Multiple Word Alignment with Profile Hidden Markov Models

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Multiple word alignment

- Given multiple words, align them all to each other
- Our approach: Profile HMMs, used in biological sequence analysis
- Use match, insert, and delete states to model changes
- Evaluate on cognate set matching
  - Beat baselines of average and minimum edit distance

What you can expect

- Introduction: word alignment
- Profile hidden Markov models
  - For bioinformatics
  - For words?
- Experiments
- Conclusions & future work

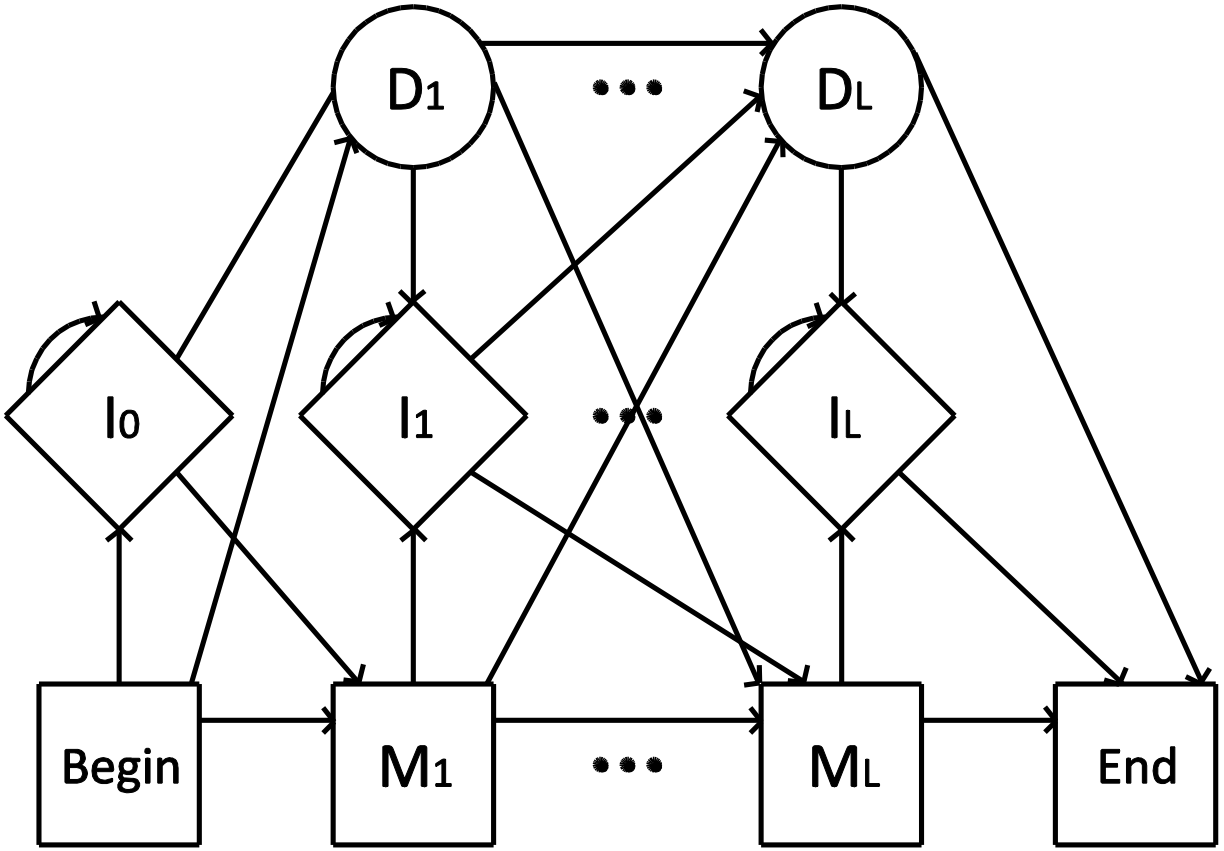
Introduction

- Multiple word alignment:
  - Take a set of words
  - Generate some alignment of these words
  - Similar and equivalent characters should be aligned together
- Pairwise alignment gets us:
  - String similarity and word distances
  - Cognate identification
  - Comparative reconstruction

Introduction

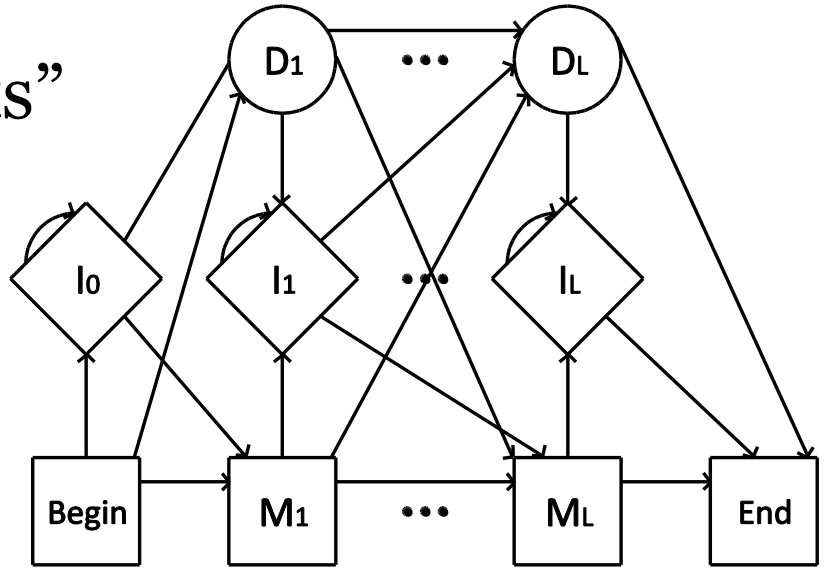
- Extending to multiple words gets us:
  - String similarity with multiple words
  - Better-informed cognate identification
  - Better-informed comparative reconstruction
- We propose Profile HMMs for multiple alignment
  - Test on cognate set matching

Profile hidden Markov models



Profile hidden Markov models

- Match states are “defaults”
- Insert states are used to represent insert symbols
- Delete states are used to represent the absence of symbols



Profile hidden Markov models

MMIIIM

AG...C

A-AG.C

AG.AA-

--AAAC

AG...C

- In this sample DNA alignment, dashes represent deletes and periods represent skipped inserts

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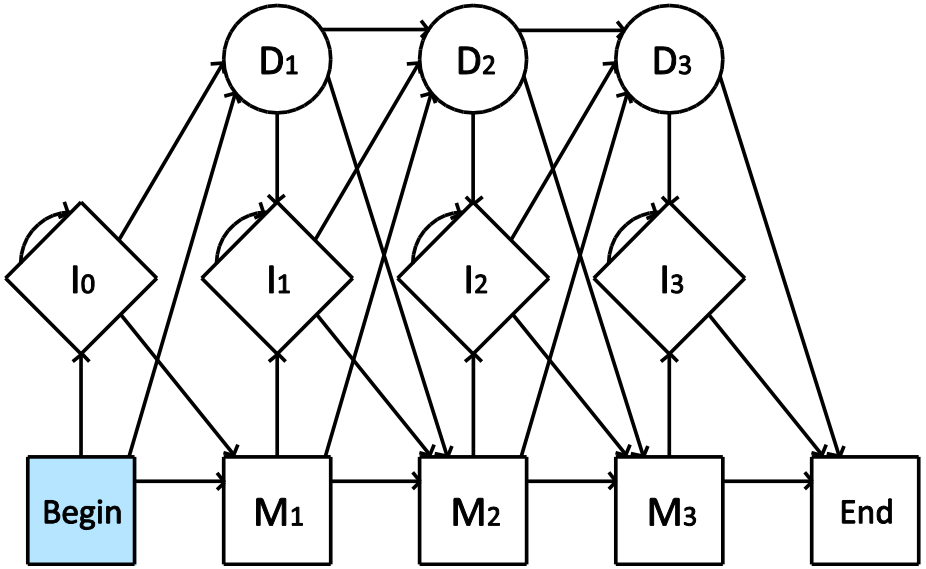

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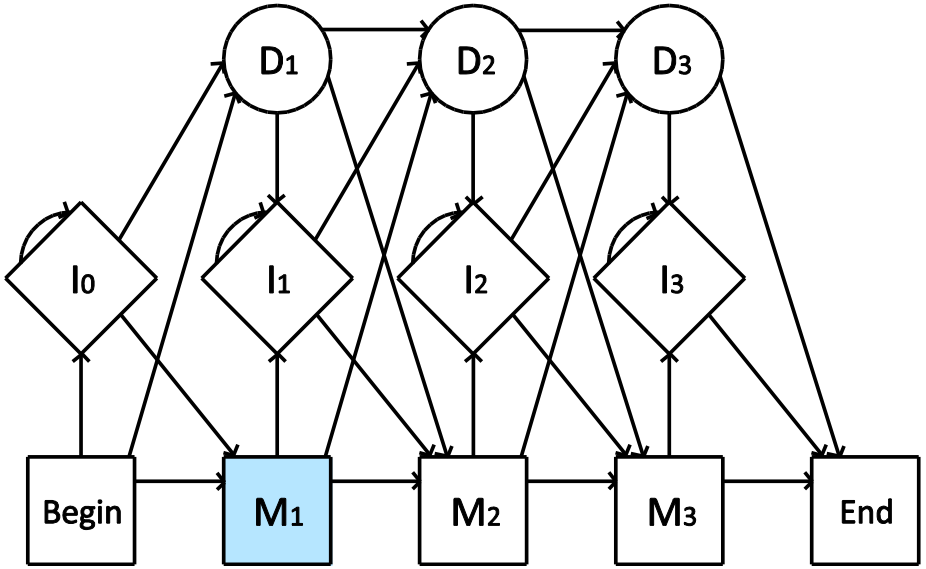

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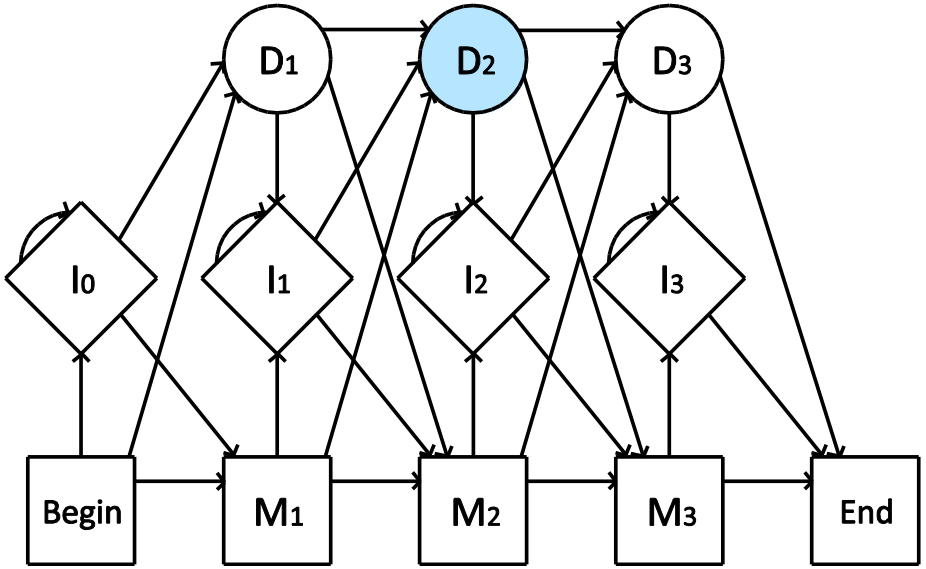

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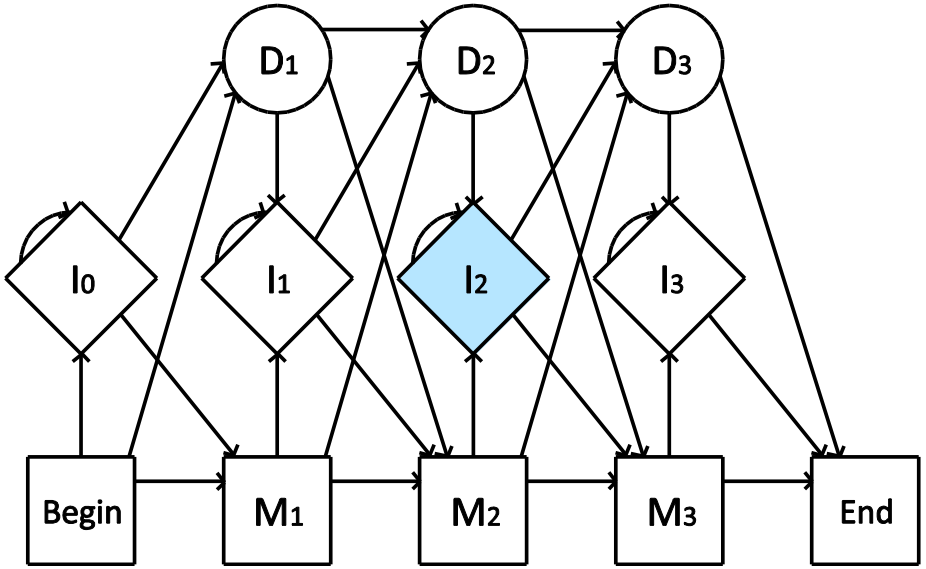

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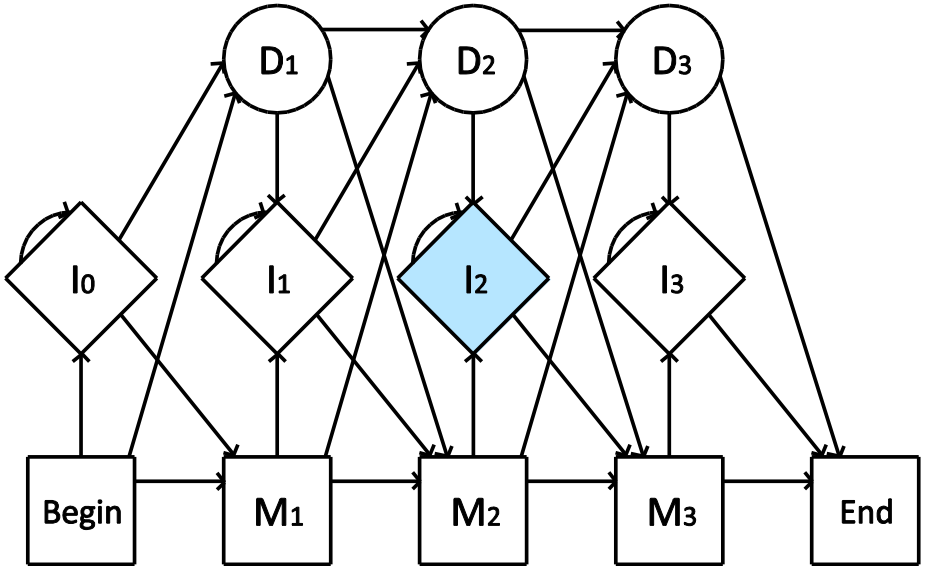

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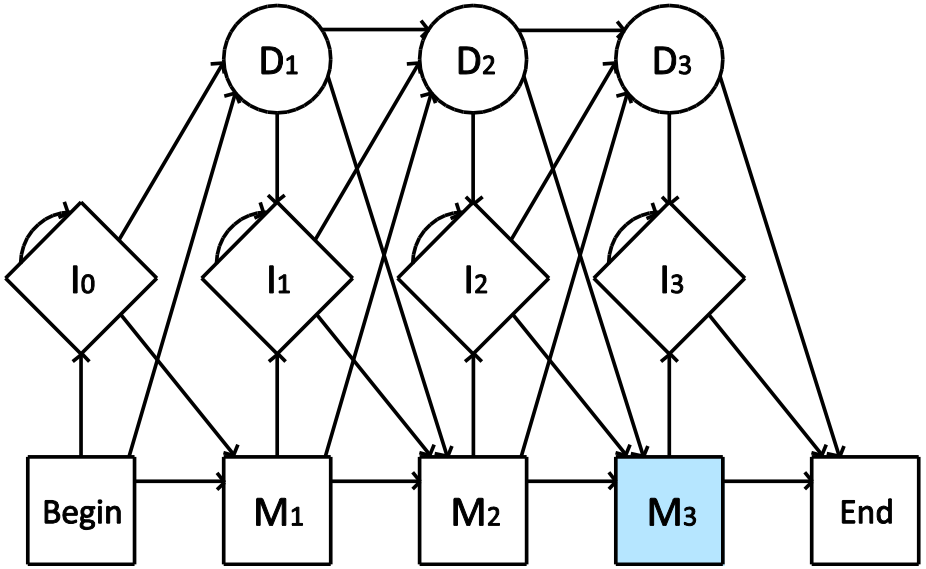

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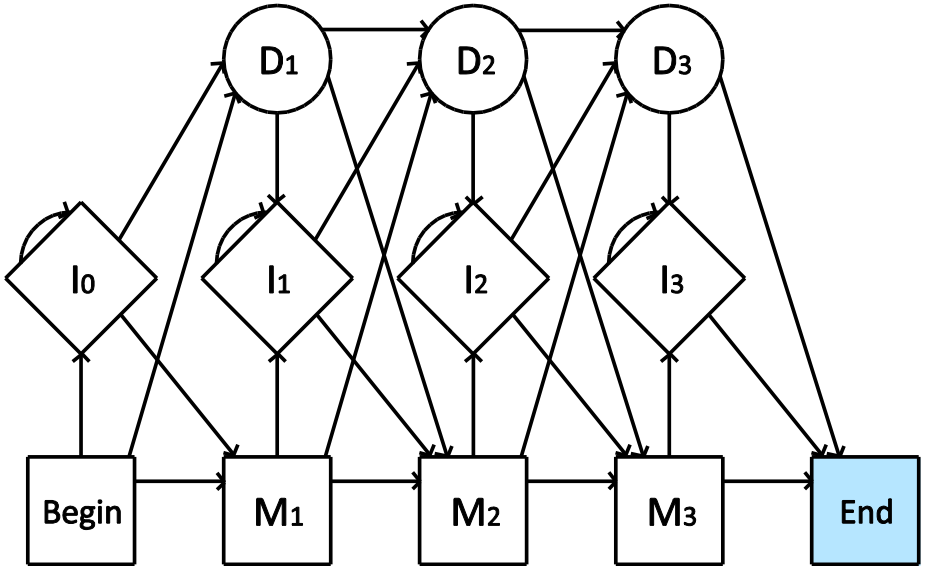


Profile hidden Markov models

- To construct a Profile HMM from aligned sequences:
  - Determine which columns are match columns and which are insert columns, then estimate transition and emission probabilities directly from counts
- To construct a Profile HMM from unaligned sequences:
  - Choose a model length, initialize the model, then train it to the sequences using Baum-Welch

Profile hidden Markov models

- Evaluating a sequence for membership in a family
  - Use the forward algorithm to get the probability
  - Use Viterbi to align the sequence
- Multiple alignment of unaligned sequences
  - Construct & train a Profile HMM
  - Use Viterbi to align the sequences

Profile hidden Markov models

- Profile HMMs are generalizations of Pair HMMs
  - Word similarity and cognate identification
- Unlike Pair HMMs, Profile HMMs are position-specific
  - Each model is constructed from a specific family of sequences
  - Pair HMMs are trained over many pairs of words

Profile HMMs for words

- Words are also sequences!
- Similar to their use for biological sequences, we apply Profile HMMs to multiple word alignment
- We also test Profile HMMs on matching words to cognate sets
- We made our own implementation and investigated several parameters

Profile HMMs: parameters

- Favour match states?
- Pseudocount methods
  - Constant-value, background frequency, substitution matrix
- Pseudocount weight
- Pseudocounts added during Baum-Welch

Experiments: Data

- Comparative Indoeuropean Data Corpus
  - Cognation data for words in 95 languages corresponding to 200 meanings
- Each meaning reorganized into disjoint cognate sets

Experiments: Multiple cognate alignment

```
MIIMIIMI
D--E--N-
D--E--NY
Z--E--N-
DZ-E--N-
DZIE--N-
D--A--N-
DI-E--NA
D--E--IZ
D--E----
D--Y--DD
D--I--A-
D--I--E-
D-----I-
Z-----I-
Z--U--E-
Z-----U-
J--O--UR
DJ-O--U-
J--O--UR
G--IORNO
```

- Parameters determined from cognate set matching experiments (later)
- Pseudocount weight set to 100 to bias the model using a substitution matrix
- Highly-conserved columns are aligned correctly
- Similar-sounding characters are aligned also correctly, thanks to the substitution matrix method
- Insert columns should not be considered aligned
- Problems with multi-character phonemes
  - An expected problem when using the English alphabet instead of e.g. IPA

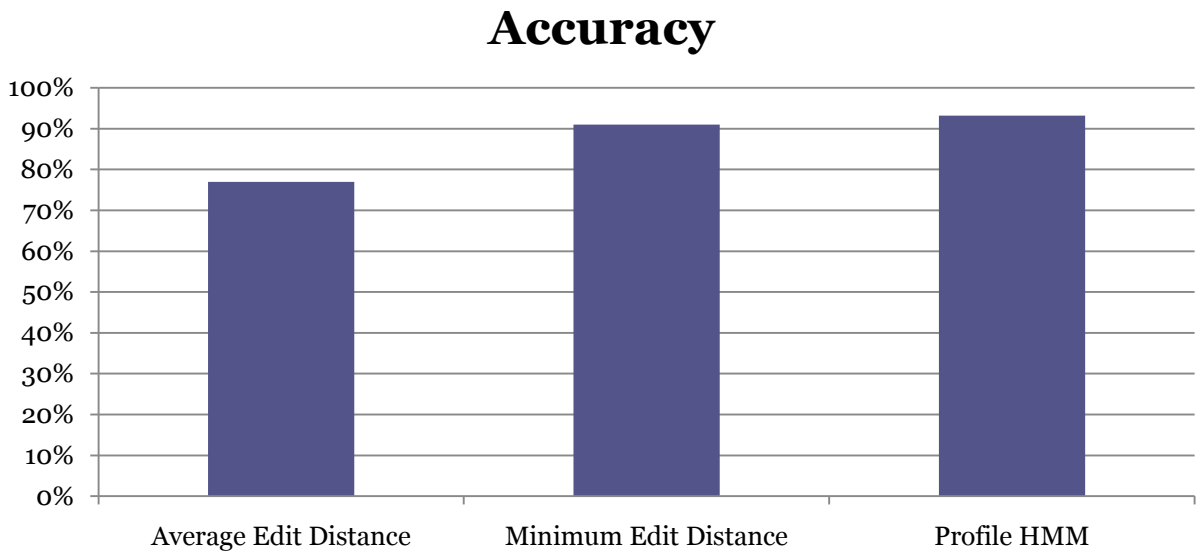
Experiments: Cognate set matching

- How can we evaluate the alignments in a principled way? There is no gold standard!
- We emulate the biological sequence analysis task of matching a sequence to a family; we match a word to a cognate set
- The task is to correctly identify the cognate set to which a word belongs given a number of cognate sets having the same meaning as the word; we choose the model yielding the highest score

Experiments: Cognate set matching

- Development set of 10 meanings (~5% of the data)
- Substitution matrix derived from Pair HMM method
- Best parameters:
  - Favour match states
  - Use substitution matrix pseudocount
  - Use 0.5 for pseudocount weight
  - Add pseudocounts during Baum-Welch

Experiments: Cognate set matching



Average Edit Distance: **77.0%**

Minimum Edit Distance: **91.0%**

Profile HMM: **93.2%**

Experiments: Cognate set matching

- Accuracy better than both average and minimum edit distance
- Why so close to MED?
  - Many sets had duplicate words (same orthographic representation for different languages)

Conclusions

- Profile HMMs can work for word-related tasks
- Multiple alignments are reasonable
- Cognate set matching performance exceeds minimum and average edit distance
- If multiple words need to be considered, Profile HMMs present a viable method

Future work

- Better model construction from aligned sequences
- Better initial models for unaligned sequences
- Better pseudocount methods
- N-gram output symbols