MEMM inference in systems

- For a Conditional Markov Model (CMM) a.k.a. a Maximum Entropy Markov Model (MEMM), the classifier makes a single decision at a time, conditioned on evidence from observations and previous decisions.
- · A larger space of sequences is explored via search

Decision Point

Local Context

-3 -2 -1 0 +1

DT NNP VBD ???? 7???

The Dow fell 22.6 %

(Ratnaparkhi 1996; Toutanova et al. 2003, etc.)

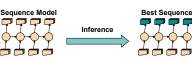
Features W₀ 22.6 W₊₁ % W₁ fell T₋₁ VBD T₋₁-T₋₂ NNP-VBD hasDigit? true

Beam Inference



- · Beam inference:
- At each position keep the top k complete sequences.
- Extend each sequence in each local way.
- The extensions compete for the k slots at the next position.
- Advantages:
 - Fast, and beam sizes of 3–5 are as good or almost as good as exact inference in many cases.
 - Easy to implement (no dynamic programming required).
- Disadvantage:
 - Inexact: the globally best sequence can fall off the beam.

Viterbi Inference



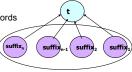
- · Viterbi inference:
 - Dynamic programming or memoization.
 - Requires small window of state influence (e.g., past two states are relevant).
- Advantage:
- Exact: the global best sequence is returned.
- · Disadvantage:
 - Harder to implement long-distance state-state interactions (but beam inference tends not to allow long-distance resurrection of sequences anyway).

HMM Part-of-speech Tagging Models -Brants 2000

- · Highly competitive with other state-of-the art models
- · Trigram HMM with smoothed transition probabilities
- Capitalization feature becomes part of the state each tag state is split into two e.g.

NN → <NN,cap>,<NN,not cap>
• Suffix features for unknown words

P(w | tag) = P(suffix | tag)(w | suffix) $\approx \hat{P}(suffix)\tilde{P}(tag | suffix)/\hat{P}(tag)$



 $\widetilde{P}(tag \mid suffix_n) = \lambda_1 \widehat{P}(tag \mid suffix_n) + \lambda_2 \widehat{P}(tag \mid suffix_{n-1}) + \dots + \lambda_n \widehat{P}(tag)$

MEMM Tagging Models -II

- Ratnaparkhi (1996): local distributions are estimated using maximum entropy models
 - Previous two tags, current word, previous two words, next two words, suffix, prefix, hyphenation, and capitalization features for unknown words
- · Toutanova et al. (2003)
 - Richer features, bidirectional inference, better smoothing, better unknown word handling

Model	Overall Accuracy	Unknown Words
HMM (Brants 2000)	96.7	85.5
MEMM (Ratn. 1996)	96.63	85.56
MEMM (T. et al 2003)	97.24	89.04

CRFs [Lafferty, Pereira, and McCallum 2001]

- Another sequence model: Conditional Random Fields (CRFs)
- A whole-sequence conditional model rather than a chaining of local models.

pidels.
$$P(c \mid d, \lambda) = \frac{\exp \sum_{c} \lambda_{i} f_{i}(c, d)}{\sum_{c'} \exp \sum_{i} \lambda_{i} f_{i}(c', d)}$$

- The space of c's is now the space of sequences
 - But if the features f_i remain local, the conditional sequence likelihood can be calculated exactly using dynamic programming
- Training is slow, but CRFs avoid causal-competition biases
- These (or a variant using a max margin criterion) are seen as the state-of-the-art these days

Summary of Tagging

- For tagging, the change from generative to discriminative model **does not by itself** result in great improvement
- One profits from discriminative models for specifying dependence on **overlapping features of the observation** such as spelling, suffix analysis,etc
- A CMM allows integration of rich features of the observations, but can suffer strongly from assuming independence from following observations; this effect can be relieved by adding dependence on following words
- This additional power (of the CMM ,CRF, Perceptron models) has been shown to result in improvements in accuracy
- The **higher accuracy** of discriminative models comes at the price of **much slower training**

Biomedical NER Motivation

- The biomedical field contains a large body of information, which is growing rapidly.
 - MEDLINE, the primary research database serving the biomedical community, currently contains over 12 million abstracts, with 60,000 new abstracts appearing each month.
 - There is also an impressive number of biological databases containing information on genes, proteins, nucleotide and amino acid sequences, including GenBank, Swiss-Prot, and Fly-Base; each contains entries numbering from the thousands to the millions and are multiplying rapidly.

Motivation

- Currently, all of these resources are curated by hand by expert annotators at enormous expense.
- The information overload from the massive growth in the scientific literature has shown the necessity to automatically locate, organize and manage facts relating to experimental results
- Natural Language Processing can aid researchers and curators of biomedical databases by automating these tasks

Named Entity Recognition

· General NER vs. Biomedical NER

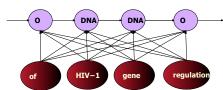
<PER> Christopher Manning /PER> is a professor at <ORG>
Stanford University </ORG>, in <LOC> Palo Alto </LOC>.

<RNA> TAR
TAT
Tat
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/PROTEIN> in cells derived from the <CELL> CNS </CELL> - a novel mechanism of <DNA> HIV-1 gene </DNA> regulation.

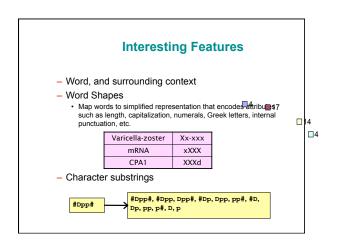
Why is this difficult?

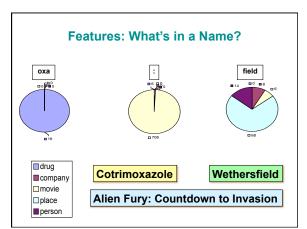
- The list of biomedical entities is growing.
 - New genes and proteins are constantly being discovered, so explicitly enumerating and searching against a list of known entities is not scalable.
 - Part of the difficulty lies in identifying previously unseen entities based on contextual, orthographic, and other clues.
- · Biomedical entities don't have strict naming conventions.
 - Common English words such as period, curved, and for are used for gene names.
 - Entity names can be ambiguous. For example, in FlyBase, "clk" is the gene symbol for the "Clock" gene but it also is used as a synonym of the "period" gene.
- · Biomedical entity names are ambiguous
 - Experts only agree on whether a word is even a gene or protein 69% of the time. (Krauthammer et al., 2000)
 - Often systematic polysemies between gene, RNA, DNA, etc.

Maximum Entropy Markov Model



$$P(t \mid h) = \frac{\exp(\sum_{j=1}^{m} f_j(h, t)\lambda_j)}{\sum_{k=1}^{K} \exp(\sum_{i=1}^{m} f_j(h, t_k)\lambda_j)}$$





241

Interesting Features

- Part-of-Speech tags
- Parsing information
- Searching the web for the word in a given context
 - X gene, X mutation, X antagonist
- Gazetteer
 - · list words whose classification is known
- Abbreviation extraction (Schwartz and Hearst, 2003)
 - Identify short and long forms when occurring together in text

... Zn finger homeodomain 2 (Zfh 2)

Finkel et al. (2004) Results · BioCreative task - Identify genes and proteins Precision Recall F1 83.6 81.3% 86.1% 83.6% 83.4 83.2 ■ Precision precision = tp / (tp + fp) 83 Recall recall = tp / (tp + fn) F1 F1 = 2(precision)(recall) / (precision + recall) 82.6

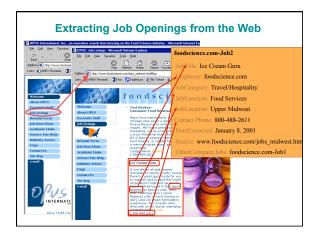
Finkel et al. (2004) Results · BioNLP task - Identify genes, proteins, DNA, RNA, and cell types Precision Recall F1 68.6% 71.6% 70.1% 71.5 70.5 precision = tp / (tp + fp) ■ Precision 70 recall = tp / (tp + fn) 69.5 Recall F1 F1 = 2(precision)(recall) / (precision + recall) 68.5 68 -67.5

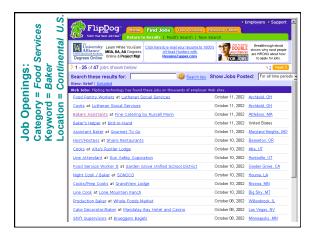
Information Extraction and Integration Following slides from: William Cohen Andrew McCallum Eugene Agichtein Sunita Sarawagi

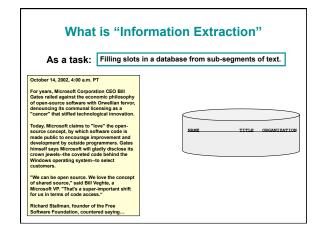
The Value of Text Data

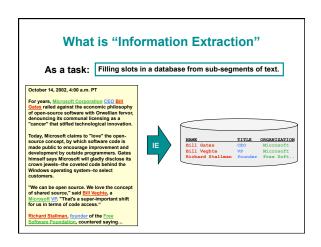
- "Unstructured" text data is the primary source of humangenerated information
 - Citeseer, comparison shopping, PIM systems, web search, data warehousing
- Managing and utilizing text: information extraction and integration
- · Scalability: a bottleneck for deployment
- · Relevance to data mining community

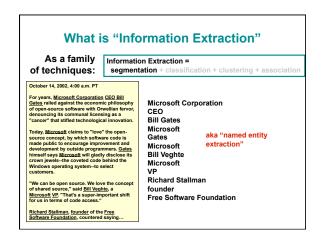


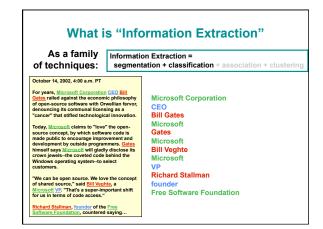


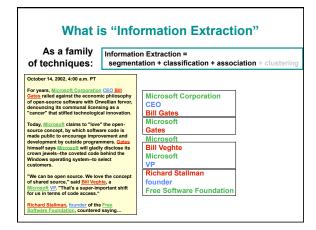


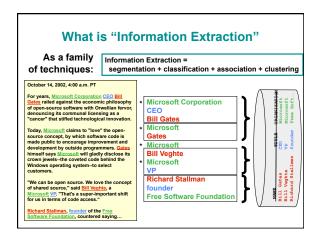


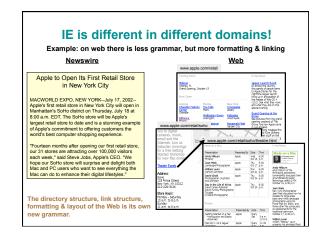


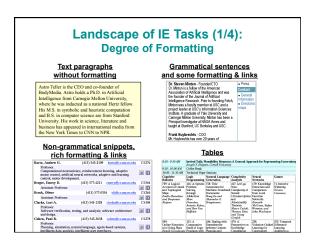


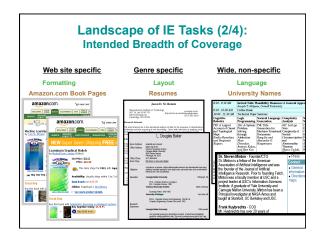


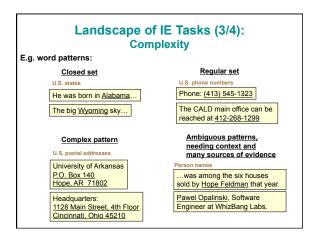


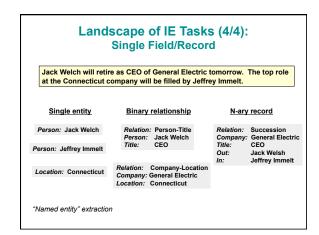


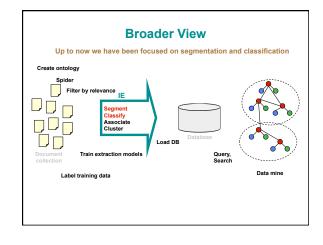












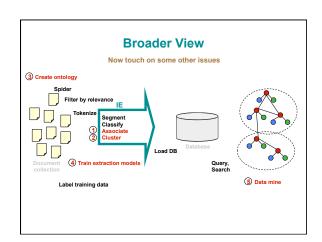
Steps 1 & 2: Hand Coded Rule Example: Conference Name # These are subordinate patterns Sword Ordinals="(?firstepscond(third(fourth)fifth)sixth)seventh|eighth|ninth|tenth|eleventh|twelfth|thirter fourteenth|fifteenth|"; my SnumberOrdinals="(?firstepscond(third(fourth)fifth)sixth)seventh|eighth|nith|tenth|eleventh|twelfth|thirter fourteenth|fifteenth|"; my Sordinals="(?swordOrdinals|SnumberOrdinals)"; my Sordinals="(?swordOrdinals|SnumberOrdinals)"; my Sordinals="(?swordOrdinals|SnumberOrdinals)"; my Swords="(?fixAZ)|w+lis]"; #A word starting with a capital letter and ending with 0 or more spaces my ScontDescriptors="(?internationals|fiXZ]*\u00e4\u00e4)"; #a, g. "International Conference ..." or the confer name for workshops (e.g. "VLDB Workshop ...") my Sconnectors="(?confo)fi"; my Sabbreviations="(?ix[(A-Z)|w+liv+|\u00e4\u00e4)\u00e4]\u00e4\u00e

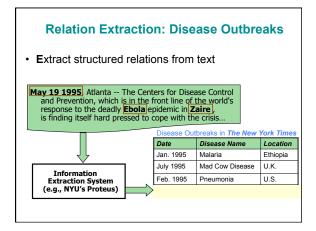
Machine Learning Methods

- · Sequence models: HMMs, CMMs/MEMMs, CRFs
- Can work well when training data is easy to construct and is plentiful
- Can capture complex patterns that are hard to encode with hand-crafted rules
- e.g., determine whether a review is positive or negative
- extract long complex gene names

The human T cell leukemia lymphotropic virus type 1 Tax protein represses MyoD-dependent transcription by inhibiting MyoD-binding to the KIX domain of p300."

- Can be labor intensive to construct training data
 - Question: how much training data is sufficient?





Relation Extraction

Typically requires Entity Tagging as preprocessing

Rules defined over parsed text
"((Obj <company>) (Verb located) (*) (Subj <location>))"
Proteus, GATE, ...

Dan Roth 2005, Cardie 2006, Mooney 2005, ...
Partially-supervised: bootstrap from "seed" examples
Agichtein & Gravano 2000, Etzioni et al., 2004, ...

Knowledge Engineering

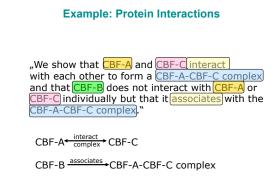
Rules defined over lexical items

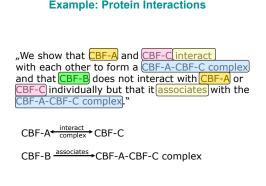
"<company> located in <location>"

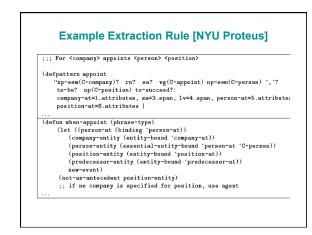
Machine Learning-based

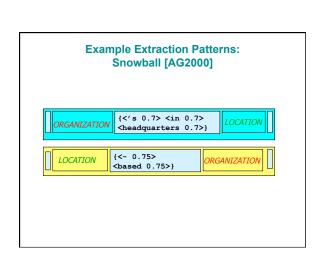
- Learn rules/patterns from examples

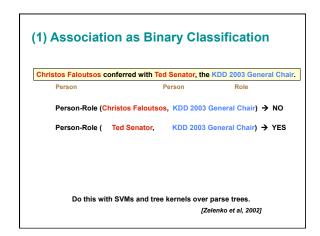
Recently, hybrid models [Feldman2004, 2006]

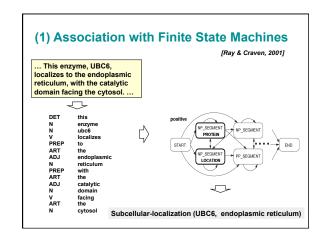


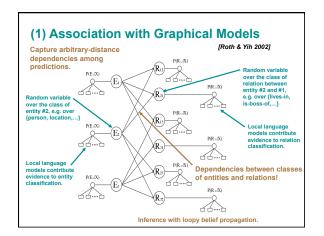


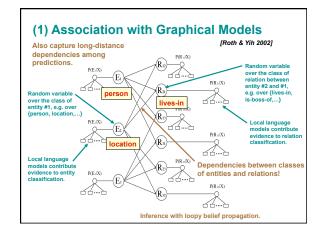


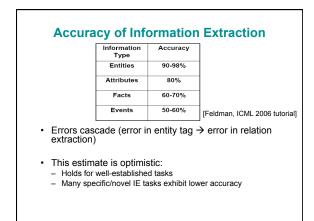


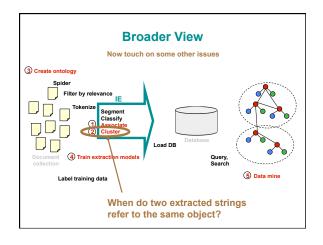












Extracted Entities: Resolving Duplicates





Document 1: The States Department has officially ended its induiry into the assassinations of John F. Kennedy and Marin Luther King Jr., finding "no persuasive evidence" to support conspiracy theories, according to department documents. The Holse Assassinations Committee concluded in 1978 that Kennedy was "psobably" assassinated as the result of a conspiracy involving a second gumman, a finding that trade from the Warren Commission's belief that Lee Harvey Oswald acted alone in Pullas on Nov. 72–1963.

Document 2: In 1953, Massachusetts Sept John F. Kennedy married Jacqueline Lee Bouvier in Newport, R.l. In 1960, Democratic presidential candidate John F. Kennedy confronted the issue of his Roman Johnolic faith by telling a Protestant group in Houston, "I do not speak for my church on gublic matters, and the church does not speak for my.e."

Document 3: David Kennedy was born in Leicester, England in 1959. ...Kennedy coedited The New Poetry (Bloodaxe Books 1993), and is the author of New Relations: The Refashioning Of British Poetry 1980-1994 (Seren 1996).

[From Li, Morie, & Roth, Al Magazine, 2005]

Important Problem

- Appears in numerous real-world contexts
- Plagues many applications
 - Citeseer, DBLife, AliBaba, Rexa, etc.

(2) Information Integration [Minton, Knoblock, et al 2001], [Doan, Domingos, Halevy 2001], [Richardson & Domingos 2003] Goal might be to merge results of two IE systems: Intro. to Comp. Sci. Introduction to Computer Science Title: Name: Num: Number: CS 101 Computer Science Dept: Teacher: M. A. Kludge Dr. Klüdge Teacher: TA: John Smith Name: Data Structures in Topic: Java Programming Java 9:10 AM Room: 5032 Wean Hall