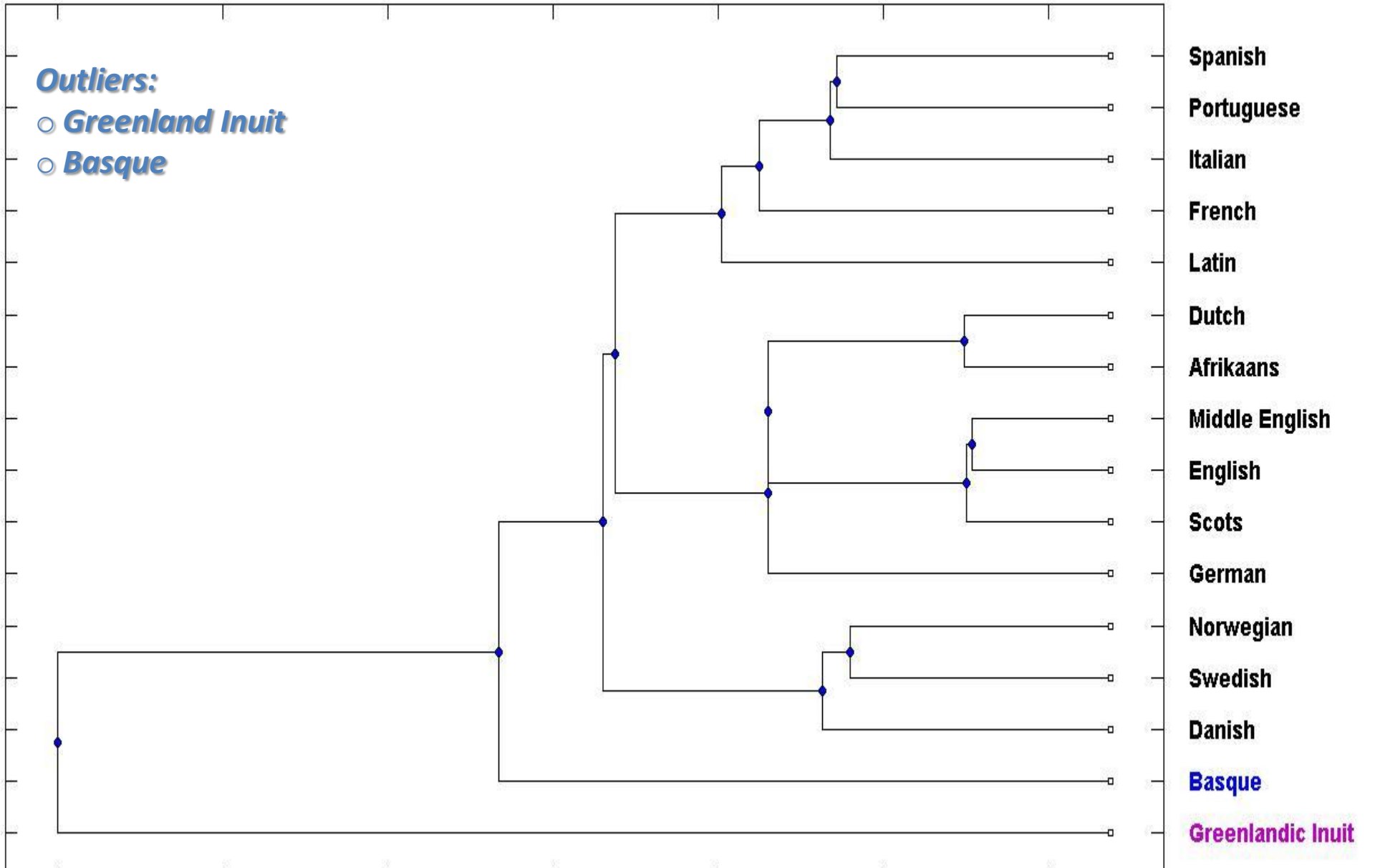
C	GTA
D	GAA
T	GTT
Z	GTG

S	ATG
X	TTG
H	TTT
L	CCC
M	CTA
N	CTC
R	AGC

Results (I): subset of 'familiar' languages: ***WORKS!***



Results (II): detecting the outliers: *WORKS!*



Conclusions and future directions

- ✓ Even with such small amount of data (10 numbers!!), results are promising
- ✓ Refine mapping criteria to take into account different linguistic properties
- ✓ Extend to different alphabets

ACKNOWLEDGMENTS: D.E. Smith (SFI)