Maximum parsimony method in the subgrouping of Dravidian languages

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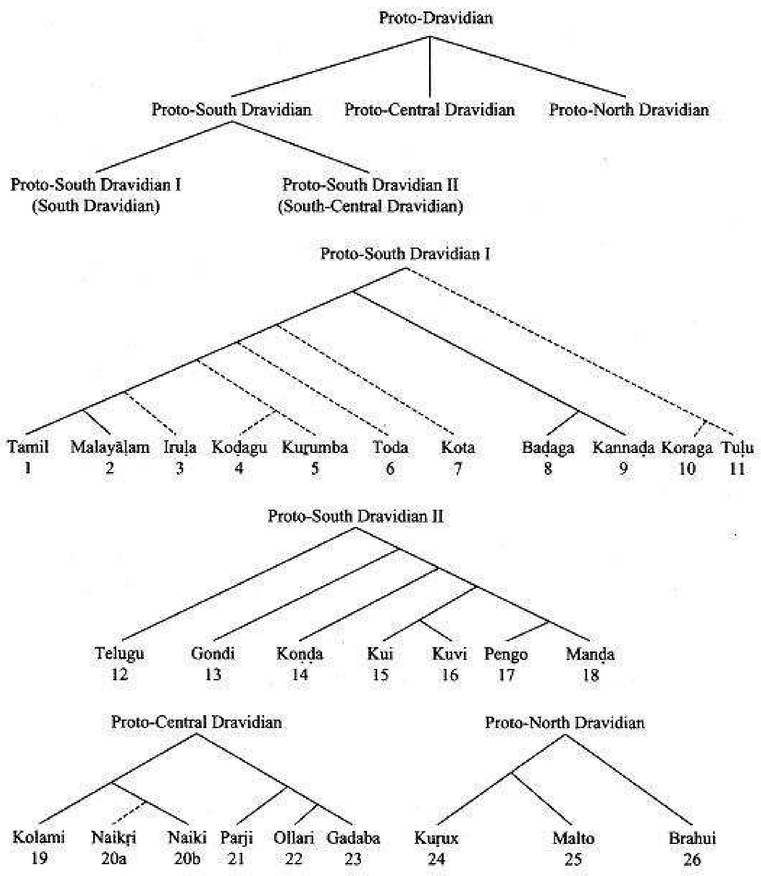
Introduction

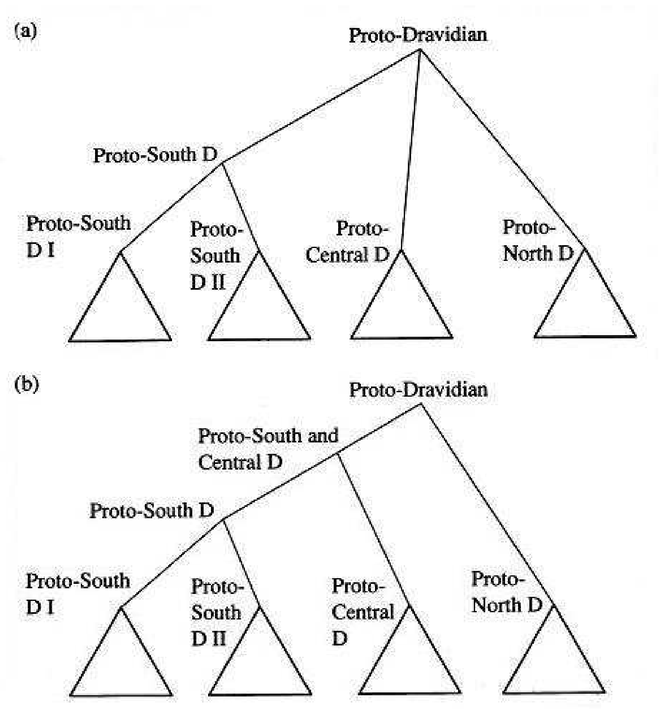
- **Subgrouping**: internal classification of languages within a language family
- **Dravidian language family**
  - consists of 26 languages spoken by over 200 million people in South Asia
  - family tree shown in Figure 1 (taken from (Krishnamurti 2003))



Broken lines reflect uncertainty as to a language's position within the group.

Subgrouping of the Dravidian languages

- Two possible subgroupings of the Dravidian languages according to (Krishnamurti 2003)



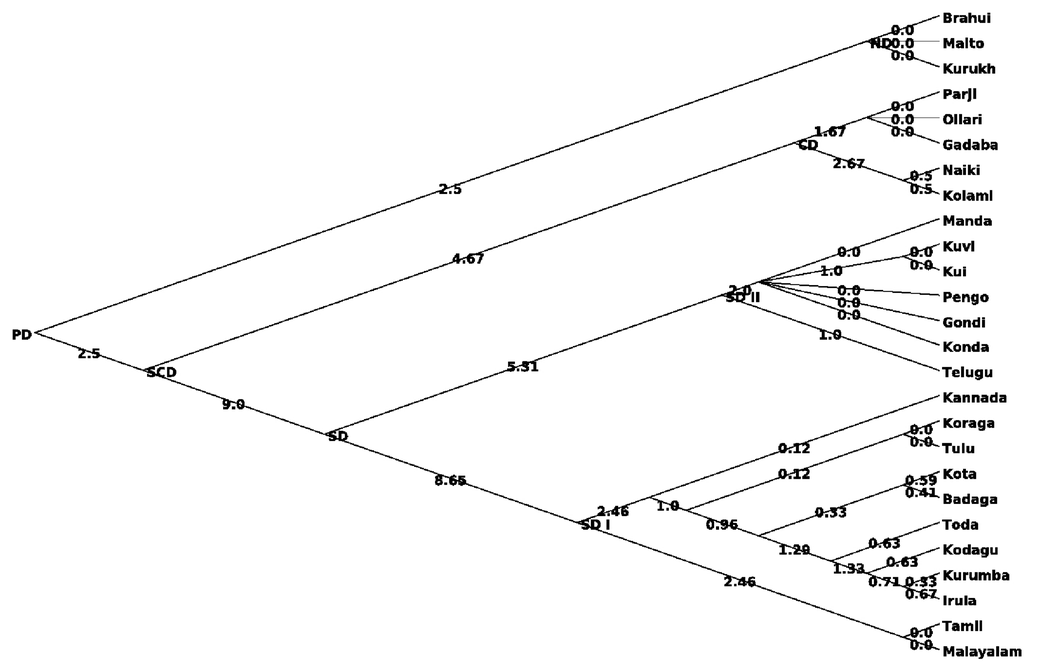
- **Aim**: To address this specific question of ternary versus binary branching of Proto-Dravidian via application of the Maximum Parsimony method (MP) to the Dravidian data
- **Dataset**: Features from comparative phonology, morphology and syntax used for subgrouping (Krishnamurti 2003) (available on request)
- **Intuition**: Binary branching of speech communities more likely than ternary
- **Procedure**: Apply MP to the same dataset and compare inferred tree to the tree constructed using traditional methodology

Maximum Parsimony (MP) method

- MP infers phylogeny by searching for the phylogeny with the minimum number of evolutionary events
- MP shown to be the most efficient for inferring the phylogenetic tree that is closest to the traditional standard tree (Nakhleh et al. 2005)
- Implementation of MP used in our experiments: *pars* program in PHYLIP
- Reason: *pars* searches over the space of both bifurcating and multifurcating trees

Experimental setup

- Bootstrapping procedure run for 10000 times with 'sampling with replacement'
- *pars* applied to the bootstrapped datasets to get multiple parsimonious trees
- Consensus tree *a*) estimated using majority consensus *b*) rooted using the North Dravidian (ND) clade as the outgroup
- *pars* applied to the dataset again, this time giving the rooted consensus tree as additional input
- Branch lengths on the consensus tree re-estimated using *pars*



Results

- Phylogenetic tree inferred using MP shown above
- Notes on interpreting the inferred tree
  - Ternary branching can show up as binary branching with zero branch length
  - A binary branching internal node can be eliminated if the number of state changes (indicated by branch lengths) along its two branches is equal
  - Difference in branch lengths between SCD and SD, and SCD and CD is 4.33 and hence, SCD cannot be eliminated

Conclusions and Future Work

- Main conclusion: MP Tree inferred clearly shows binary branching of Proto-Dravidian and not ternary as suggested in (Krishnamurti 2003)
- Features shared by CD and SD II ignored in the subgrouping using the traditional method (Figure 2(a))
- It treats these similarities between CD and SD II as a result of a common stage in their evolution: Proto South-Central Dravidian (SCD)
- Additional outcomes: MP resolves other uncertainties such as position of Nilgiri languages
- In future,
  - Experiment with weighted Maximum Parsimony (WMP) by weighting different kinds of features
  - Experiment with a much larger set of features by including lexical features
  - Explore network-based methods to address borrowing and homoplasy

References

Krishnamurti, B. (2003), *The Dravidian languages*, Cambridge Univ Press.

Nakhleh, L., Warnow, T., Ringe, D. & Evans, S. (2005), 'A comparison of phylogenetic reconstruction methods on an Indo-European dataset', *Transactions of the Philological Society* **103**(2), 171–192.

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