

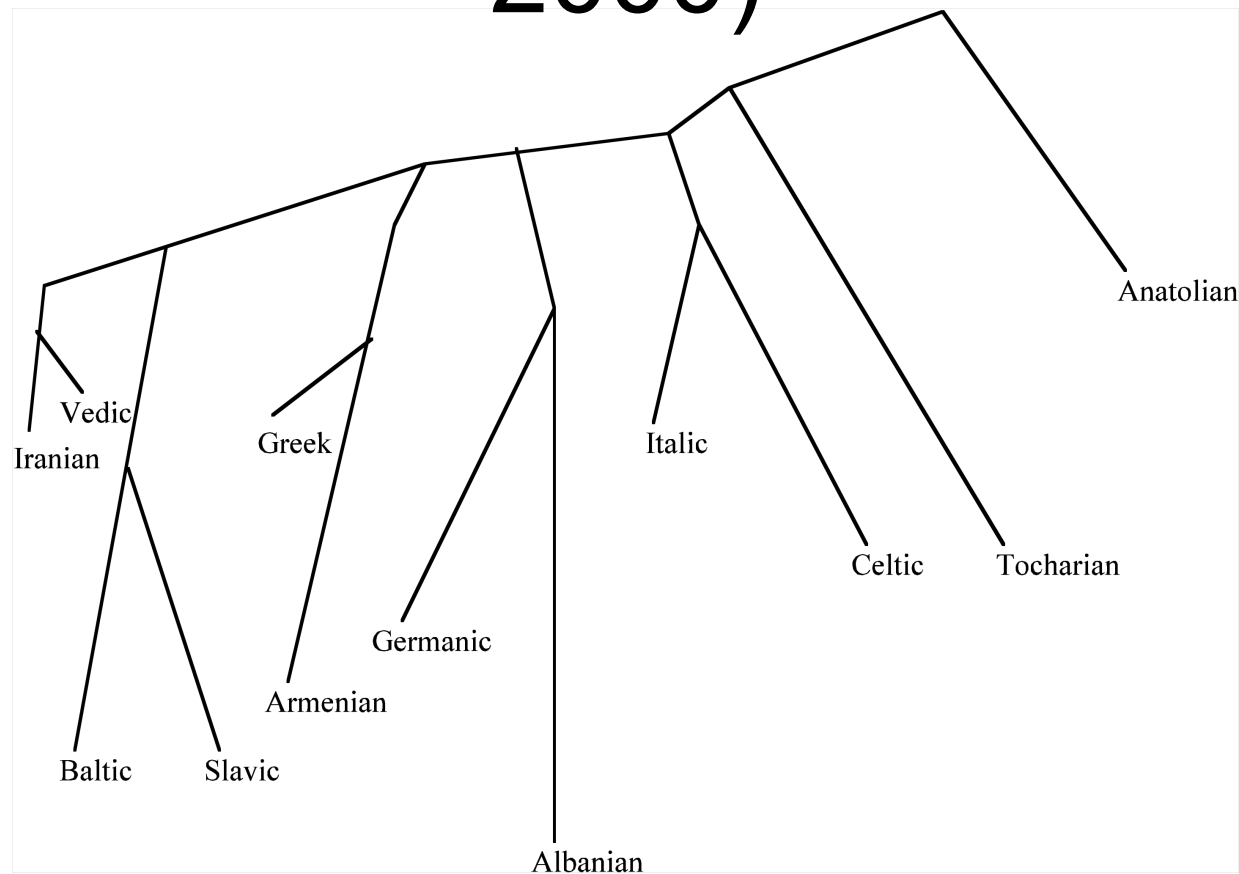
# Phylogeny Reconstruction Methods in Linguistics

Tandy Warnow

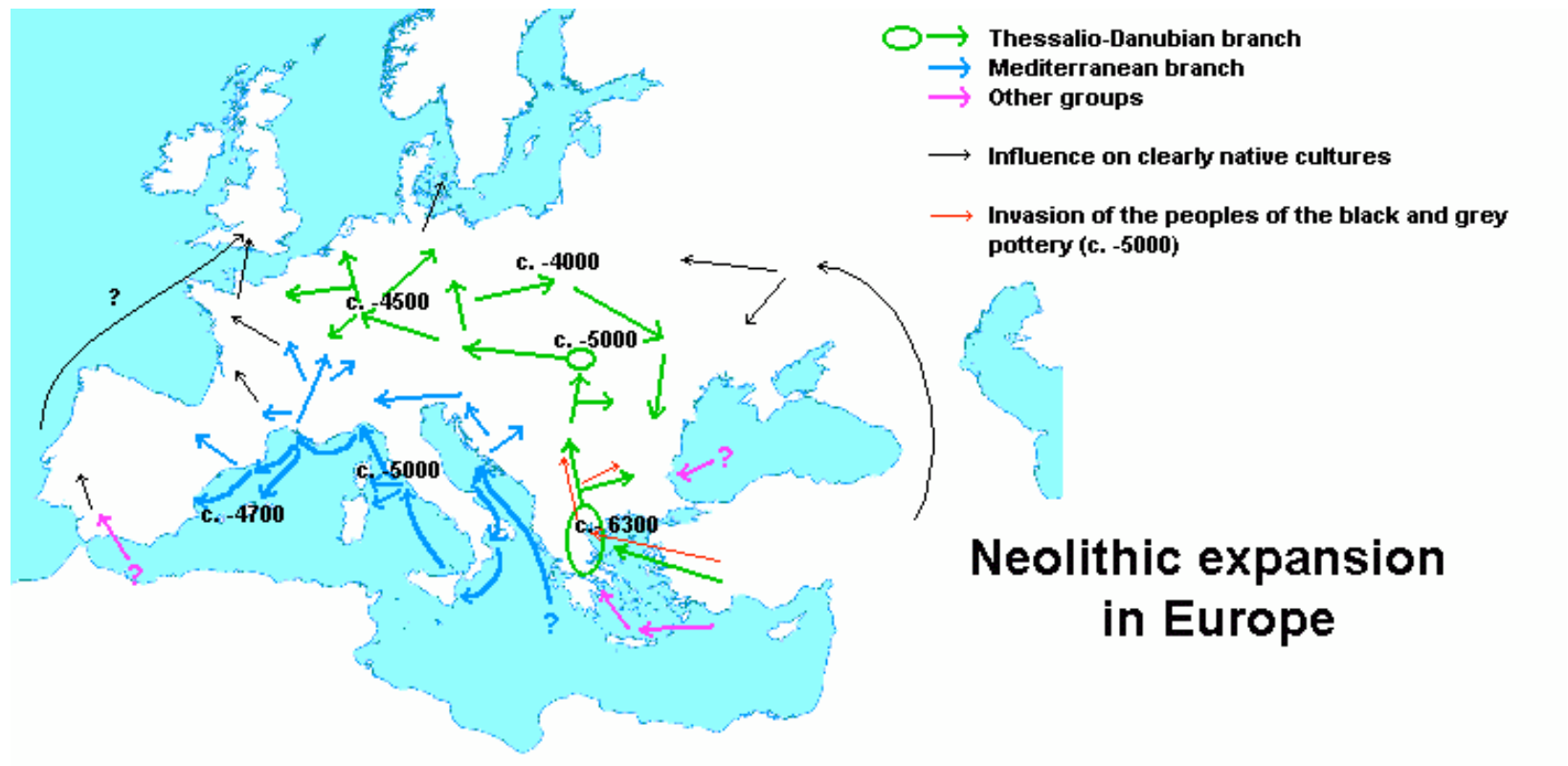
The University of Texas at Austin

with Francois Barbancon, Steve Evans,  
Luay Nakhleh, Don Ringe, and Ann Taylor

# Possible Indo-European tree (Ringe, Warnow and Taylor 2000)



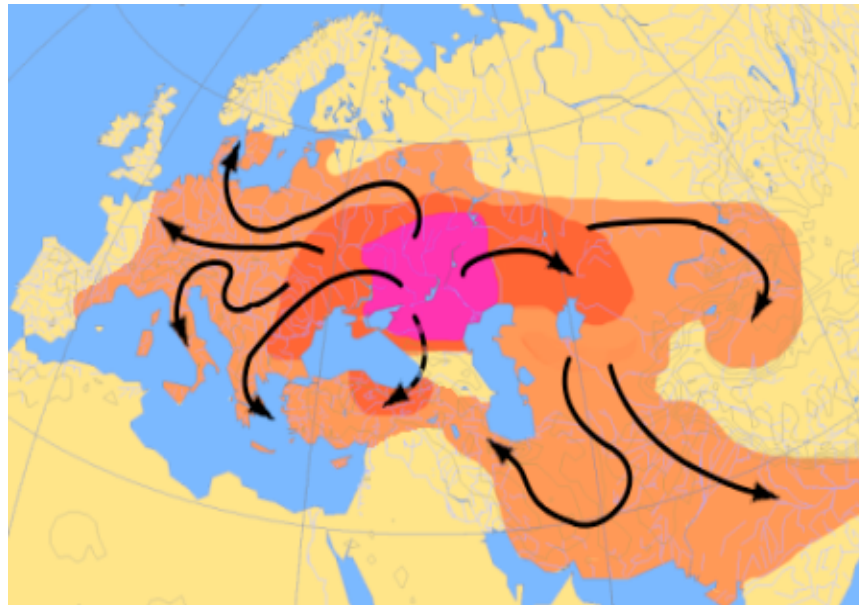
# The Anatolian hypothesis (from wikipedia.org)



Date for PIE ~7000 BCE

# The Kurgan Expansion

- Date of PIE ~4000 BCE.
- Map of Indo-European migrations from ca. 4000 to 1000 BC according to the Kurgan model
- From <http://indo-european.eu/wiki>



# Controversies for IE history

- Subgrouping: Other than the 10 major subgroups, what is likely to be true? In particular, what about
  - Italo-Celtic
  - Greco-Armenian
  - Anatolian + Tocharian
  - Satem Core (Indo-Iranian and Balto-Slavic)
  - Location of Germanic
- Dates?
- PIE homeland?
- How tree-like is IE?

# Estimating the date and homeland of the proto-Indo-Europeans (PIE)

- Step 1: Estimate the phylogeny
- Step 2: Reconstruct words for PIE (and for intermediate proto-languages)
- Step 3: Use archaeological evidence to constrain dates and geographic locations of the proto-languages

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# This talk

- Linguistic data
- Ringe-Warnow-Taylor tree for IE
- Nakhleh, Ringe and Warnow IE network
- Comparison of different phylogenetic analyses of Indo-European
- Simulation study
- Future work

# Lexical data (word lists)

**An Indo-European lexical character: 'hand'.**

**Data.**

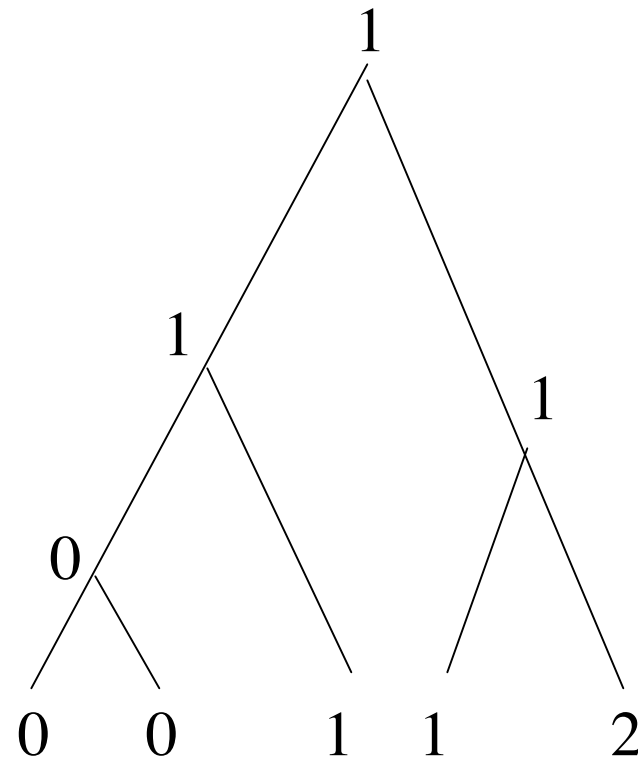
Hittite	kissar	Lithuanian	rankà	Old Prussian	rānkan (acc.)
Armenian	jeřn	Old English	hand	Latvian	ròka
Greek	xeřr /k <sup>h</sup> é:r/	Old Irish	lám	Gothic	handus
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# Historical Linguistic Data

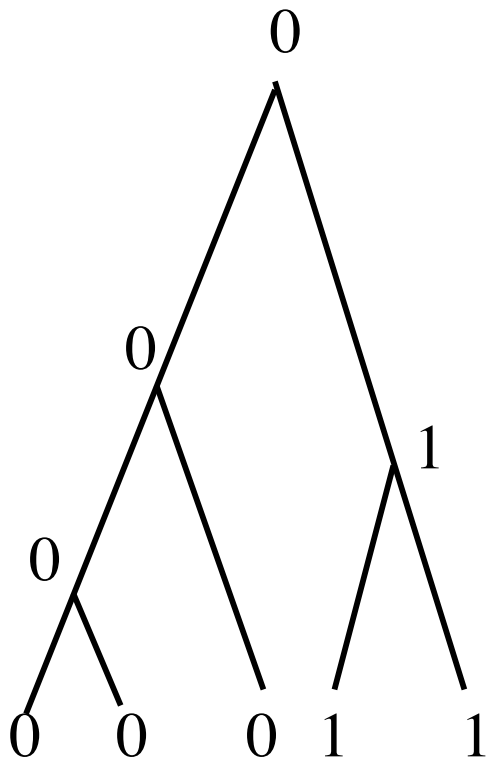
- A character is a function that maps a set of languages,  $L$ , to a set of states.
- Three kinds of characters:
  - Phonological (sound changes)
  - Lexical (meanings based on a wordlist)
  - Morphological (especially inflectional)

# Homoplasy-free characters

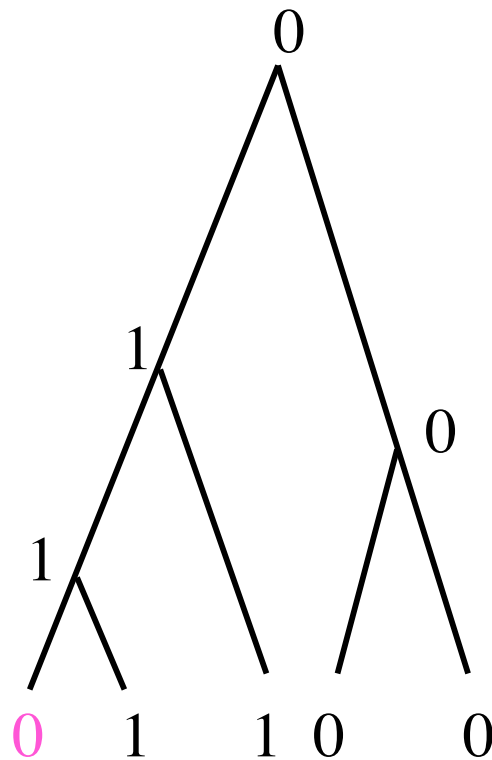
- When the character changes state, it evolves without borrowing, parallel evolution, or back-mutation
- These characters are “compatible on the true tree”



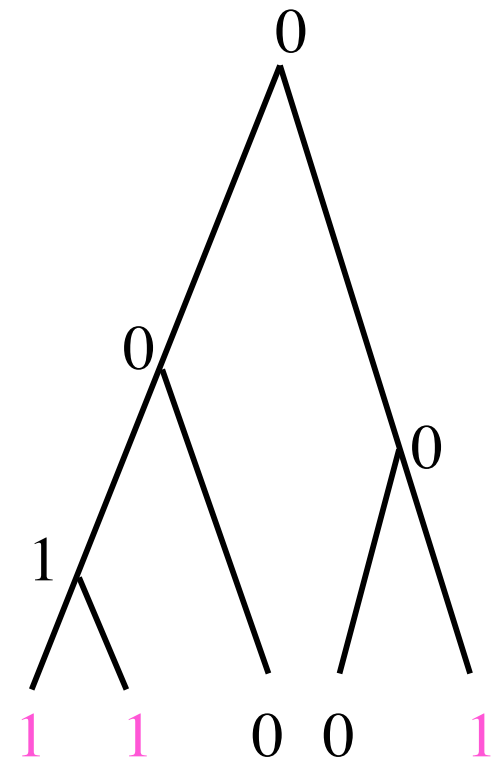
# Homoplastic Evolution



no homoplasy



back-mutation



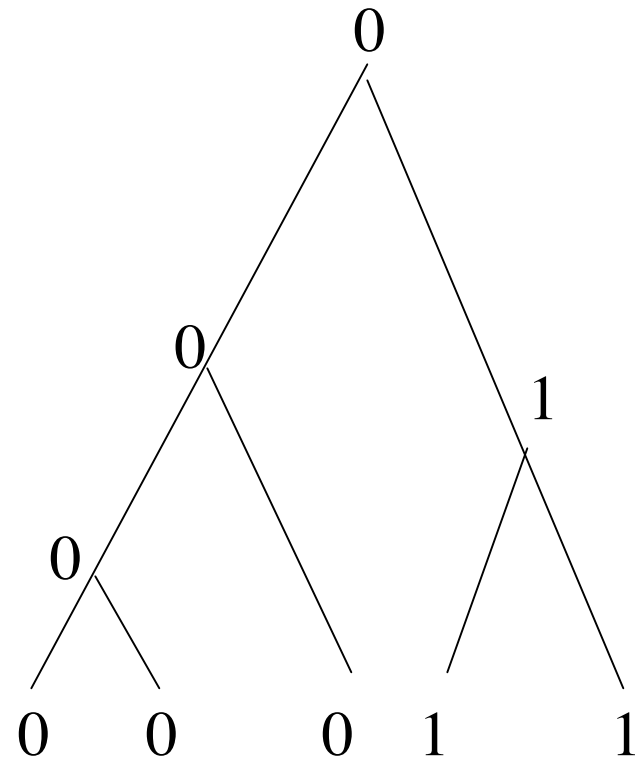
parallel evolution

# Sound changes

- Many sound changes are natural, and should not be used for phylogenetic reconstruction.
- Others are bizarre, or are composed of a sequence of simple sound changes. These are useful for subgrouping purposes.
- Grimm's Law:
  1. Proto-Indo-European voiceless stops change into voiceless fricatives.
  2. Proto-Indo-European voiced stops become voiceless stops.
  3. Proto-Indo-European voiced aspirated stops become voiced fricatives.

# Indo-European subgrouping based upon homoplasy-free characters

- First inferred for *weird innovations* in phonological characters and morphological characters in the 19th century
- Used to establish all the major subgroups within Indo-European



# Indo-European languages

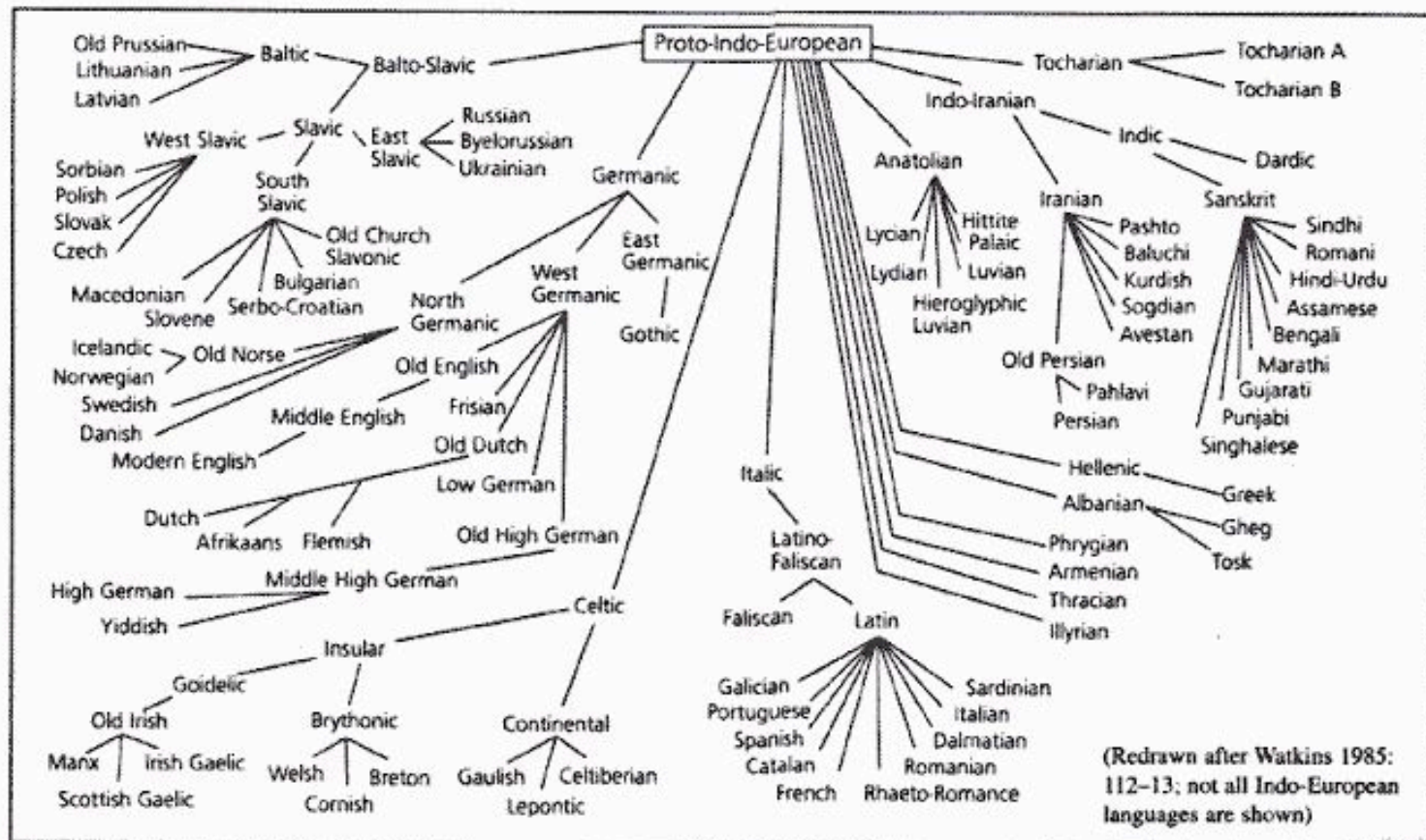


FIGURE 6.1: The Indo-European family tree

From [linguistica.tribe.net](http://linguistica.tribe.net)

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# Cognates

- Two words are *cognate* if they are derived from an ancestral word via *regular sound changes*
- Examples: **mano** and **main**
- But **mucho** and **much** are not cognate, nor are the words for ‘television’ in Japanese and English

# Coding lexical characters

- For each *basic meaning*, assign two languages the same state if they contain cognates
- Example: basic meaning ‘hand’
  - English **hand**, German **hand**,
  - French **main**, Italian **mano**, Spanish **mano**
  - Russian **ruká**
- Mathematically this is:
  - Eng. 1, Ger. 1, Fr. 2, It. 2, Sp. 2, Rus. 3

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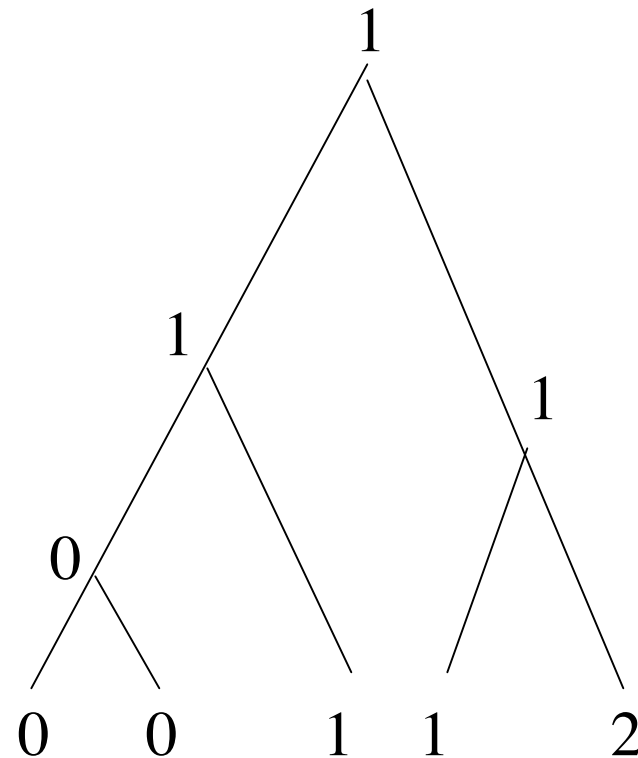
## ‘hand’ coded as a character

### **Coding.**

Hittite	1	Lithuanian	2	Old Prussian	2
Armenian	1	Old English	3	Latvian	2
Greek	1	Old Irish	4	Gothic	3
Albanian	1	Latin	5	Old Norse	3
Tocharian B	1	Luvian	1	OHG	3
Vedic	1a	Lycian	1	Welsh	4
Avestan	1a	Tocharian A	1	Oscan	5
OCS	2	Old Persian	1a	Umbrian	5

# Lexical characters can also evolve without homoplasy

- For every cognate class, the nodes of the tree in that class should form a connected subset - *as long as there is no undetected borrowing nor parallel semantic shift.*



# Our group

- Don Ringe (Penn)
- Luay Nakhleh (Rice)
- Francois Barbancon (Microsoft)
- Tandy Warnow (Texas)
- Ann Taylor (York)
- Steve Evans (Berkeley)



*Don Ringe*



# Our approach

- We estimate the phylogeny through intensive analysis of a relatively small amount of data
  - a few hundred lexical items, plus
  - a small number of morphological, grammatical, and phonological features
- All data preprocessed for homology assessment and cognate judgments
- All *character incompatibility (homoplasy)* must be explained and linguistically believable (via borrowing, parallel evolution, or back-mutation)

Table 1: The 24 IE languages analyzed.

Language	Abbreviation	Language	Abbreviation
Hittite	HI	Old English	OE
Luvian	LU	Old High German	OG
Lycian	LY	Classical Armenian	AR
Vedic	VE	Tocharian A	TA
Avestan	AV	Tocharian B	TB
Old Persian	PE	Old Irish	OI
Ancient Greek	GK	Welsh	WE
Latin	LA	Old Church Slavonic	OC
Oscan	OS	Old Prussian	PR
Umbrian	UM	Lithuanian	LI
Gothic	GO	Latvian	LT
Old Norse	ON	Albanian	AL

# Our (RWT) Data

- Ringe & Taylor (2002)
  - 259 lexical
  - 13 morphological
  - 22 phonological
- These data have cognate judgments estimated by Ringe and Taylor, and vetted by other Indo-Europeanists. (Alternate encodings were tested, and mostly did not change the reconstruction.)
- Polymorphic characters, and characters known to evolve in parallel, were removed.

# Differences between different characters

- **Lexical**: most easily borrowed (most borrowings detectable), and homoplasy relatively frequent (we estimate about 25-30% overall for our wordlist, but a much smaller percentage for basic vocabulary).
- **Phonological**: can still be borrowed but much less likely than lexical. Complex phonological characters are infrequently (if ever) homoplastic, although simple phonological characters very often homoplastic.
- **Morphological**: least easily borrowed, least likely to be homoplastic.

# Our methods/models

- Ringe & Warnow “[Almost Perfect Phylogeny](#)”: most characters evolve without homoplasy under a no-common-mechanism assumption (various publications since 1995)
- Ringe, Warnow, & Nakhleh “[Perfect Phylogenetic Network](#)”: extends APP model to allow for borrowing, but assumes homoplasy-free evolution for all characters (Language, 2005)
- Warnow, Evans, Ringe & Nakhleh “[Extended Markov model](#)”: parameterizes PPN and allows for homoplasy provided that homoplastic states can be identified from the data. Under this model, trees and some networks are identifiable, and likelihood on a tree can be calculated in linear time (Cambridge University Press, 2006)
- Ongoing work: incorporating unidentified homoplasy and polymorphism (two or more words for a single meaning)

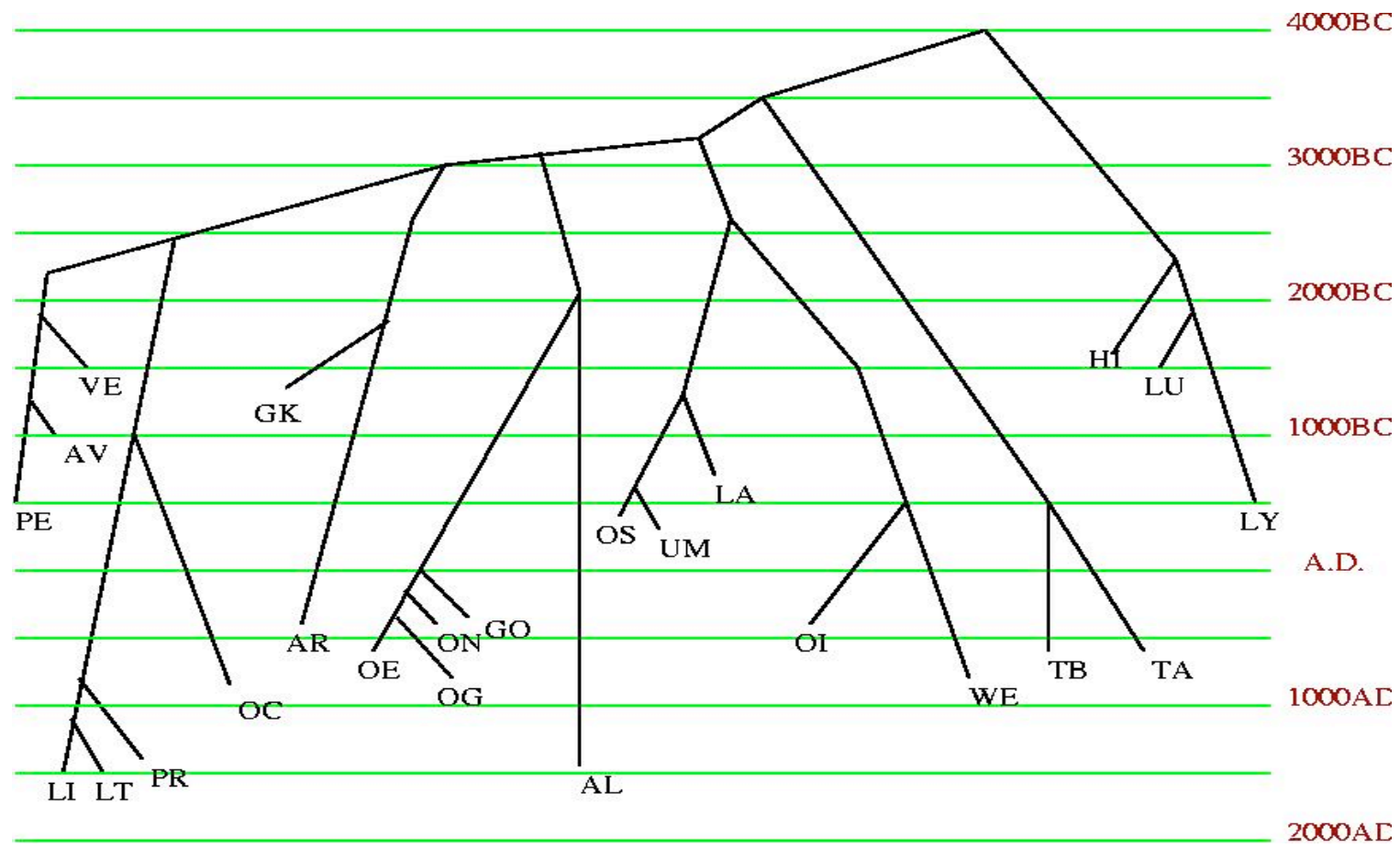
# First Ringe-Warnow-Taylor analysis: “Weighted Maximum Compatibility”

- Input: set L of languages described by characters
- Output: Tree with leaves labelled by L, such that the number of homoplasy-free (compatible) characters is maximized.
- In our analyses, we required that certain of the morphological and phonological characters be compatible.

# The WMC Tree

dates are approximate

95% of the characters are compatible



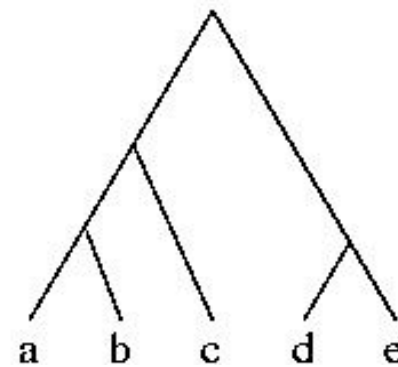
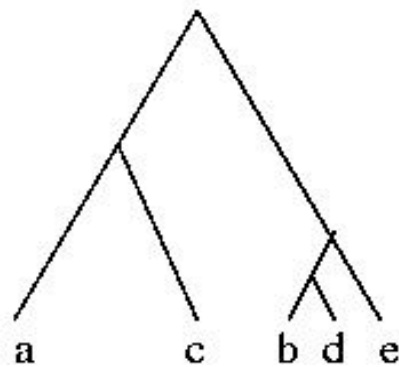
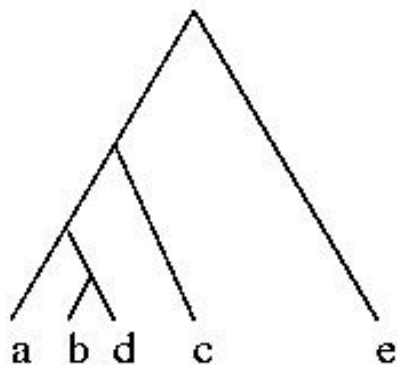
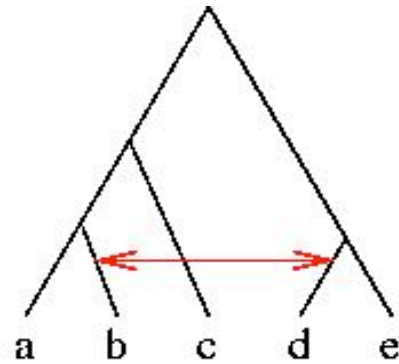
# Second analysis

- Objective: explain the remaining character incompatibilities in the tree
- Observation: all incompatible characters are lexical
- Possible explanations:
  - Undetected borrowing
  - Parallel semantic shift
  - Incorrect cognate judgments
  - Undetected polymorphism

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# Modelling borrowing: Networks and Trees within Networks



# Perfect Phylogenetic Networks

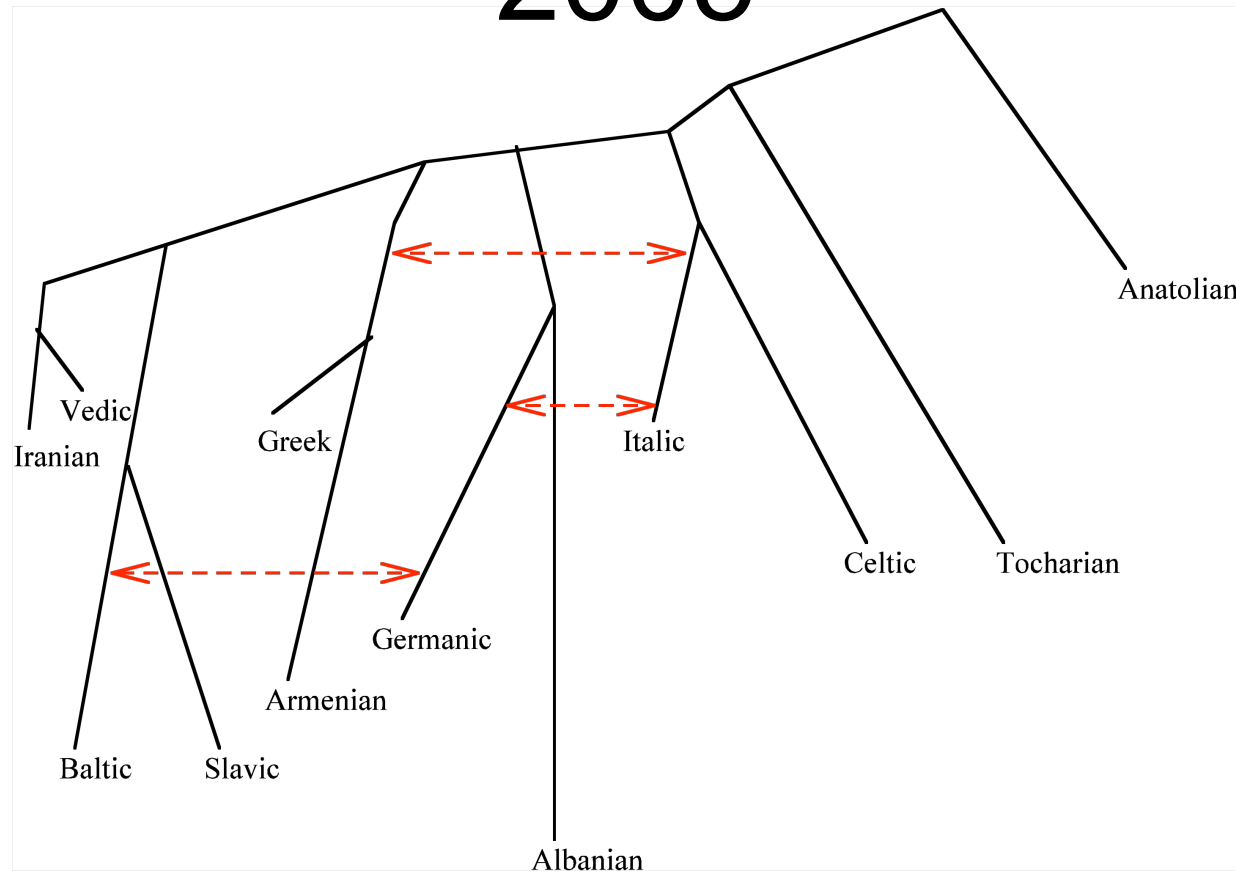
## Problem formulation

- Input: set of languages described by characters
- Output: Network on which all characters evolve without homoplasy, but can be borrowed

Nakhleh, Ringe, and Warnow, 2005. Language.

# Phylogenetic Network for IE

Nakhleh *et al.*, Language  
2005



# Comments

- This network is very “tree-like” (only three contact edges needed to explain the data).
- Two of the three contact edges are strongly supported by the data (many characters are borrowed).
- If the third contact edge is removed, then the evolution of the remaining (two) incompatible characters needs to be explained. Probably this is parallel semantic shift.

# Other IE analyses

Note: many reconstructions of IE have been done, but produce different histories which differ in significant ways

Possible issues:

Dataset (modern vs. ancient data, errors in the cognancy judgments, lexical vs. all types of characters, screened vs. unscreened)

Translation of multi-state data to binary data

Reconstruction method

## The performance of methods on an IE data set (Transactions of the Philological Society, Nakhleh et al. 2005)

**Observation:** Different datasets (not just different methods) can give different reconstructed phylogenies.

**Objective:** Explore the differences in reconstructions as a function of data (lexical alone versus lexical, morphological, and phonological), screening (to remove obviously homoplastic characters), and methods. However, we use a *better basic dataset* (where cognancy judgments are more reliable).

# Phylogeny reconstruction methods

- Neighbor joining (distance based method)
- UPGMA (distance-based method, same as glottochronology)
- Maximum parsimony (minimize number of changes)
- Maximum compatibility (weighted and unweighted)
- Gray and Atkinson (Bayesian estimation based upon presence/absence of cognates, as described in Nature 2003)

# Four datasets

- Ringe & Taylor
  - The screened full dataset of 294 characters (259 lexical, 13 morphological, 22 phonological)
  - The unscreened full dataset of 336 characters (297 lexical, 17 morphological, 22 phonological)
  - The screened lexical dataset of 259 characters.
  - The unscreened lexical dataset of 297 characters.

# Likely Subgroups

Other than UPGMA, all methods reconstruct

- the ten major subgroups
- **Anatolian + Tocharian** (that under the assumption that Anatolian is the first daughter, then Tocharian is the second daughter)
- **Greco-Armenian** (that Greek and Armenian are sisters)

## Other observations

- UPGMA (i.e., the tree-building technique for glottochronology) does the worst (e.g. splits Italic and Iranian groups).
- The Satem Core (Indo-Iranian plus Balto-Slavic) is not always reconstructed.
- Almost all analyses put Italic, Celtic, and Germanic together. (The only exception is weighted maximum compatibility on datasets that include morphological characters.)

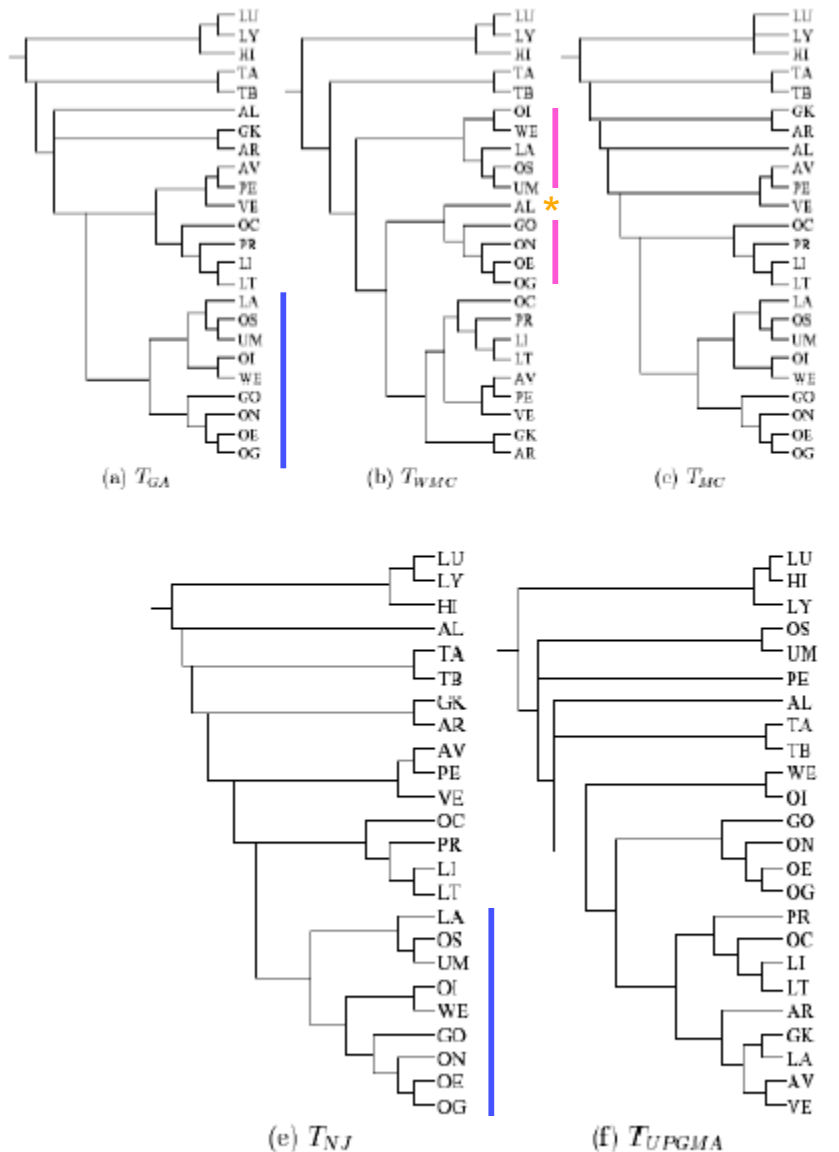


Figure 1. Five trees inferred on the screened full dataset

GA = Gray+Atkinson Bayesian MCMC method

WMC = weighted maximum compatibility

MC = maximum compatibility (identical to maximum parsimony on this dataset)

NJ = neighbor joining (distance-based method, based upon corrected distance)

UPGMA = agglomerative clustering technique used in glottochronology.

Different methods/data  
give different answers.

We don't know  
which answer is correct.

Which method(s)/data  
should we use?

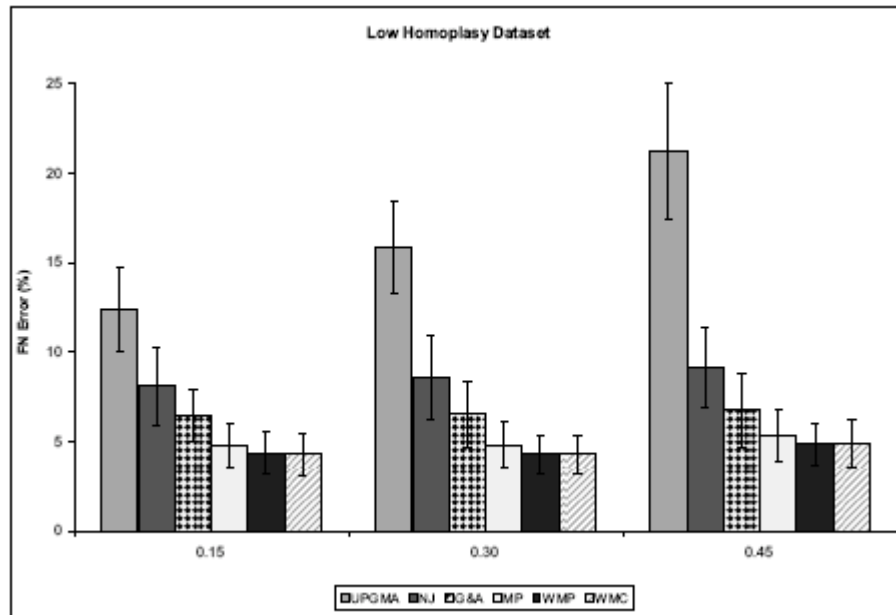
# Our simulation

## (Barbancon et al., in press)

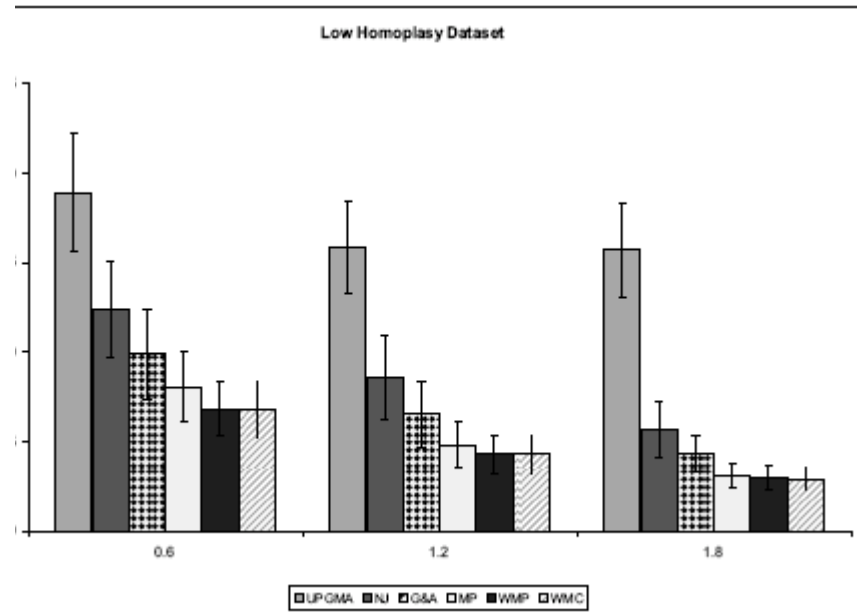
- Lexical and morphological characters
- Networks with 1-3 contact edges, and also trees
- “Moderate homoplasy”:
  - morphology: 24% homoplastic, no borrowing
  - lexical: 13% homoplastic, 7% borrowing
- “Low homoplasy”:
  - morphology: no borrowing, no homoplasy;
  - lexical: 1% homoplastic, 6% borrowing

# Observations

1. Choice of reconstruction method does matter.
2. Relative performance between methods is quite stable (distance-based methods worse than character-based methods).
3. Choice of data does matter (good idea to add morphological characters).
4. Accuracy only slightly lessened with small increases in homoplasy, borrowing, or deviation from the lexical clock.
5. Some amount of heterotachy helps!



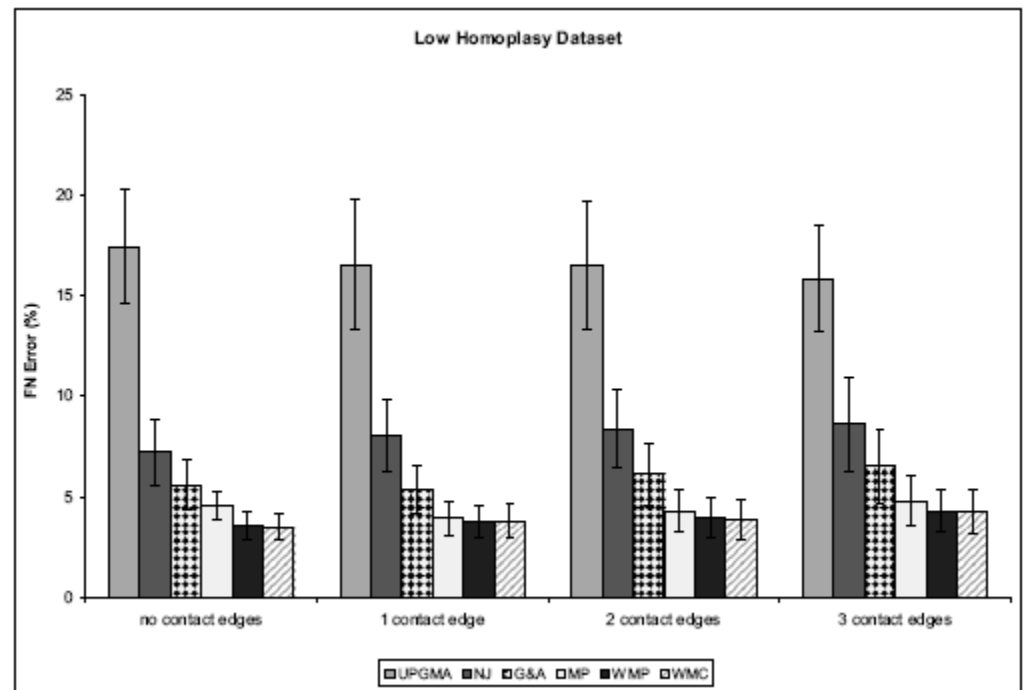
(i)



(ii)

Relative performance of methods for **low homoplasy datasets** under various model conditions:

- (i) Varying the deviation from the lexical clock,
- (ii) Varying the heterotachy, and
- (iii) Varying the number of contact edges.



(iii)

# Future research

- We need more investigation of methods based on stochastic models (Bayesian beyond G+A, maximum likelihood, NJ with better distance corrections), as these are now the methods of choice in biology. This requires ***better models of linguistic evolution*** and hence ***input from linguists!***

# Future research (continued)

- Should we screen? The simulation uses low homoplasy as a proxy for screening, but real screening throws away data and may introduce bias.
- How do we detect/reconstruct borrowing?
- How do we handle missing data in methods based on stochastic models?
- How do we handle polymorphism?

# Acknowledgements

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- Collaborators: Don Ringe (Penn), Steve Evans (Berkeley), Luay Nakhleh (Rice), and Francois Barbancon (Microsoft)
- Please see <http://www.cs.rice.edu/~nakhleh/CPHL> for papers and data