Structured Linear Models

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Goals

• **What**: link document and structured databases

• **How**: *information extraction*:
  - *Tag* entity and relation mentions in text
  - Map (“normalize”) the mentions to database entities and relations

• *Example*: biomedical databases
Nance, who is also a paid consultant to ABC News, said …
Biomedical Examples

• Gene/protein mentions:

In the absence of MHC class II, purified soluble D10 TCR bound to Staphylococcus aureus enterotoxin C2 with an association rate of 1.

• Variation events: type, location, and state change

One ER showed a G to T point mutation in the second position of codon 12
Approach

• Develop text annotation guidelines
• Annotate initial training documents
• Train machine learning algorithms for extraction
• Automatically label more documents and correct (active annotation)
Annotation Tool

Laboratorio di Ematologia Sperimentale e Genetica Molecolare, Servizio di Ematologia, Università degli Studi di Milano, Ospedale Maggiore IRCCS, Milano, Italy.

Chromosomal translocations involving the immunoglobulin heavy chain (IGH) locus at chromosome 14q32 represent a common mechanism of oncogene activation in lymphoid malignancies. In multiple myeloma (MM), the most consistent chromosomal abnormality is the 14q+ marker, which originates in one third of cases through a t(11, 14)(q13, q32) chromosomal translocation, in the

- pm9351876.txt.ann
- yajin (gene#5) 483,486 1 6740
Analyzing Text

• Segmentation
  • units (paragraphs, sentences)
  • layout (lists, FAQs,...)
• Tagging
  • part of speech
  • sense
• Information extraction
• Parsing
Structured Classification

- Learn mapping from objects (documents, sentences,...) to structures
Challenges

• Interacting decisions

• Many types of sequence features

• Computing an answer is relatively costly
Analysis by Tagging

\[ \mathbf{x} = x_1 \cdots x_n \rightarrow \text{Structured classifier} \rightarrow \mathbf{y} = y_1 \cdots y_n \]

- Labels give the role of corresponding inputs
  - Information extraction
  - Part-of-speech tagging
  - Shallow parsing
  - Other segmentation/labeling tasks (speech, genomic sequences,...)
Rockwell International Corp. ’s Tulsa unit said it signed a tentative agreement extending its contract with Boeing Co. to provide structural parts for Boeing ’s 747 jetliners
Traditional Approaches

• *Generative modeling*: probabilistic generators of sequence-structure pairs
• HMMs, probabilistic CFGs
• Hard to model non-independent features

• *Sequential classification*: decompose structure assignment into a sequence of structural decisions
• Cannot trade-off decisions at different locations: *label-bias* problem
Hidden Markov Model

- Instances: symbol sequences
- Labels: state sequences

\[ p(x, y) = p(y_1) p(x_1 | y_1) \prod_{i=2}^{n} p(y_i | y_{i-1}) p(x_i | y_i) \]
HMMs in IE

[Seymore & McCallum 99, Freitag & McCallum 99]

- **Inputs** $x$: words
  \[ p(x, y) = \prod_i p(y_i | y_{i-1}) p(x_i | y_i) \]

- **States** $y$: fields to extract
Problems with HMMs

• Applications need richer input representation

<table>
<thead>
<tr>
<th>Word features</th>
<th>Formatting features</th>
</tr>
</thead>
<tbody>
<tr>
<td>word identity</td>
<td>centered</td>
</tr>
<tr>
<td>capitalization</td>
<td>indentation</td>
</tr>
<tr>
<td>ends in “-tion”</td>
<td>white space ratio</td>
</tr>
<tr>
<td>word in word list</td>
<td>begins with number</td>
</tr>
<tr>
<td>word font</td>
<td>ends with “?”</td>
</tr>
</tbody>
</table>
Generating Multiple Features

- Relax conditional independence of features on labels ⇒ intractability
Structured Linear Models

- Generalize linear classification
  \[ y^* = \arg \max_y w \cdot F(x, y) \]

- Features based on local domains
  \[ F(x, y) = \sum_{C \in C(x)} f_C(x, y) \]
  \[ f_C(x, y) = f_C(x, y_C) \]

- Efficient Viterbi decoding for tree-structured interactions
Learning

- Prior knowledge
- local domains $C(x)$
- local feature functions $f_C$
- Adjust $w$ to optimize objective function on some training data

$$w^* = \arg \min_w \lambda \|w\|^2 + \sum_i L(x_i, y_i; w)$$

regularizer loss
Margin

- Score advantage between correct and candidate classifications

\[ m(x, y, y'; w) = w \cdot F(x, y) - w \cdot F(x, y') \]
Losses

• Log loss ⇒ maximize probability of correct output
  \[ L(x, y; w) = \log \sum_{y'} e^{-m(x, y, y'; w)} \]

• Hamming loss ⇒ minimize distance-adjusted misclassification
  \[ L(x, y; w) = \max_{y'} [d(y, y') - m(x, y, y'; w)]_+ \]

• Search over \( y' \): dynamic programming on “good” graphs
• Combine the best of generative and classification models:
  • Trade off labeling decisions at different positions
  • Allow overlapping features
• Modular
  • factored scoring
  • loss function

Why?
Probabilistic Version

- Sequence *conditional random fields (CRFs)*

\[
p(\mathbf{y} | \mathbf{x}; \mathbf{w}) = \frac{\exp \mathbf{w} \cdot F(\mathbf{x}, \mathbf{y})}{Z(\mathbf{x}; \mathbf{w})}
\]

\[
Z(\mathbf{x}; \mathbf{w}) = \sum_{\mathbf{y}} \exp \mathbf{w} \cdot F(\mathbf{x}, \mathbf{y})
\]

\[
F(\mathbf{x}, \mathbf{y}) = \sum_{i} f_i(\mathbf{x}, \mathbf{y})
\]

\[
f_i(\mathbf{x}, \mathbf{y}) = f_i(y_{i-1}, y_i, \mathbf{x})
\]

- Training criterion: log loss
Features

- Conjunctions of
  - Label configuration
  - Input properties
    - Term identity
    - Membership in term list
    - Orthographic patterns
  - Conjunctions of the these for current and surrounding words
- *Feature induction*: generate only those conjunctions that help prediction
MALLET is an integrated collection of Java code useful for statistical natural language processing, document classification, clustering, information extraction, and other machine learning applications to text.

### Table of contents
1. Getting Started
2. Features
3. Developing in MALLET
4. About the MALLET project
5. Mailing Lists
6. Other relevant software

### Getting Started
Find out about obtaining MALLET and look at a few tutorials.

### Features
The toolkit provides facilities for:

- Several classification methods including naive Bayes, maximum entropy, Boosting, Winnow.
- Maximum entropy classifier training is highly efficient, making use of Nocedal's "Limited-Memory BFGS", an efficient quasi-Newton optimization technique. It also handles arbitrary real-valued features.
- A general framework for finite state transducers.
- An implementation of finite-state Conditional Random Fields, also trained by Limited-Memory BFGS.
- A general framework for optimization (based on "Numerical Recipes in C").
- Recursively descending directories, finding text files.
- Quite arbitrary pipelines of text processing steps.
- Tokenizing a text file, according to arbitrary regular expressions.
- Including N-grams among the tokens.
- Creating real-valued feature vectors, and feature vector sequences.
- Mapping strings to integers and back again, very efficiently.
- Selecting features by information gain, or other measures.
- Building and manipulating feature vectors.
- Saving trained models to disk.
- Performing test-train splits.
- Various evaluation procedures for performing multiple trials, calculating accuracy, precision, recall, F1, etc.

Evaluation

- **Precision** $P$: what proportion of predicted entities are correct
- **Recall** $R$: what proportion of correct entities are predicted
- $F_1$ measure:
  
  $$\frac{2PR}{P + R}$$
Gene/protein results

<table>
<thead>
<tr>
<th></th>
<th>Precision</th>
<th>Recall</th>
<th>F₁</th>
</tr>
</thead>
<tbody>
<tr>
<td>AbGene</td>
<td>63</td>
<td>65</td>
<td>64</td>
</tr>
<tr>
<td>CRF</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>words + spelling</td>
<td>83</td>
<td>77.3</td>
<td>80.1</td>
</tr>
<tr>
<td>(non-)gene tokens + rare trigrams</td>
<td>86.4</td>
<td>78.7</td>
<td>82.4</td>
</tr>
</tbody>
</table>

- Exact match
- AbGene: Brill-style POS and gene tagger, post-processor
## Variation Results

<table>
<thead>
<tr>
<th></th>
<th>Precision</th>
<th>Recall</th>
<th>F</th>
</tr>
</thead>
<tbody>
<tr>
<td><strong>Type</strong></td>
<td>0.80</td>
<td>0.72</td>
<td>0.76</td>
</tr>
<tr>
<td><strong>Location</strong></td>
<td>0.85</td>
<td>0.73</td>
<td>0.79</td>
</tr>
<tr>
<td><strong>State</strong></td>
<td>0.90</td>
<td>0.80</td>
<td>0.85</td>
</tr>
</tbody>
</table>
University of Pennsylvania BioTagger

This is a quick and dirty web-page for information on the UPenn BioTagger software suite. Currently the tagger supports three types of entities – gene entities, genomic variations entities and malignancy type entities.

Please view the README file to learn about usage and input/output format.

Tagger

- [Download tagger](http://www.cis.upenn.edu/~ryantm/software/BioTagger/)
- [View the README file](http://www.cis.upenn.edu/~ryantm/software/BioTagger/)
- [JavaDoc](http://www.cis.upenn.edu/~ryantm/software/BioTagger/)

The core of the tagger is derived from the machine learning package [MALLET](http://www.cis.upenn.edu/~ryantm/software/BioTagger/)

These taggers are based on those discussed in:

- **Identifying and Extracting Malignancy Types in Cancer Literature**
  Y. Jin, R. McDonald, K. Lerman, M. Mandel, M. Liberman, F. Pereira, R.S. Winters and P.S. White
  Linking Literature, Information and Knowledge for Biology, BioLink 2005
  [PDF](http://www.cis.upenn.edu/~ryantm/software/BioTagger/)

- **Identifying gene and protein mentions in text using conditional random fields**
  Ryan McDonald and Fernando Pereira
  BMC Bioinformatics 2005, 6(Suppl 1):S6
  [PDF](http://www.cis.upenn.edu/~ryantm/software/BioTagger/)

- **An entity tagger for recognizing acquired genomic variations in cancer literature**
  R. McDonald, R.S. Winters, M. Mandel, Y. Jin, P.S. White and F. Pereira
  [PDF](http://www.cis.upenn.edu/~ryantm/software/BioTagger/)

Programming Credits: Kevin Lerman, Yang Jin, Eric Pancoast and Ryan McDonald.
Questions: ryantm at cis dot upenn dot edu

Why use FABLE?

FABLE finds MEDLINE articles that mention human genes and proteins more thoroughly than other systems. To search FABLE, type a human gene or protein name into the search bar at the top right, choose search options, and click submit. The result will list MEDLINE articles mentioning this gene. Learn more...

4/5/2006: FABLE release v1.0 provides a way to search MEDLINE for human genes and proteins. Learn more...

http://fable.chop.edu/index.jsp
Technical challenges

- Very large number of features:
  - 820,000 at least once on training set
  - 3,800,000 input tests true at least once
  - most features are term-based

- Slow training
  - online methods
  - stochastic gradient

- Overfitting
  - improve term lists
  - large margin methods
Alternative: online training

- Process one training instance at a time
- Very simple
- Predictable runtime, small memory
- Adaptable to different loss functions

Basic idea:

\[
\begin{align*}
\mathbf{w} &= 0 \\
\text{for } t = 1, \ldots, T : \\
&\quad \text{for } i = 1, \ldots, N : \\
&\quad \text{classify } \mathbf{x}_i \text{ incurring loss } l \\
&\quad \text{update } \mathbf{w} \text{ to reduce } l
\end{align*}
\]
Online maximum margin
(MIRA)

• Project onto subspace where the correct structure scores “far enough” above all incorrect ones

\[ w = 0 \]
for \( t = 1, \ldots, T \):
  for \( i = 1, \ldots, N \):
    \[ w \leftarrow \arg \min_{w'} \frac{1}{2} \|w' - w\|^2 \]
    s.t. \( \forall y : w' \cdot F(x_i, y_i) - w' \cdot F(x_i, y) \geq d(y_i, y) \)

• Exponentially many \( ys \): select best \( k \) instead

• Related to Hamming loss
Lists and Unlabeled Text

Context Pattern Inducer and Entity Extractor

Morgan-Stanley
Google

companies such as <ENT>, joint venture between <ENT> ( analyst at <ENT>)

Morgan Stanley
Google
Goldman-Sachs
Sun
Lists and Unlabeled Text

Context Pattern Inducer and Entity Extractor

- Morgan Stanley
- Google

- analyst at <ENT>
- companies such as <ENT>
- joint venture between <ENT>

Unlabeled Text
Pattern Induction

Seed

Unlabeled Data

Extract Context

Find Triggers

Induce & Prune Automata

Rank

Automata as Extractor

Rank

Extended List

Entity tagger
Person Names


Tiger Woods Andre Agassi Lleyton Hewitt Ernie Els Serena Williams Andy Roddick Retief Goosen Vijay Singh Jennifer Capriati Roger Federer ...
## Improving CRF Tagger

### PER, LOC, ORG

<table>
<thead>
<tr>
<th>Training Data (Tokens)</th>
<th>Test-a</th>
<th>Test-b</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>No List</td>
<td>Seed List</td>
</tr>
<tr>
<td>9268</td>
<td>68.16</td>
<td>70.91</td>
</tr>
<tr>
<td>23385</td>
<td>78.36</td>
<td>79.21</td>
</tr>
<tr>
<td>46816</td>
<td>82.08</td>
<td>80.79</td>
</tr>
<tr>
<td>92921</td>
<td>85.34</td>
<td>83.03</td>
</tr>
<tr>
<td>203621</td>
<td>89.71</td>
<td>84.50</td>
</tr>
</tbody>
</table>

### PER, LOC, ORG, MISC

<table>
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<th>Test-b</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>No List</td>
<td>Seed List</td>
</tr>
<tr>
<td>9229</td>
<td>68.27</td>
<td>70.93</td>
</tr>
<tr>
<td>204657</td>
<td>89.52</td>
<td>84.30</td>
</tr>
</tbody>
</table>

Test Data Sizes: Test-a 51362 tokens, Test-b 46435 tokens
Extensions

• Reducing training data requirements
  • *Pattern induction*
• Unsupervised domain adaptation for linear models: *structural correspondence learning*
• Deeper analysis
  • Syntactic features
    • Structured linear models for *dependency parsing*
• Joint entity-relation extraction
  • Computational challenges in inference and learning