HUMBOLDT-UNIVERSITÄT ZU BERLIN

Maschinelle Sprachverarbeitung

Named Entity Recognition

Ulf Leser

Content of this Lecture

- Named Entity Recognition
- Dictionary-based approaches
- Rule-based approaches
- ML-based approaches
- Case studies

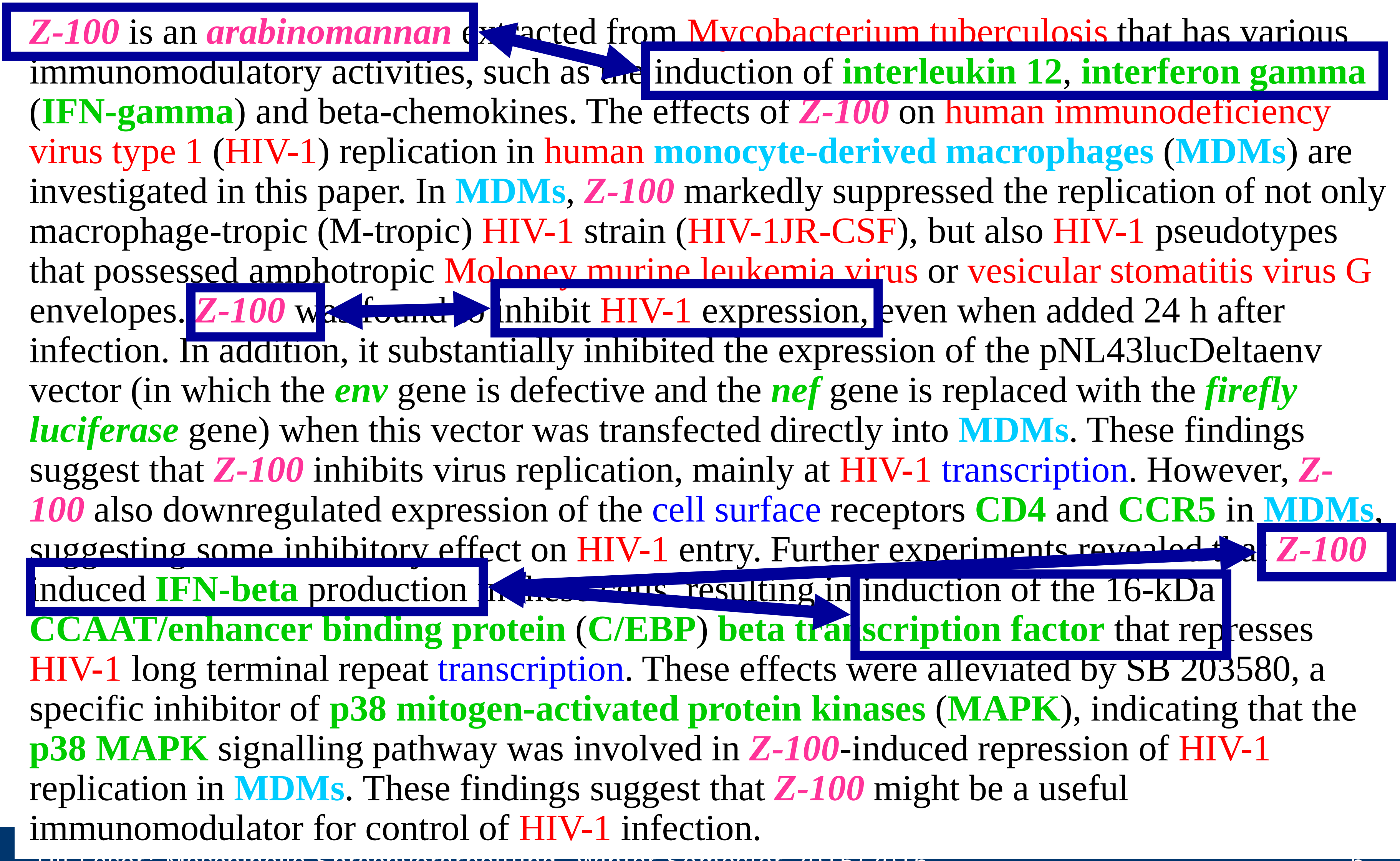
Information Extraction: What we need to do

Z-100 is an arabinomannan extracted from Mycobacterium tuberculosis that has various immunomodulatory activities, such as the induction of interleukin 12, interferon gamma (IFN-gamma) and beta-chemokines. The effects of Z-100 on human immunodeficiency virus type 1 (HIV-1) replication in human monocyte-derived macrophages (MDMs) are investigated in this paper. In MDMs, Z-100 markedly suppressed the replication of not only macrophage-tropic (M-tropic) HIV-1 strain (HIV-1JR-CSF), but also HIV-1 pseudotypes that possessed amphotropic Moloney murine leukemia virus or vesicular stomatitis virus G envelopes. Z-100 was found to inhibit HIV-1 expression, even when added 24 h after infection. In addition, it substantially inhibited the expression of the pNL43lucDeltaenv vector (in which the env gene is defective and the nef gene is replaced with the firefly luciferase gene) when this vector was transfected directly into MDMs. These findings suggest that Z-100 inhibits virus replication, mainly at HIV-1 transcription. However, Z-100 also downregulated expression of the cell surface receptors CD4 and CCR5 in MDMs, suggesting some inhibitory effect on HIV-1 entry. Further experiments revealed that Z-100 induced IFN-beta production in these cells, resulting in induction of the 16-kDa CCAAT/enhancer binding protein (C/EBP) beta transcription factor that represses HIV-1 long terminal repeat transcription. These effects were alleviated by SB 203580, a specific inhibitor of p38 mitogen-activated protein kinases (MAPK), indicating that the p38 MAPK signalling pathway was involved in Z-100-induced repression of HIV-1 replication in MDMs. These findings suggest that Z-100 might be a useful immunomodulator for control of HIV-1 infection.

Find Entity Names (Multiple Classes)

Z-100 is an ***arabinomannan*** extracted from Mycobacterium tuberculosis that has various immunomodulatory activities, such as the induction of **interleukin 12**, **interferon gamma** (**IFN-gamma**) and beta-chemokines. The effects of ***Z-100*** on human immunodeficiency virus type 1 (HIV-1) replication in human **monocyte-derived macrophages** (**MDMs**) are investigated in this paper. In **MDMs**, ***Z-100*** markedly suppressed the replication of not only macrophage-tropic (M-tropic) HIV-1 strain (HIV-1JR-CSF), but also HIV-1 pseudotypes that possessed amphotropic Moloney murine leukemia virus or vesicular stomatitis virus G envelopes. ***Z-100*** was found to inhibit HIV-1 expression, even when added 24 h after infection. In addition, it substantially inhibited the expression of the pNL43lucDeltaenv vector (in which the ***env*** gene is defective and the ***nef*** gene is replaced with the ***firefly luciferase*** gene) when this vector was transfected directly into **MDMs**. These findings suggest that ***Z-100*** inhibits virus replication, mainly at HIV-1 transcription. However, ***Z-100*** also downregulated expression of the cell surface receptors **CD4** and **CCR5** in **MDMs**, suggesting some inhibitory effect on HIV-1 entry. Further experiments revealed that ***Z-100*** induced **IFN-beta** production in these cells, resulting in induction of the 16-kDa **CCAAT/enhancer binding protein** (**C/EBP**) **beta transcription factor** that represses HIV-1 long terminal repeat transcription. These effects were alleviated by SB 203580, a specific inhibitor of **p38 mitogen-activated protein kinases** (**MAPK**), indicating that the **p38 MAPK** signalling pathway was involved in ***Z-100***-induced repression of HIV-1 replication in **MDMs**. These findings suggest that ***Z-100*** might be a useful immunomodulator for control of HIV-1 infection.

Relationship Extraction (RE)



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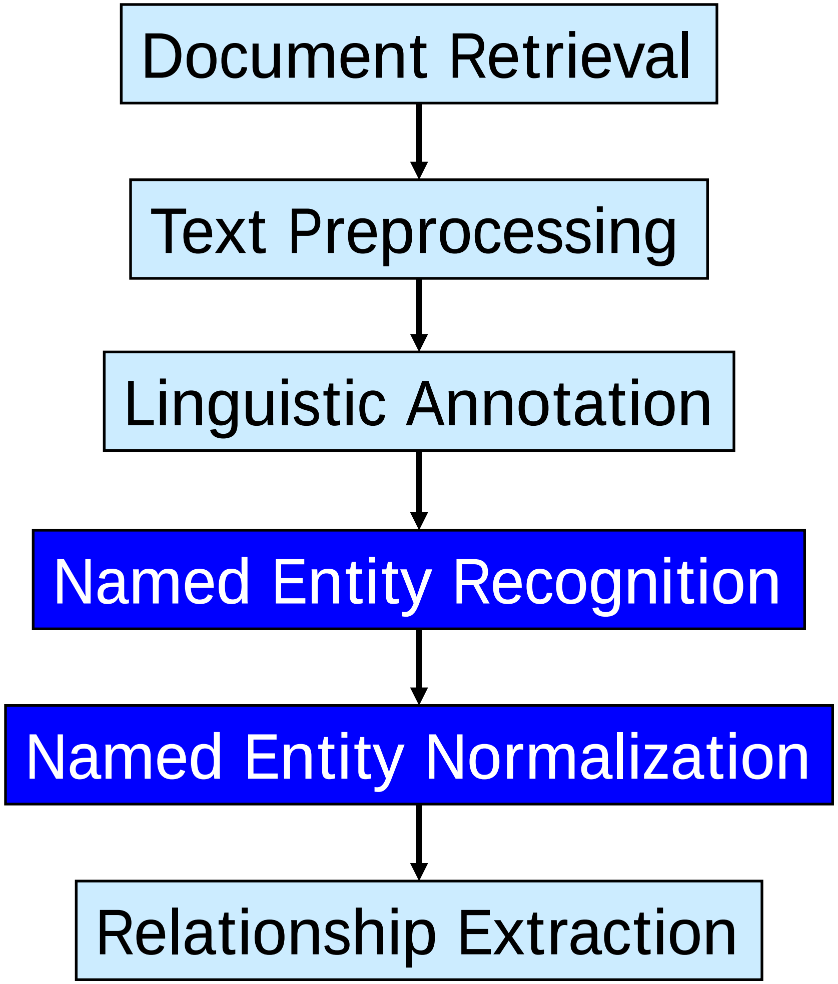
Information Extraction Workflow



Document Retrieval

Text Preprocessing

Linguistic Annotation

Named Entity Recognition

Named Entity Normalization

Relationship Extraction

Named Entity Recognition (NER)

- Named Entity Recognition (NER)
  - Find all mentions of entity names in text
  - For one class (e.g. genes) or multiple classes (e.g. genes, diseases, ...)
  - Entity names may span more than one token (also non-continuous)
  - Does usually not include referential mentions (relative pronouns)
- Word Sense Disambiguation (WSD)
  - Often, tokens (or sets of tokens) can be of multiple classes
    - Bass can be a fish or an instrument
  - WSD: Assign an entity in a text to its correct semantic class (sense)
- Named Entity Normalization (NEN)
  - Map each entity to a canonical ID
    - Highly application specific: Coordinates of geo-locations, DB-IDs of genes, passport-numbers of persons, etc.
  - Typical approach: Map names into a set of names of known entities
  - Necessary to link entities to further information (integration)

Examples

- High plasma AVP levels observed in the two cases suggest that SSRIs stimulate AVP secretion, thereby causing SIADH
- A Drosophila shc gene product is implicated in signaling by the DER receptor tyrosine kinase.
- 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.
- The tumor necrosis factor alpha and dkfzp779b086 bind to the human mono-adp-ribosyltransferase.

Examples

- High plasma AVP levels observed in the two cases suggest that SSRIs stimulate AVP secretion, thereby causing SIADH
  - Requires domain knowledge
- A Drosophila shc gene product is implicated in signaling by the DER receptor tyrosine kinase.
  - Has to deal with ambiguities (context is important)
- 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.
  - Sometimes has no clear answer (borders)
- The tumor necrosis factor alpha and dkfzp779b086 bind to the human mono-adp-ribosyltransferase.
  - May use very specific words or consist of rather common words

Some Funny Gene Names

- Dickkopf, zerknüllt, Spätzle
- a (Entrez Gene 43852)
- Lush (40136); (Protein mediates responses to alcohols)
- Van gogh (35922) (Have swirling wing-hair patterns)
- Wish
- Soul
- the
- ...
- Obviously, all of these are homonyms
- Often, a gene, the caused disease, and the mutation share the same name

Abbreviations

- ACE
  - angiotensin converting enzyme
  - affinity capillary electrophoresis
  - Acetylcholinesterase
  - ACE I, a nephrotoxic drug
  - ACE (Anevrysme de l'aorte abdominale: Chirurgie versus Endoprothese)
  - acetosyringone
  - Addenbrooke's cognitive examination
  - Dirección Médica de Fundació ACE
- Rumors say: >20 definitions for ACE in Medline
  - More than ~620 different definitions in GeneView
- Study says: 80% of all acronyms in Medline are not unique

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Dictionary-Based NER

- Gazetteer or dictionary
  - A gazetteer is a list of geographic names with their location
  - In TM, a gazetteer is a list of names with their canonical ID
- Dictionary-based NER
  - Build a dictionary of all names of entities you are interested in
    - Dictionaries usually include synonyms
  - Match every token in the text against the dictionary
- Efficiency: Build a keyword tree of all entries in the dictionary and use Aho-Corasick for searching
- Important to include fuzzy matches
  - Use algorithms for word similarity search
    - K-difference matching, PETER, LingPipe, etc.
  - But watch for precision

Dynamic Domains

- Can we always build a dictionary of all entities of a class?
  - Finding all street names in Berlin is relatively simple
  - Finding all geographic locations is more difficult
    - Places, buildings, hills, woods, ...
  - Finding all person names in Germany is even more difficult
    - New persons are born all the time
      - Mostly new combinations of known first / last names
    - New names immigrate all the time
    - Other languages are much more innovative with names (initials, J.R: junior, Schewarnadze (son), Saakaschwili (child), Hadschi Halef Omar Ben Hadschi Abul Abbas Ibn Hadschi Dawuhd al Gossarah, ...
  - Finding all company names is still even more difficult
    - Companies are created and closed all the time
    - No real naming conventions (Remember the ".com" phase)
    - Often with fixed elements (GmbH, AG, inc., ...)

Funny First Names [Berliner Zeitung, 2008]

- Regulations in Germany: „Die Schreibweise ist den Regeln der Rechtschreibung unterworfen. Biblische Namen mit negativer Assoziation wie Judas oder Kain sind nicht erlaubt, ebenso wenig Markennamen, die nicht mit Vornamen identisch sind, Adelstitel, Orts- und Städtenamen. Also nichts mit Arizona, Sierra Nevada oder Schweinfurt. Ausnahmen wie Mercedes, Paris und San Diego bestätigen allerdings die Regel. Außerdem muss der Vorname das Geschlecht erkennen lassen, weshalb ein Kind namens Kim einen zweiten Vornamen braucht.“
  - Internationale Promis hätten in Deutschland schlechte Karten. Ist der Name von Nicole Kidmans Tochter Sunday Rose weiblich? Nein, der Sonntag ist so männlich wie Freitag aus Robinson Crusoe. Und was ist mit Gwyneth Paltrows Tochter Apple? Im Deutschen wäre es der Apfel ... Da wir schon mal beim Obst sind: Eine Lehrerin in Neuseeland heißt Cherry. Kirsche. Immerhin: die Kirsche. Auch viele Frauen namens Fern gibt es im Land des Silberfarns. Und ganz im Trend der handy- und SMS-süchtigen jungen Generation kamen im vergangenen Jahr reichlich Knaben namens JJ, C, CJ, T, TJ und AJ auf die Welt. Die weibliche Antwort darauf ist Tequila. Zur besseren Verdauung aller schwer verdaulichen Vornamen.
- Genehmigt: Pepsi-Carola, Napoleon, Rasputin, Rapunzel, Sunshine, Sonne
- Abgelehnt: Möwe, Porsche, Pfefferminze, Lenin, Crazy Horse, Störenfried

Finding Gene Names

- Finding all gene names is really hard
  - New genes are found or genes are re-discovered all the time
  - Definition of a gene is not clear at all (splicing, miRNA, ...)
  - Difference between gene, transcripts, encoded proteins not clear
  - No (successful) naming convention
    - Discoverer, disease, location, phenotype, species, cell type, ...
  - Much “legacy” text which is only a couple of years old
  - Frequent use of abbreviations
  - Use of common English words (hedgehog, Dickkopf, soul, ...)
  - Highly distributed creation process, no central repository
    - Contrast: There are regional “repositories” for company names

Fuzzy Search

- Even in static areas, names need not appear exactly
  - Yahoo, yahoo, Yahoo!, yahoo.com, yaho (typo), ...
  - Die Geissens, die Geissen’s, die Geissen`s, die Geißens, ...
- Solution: Fuzzy or approximate matching
  - Solution 1: Generate a “fuzzified” dictionary
  - Solution 2: Use fuzzy string matching algorithm
- Heuristic variations: “s”, special characters (“.”, “-”, ...), ...
  - Domain-specific
- Domain-independent: Edit-Distance / string similarity
  - Does a good domain-independent similarity measure exist?
  - Even smallest deviations may make a large difference

Properties of Dictionary-Based NER

- For static (closed) classes, dictionary-based NER is perfect
- For dynamic classes
  - Performance depends on task, dictionary size, matching mode, ...
  - Usually one expects high precision
    - A match mostly is correct (provided appropriate configuration)
    - But dictionary-based NER usually disregards context
    - Ambiguous names deteriorate precision
  - ... at rather low recall (incomplete dictionaries)
- Advantages: Simple, fast, includes NEN
- Typical baseline system
- Easiest solution, lay persons use it as synonym for NER

Multi-Token Dictionary-Based NER

- Gene Ontology contains many long entities
  - "*Negative regulation of anterior neural cell fate commitment of the neural plate by fibroblast growth factor receptor signaling pathway*"
- Option 1: Only consider phrases (shallow parsing)
  - Fast, simple
  - But for k>3 token, order is flexible; tokens may be missing; interspersed new tokens; ...
- Option 2: Search all single tokens and aggregate scores
  - Break multi-token entities in single tokens and search all of them
  - Compute aggregated scores within sliding windows
    - Seeing many tokens is good, same order may be rewarded
  - Slow: Usually many matches of single tokens (tokens appearing in many of the entities)

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Rule-Based Systems

- Build on a (usually very large) set of rules that try to capture all possible situations and indications of a NE
  - Rules combine dictionary look-up, token properties (capitalization, special characters, ...), POS tags, context words, ...
  - Examples
    - [PERSON] earns [MONEY]
    - [PERSON] joined [ORGANIZATION]
    - [PERSON] joined [ORGANIZATION] as [JOBTITLE]
    - [Protein] receptor
- Manual, labor-intensive approach
- Some of the best systems are (were?) use rule-bases
  - Use ML-based NER and rules for filtering false positives
- Example: ANNIE (in GATE)

Learning Rules

- Rules can also be learned from gold standard corpora
- Find patterns characteristic for the searched entities
  - Appear (frequently) around positive instances
  - Do not (rarely) appear around elsewhere
- Rule abstraction is vital
  - Word at this position? Around this position? Word like this?
  - Must be a verb-pasttense-1stperson-sg; verb-1stperson-sg; ...
- Requires very large GS-corpora
- Still: Zipf's law implies low recall

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- Machine Learning-based approaches
  - NER as classification
  - Sequential tagging: HMMs, MEMMs, CRFs
- Case studies

Classification-Based NER

- Classify each token as entity or not
  - Learn model based on manually annotated training text
- Advantages
  - Usually high quality results, but problems with multi-token names
  - Recognizes unseen entities (provided a proper feature set)
  - We “only” need a corpus, quick adaptation to new tasks
  - Implicitly performs weak form of WSD
    - If context is encoded as features
- Disadvantages
  - Often slow (depends on ML-method)
  - Needs large amount of high-quality training data
  - Requires additional NEN step

Typical Features

- [Biased towards gene / protein name recognition]
- Surface features
  - The word itself – how often at start of / within entity name?
  - Character uni-, bi-, tri-grams
  - POS tag
  - Length
  - Discrete properties (to be defined manually)
    - Has capital letters, all capital letters, more capital letters
    - Has Greek/Roman letters, special characters, digits, all digits
      - 3’-mRNA, 5-alpha-reductase, EST94F88G, ...
    - Abstraction: is of class DDUU, DDSS, DDCDD, ...
      - Digits, small case letter, upper case letter, special characters, ...
      - Max include contraction: 1.999.000,99 -> D.DDD.DDD,DD -> D.D.D,D
  - ...

More Features

- Context features
  - POS tag of surrounding tokens (implicit sequential information)
  - NER tag of preceding tokens (implicit sequential information)
  - Presence of indicator words within a certain distance
    - Protein, human, enzyme, plasma, ...
- External knowledge
  - Token (or closed-by tokens) matches in a dictionary
- Memory
  - Most frequent tag for this token in texts
  - Most frequent tag for surrounding tokens in corpus
- Others (creativity!)
  - E.g. Number of matches in Google versus PubMed

Classifiers and Ensembles

- Popular choices: SVM / Maximum Entropy / HMMs
- Ensembles: Use different classifiers and vote
- Example results

Classification	**LOC**	**MISC**	**ORG**	**PER**
MxE24$_1$	77.81	57.49	78.83	85.41
TMB24	75.49	53.19	77.44	83.89
MxE25	78.27	58.22	78.64	85.60
TMB25$_2$	75.15	52.94	77.79	85.36
HMM$_3$	71.15	45.69	72.95	70.20
Voting$_{1,2,3}$	78.46	57.00	78.93	86.52

Source: Kozareva, JRC Workshop, 2005

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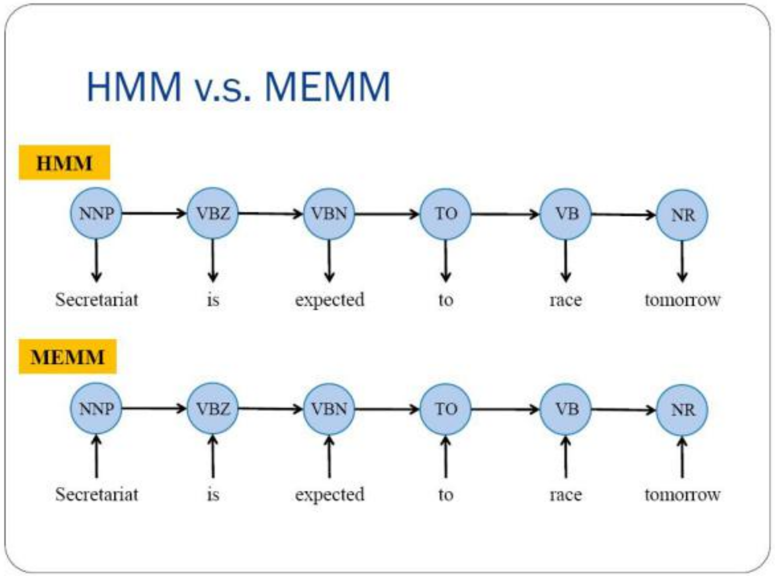
Sequential Tagging using HMMs

- Recall POS tagging with HMMs
  - Fix a set of classes (POS tags)
  - Learn probabilities as state transitions and emissions
  - Encode as Hidden Markov Model
  - Given a new text, find most probable sequence of tags (Viterbi)
- Can readily be applied to NER – with proper tag set
  - Very popular: IOB (Begin of name, In a name, Other)
- But: Using only tag sequence not enough for high quality
  - Too coarse-grained (only three classes)
  - Need to look at the words and their features, not just their tags

MEMM: Maximum Entropy Markov Models (sketch)

- HMMs are generative models (like Naive Bayes)
- MEMM: A discriminative sequential classifier
  - We predict output (e.g. IOB) from sequential observations (token)
  - MEMM model only transition probabilities, but conditional on the observations which are represented using feature functions
    - Feature functions are derived from the observation
    - May take tokens “as is” or use abstractions
      - “is a noun”, “has capital letter”, …
  - ME principle to learn conditional transition probabilities is applied separately for each transition from a state q to all next states
  - Training: GIS algorithm for each state as in ME classification
  - Decoding: Variation of Viterbi algorithm

Visual Explanation



Source: https://liqiangguo.wordpress.com/2011/04/18/

Conditional Random Fields (sketch)

- MEMM suffer from Label Bias Problem: Transitions from labels with few successor states get higher probabilities and thus dominate inference
  - Because outgoing probabilities must sum to 1 in each state
  - MEMM is a local model (in each state)
- CRF are global models and directly infer p(Y|X) over the entire sequence of labels Y and observations X
  - Lafferty, McCallum, Pereira. "Conditional random fields: Probabilistic models for segmenting and labeling sequence data.„. Technical Report, Upenn (2001).
  - Transitions probabilities may depend on future observations and future states – all combinations are considered during inference
- Decoding is simple (Viterbi), learning is more complex

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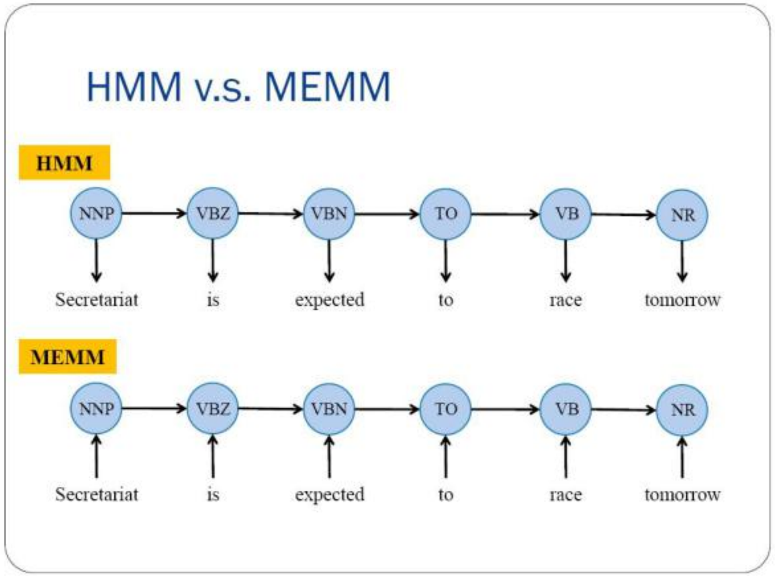
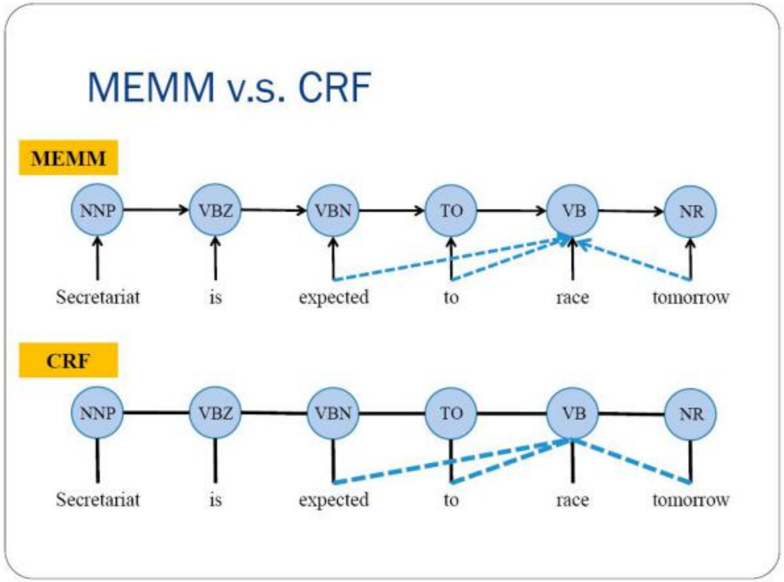
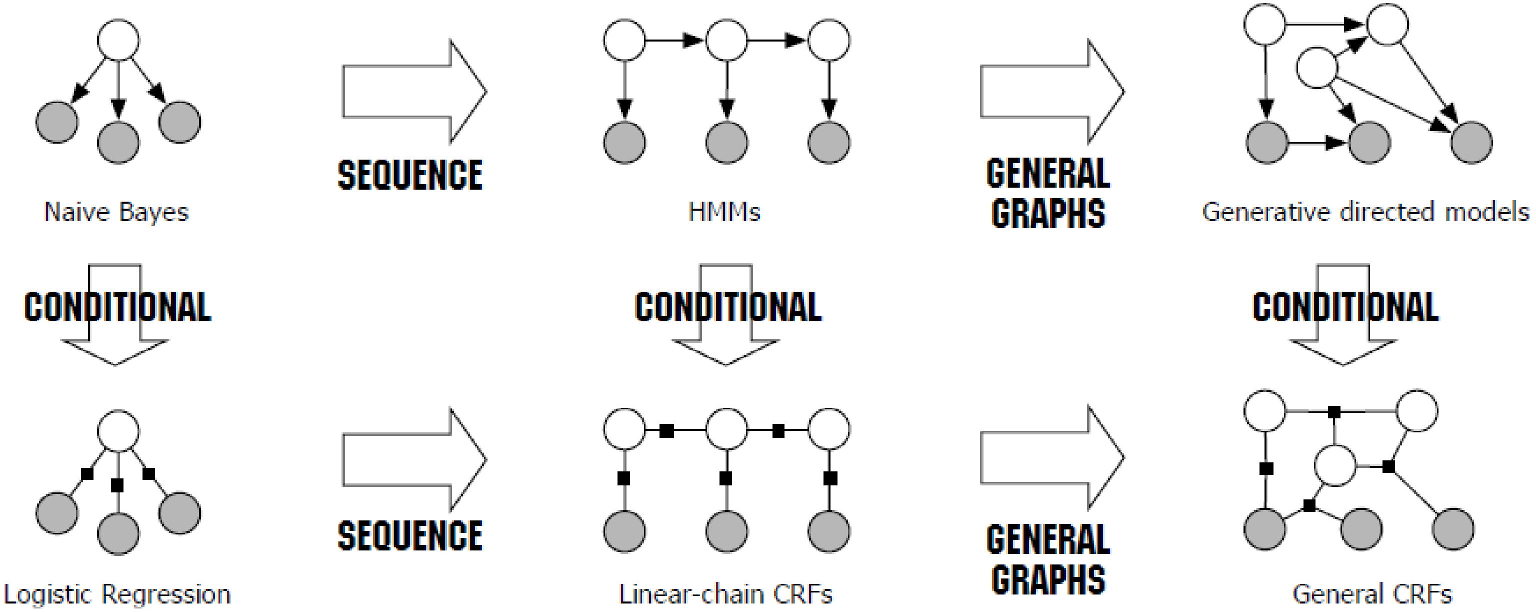




Source: https://liqiangguo.wordpress.com/2011/04/18/

Linear-Chain CRF

- General CRF may condition on every state in the sequence
- Linear-chain CRF restrict the scope of features to those of the surrounding states to make inference more efficient
    - And to make learning less data-demanding



Sutton, McCallum (2011): An Introduction to Conditional Random Fields

Comparison

	HMM	MEMM	CRF
Type	Generative	Discriminative	Discriminative
Model	Local	Local	Global
Decoding method	Viterbi-style	Viterbi-style	Viterbi-style
Independence assumption (token-next state)	Yes	No	No
Arbitrary feature functions	No (difficult)	Yes	Yes
Label bias problem	Yes	Yes	No
Learning	Fast	Fast	Slow
Decoding	Fast	Fast	Fast

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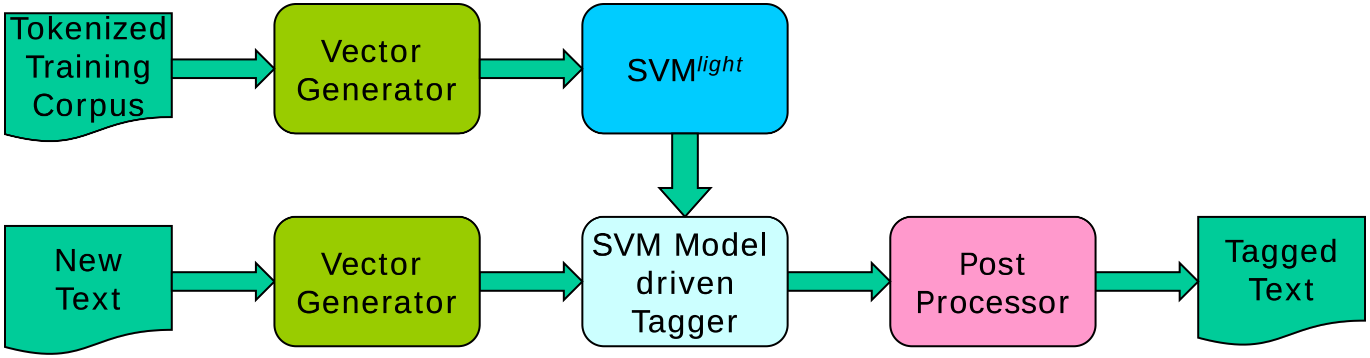
- ML-based approached
- Case studies
  - BioCreative
  - MUC conferences

BioCreative Cup 2004

- Critical Assessment of Information Extraction Systems in Biology
- International competition, three tasks
- Training data and evaluation script provided by organizers in cooperation with database curators (Swiss-Prot)
- Test data available for one week
- Evaluation of all submissions by (published) scripts
- Major boost: Top systems reached 84 F1-measure
  - Previous best systems around 60 F1-Measure
  - Possibly not much further improvements since then
  - Fields splits up: Species, NER/NEN, NER/PPI, ...

Example: SVM for NER



- Corpus of 7500 sentences
  - 140.000 non-gene words
- SVM$^{\text{light}}$ on different feature sets
- Dictionary compiled from Genbank, HUGO, MGD, YDB
- Post-processing for compound gene names

Features

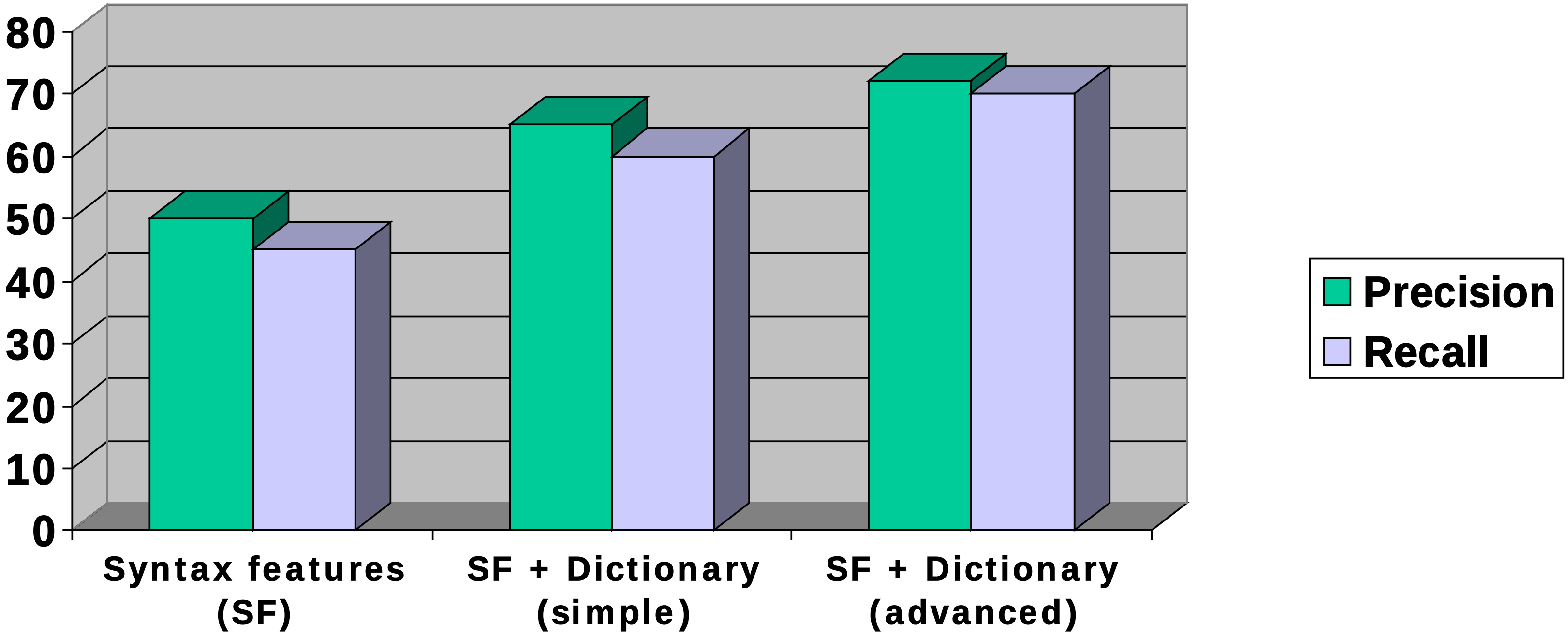
Feature	**Weight**	**Example**
Word	tf * idf	kinase
n-grams		
N=1	tf * idf	k, i, n, a, s, e
N=2	tf * idf	ki, in, na, as, se
N=3	tf * idf	kin, ina, nas, ase
Special signs		
HasNumbers	[1|0]	p300
HasCapitals	[1|0]	abLIM
AllCaps	[1|0]	DMD
InitCap	[1|0]	Pax
HasNumbers & Letters	[1|0]	cMOAT2, EST90757
Context		
predecessing word	[1|0]	Gene
succeeding word	[1|0]	Product
distance to keywords	1/(1+dist)	(list of 15)
Dictionary		
Word match	[1|0]	
Phrase match	[1|0]	

Post-processing

- SVM detects only single token candidates
- Most gene names are multi-token names
- Expand detected single-token genes based on set of heuristic rules (found in an unsystematic manner)

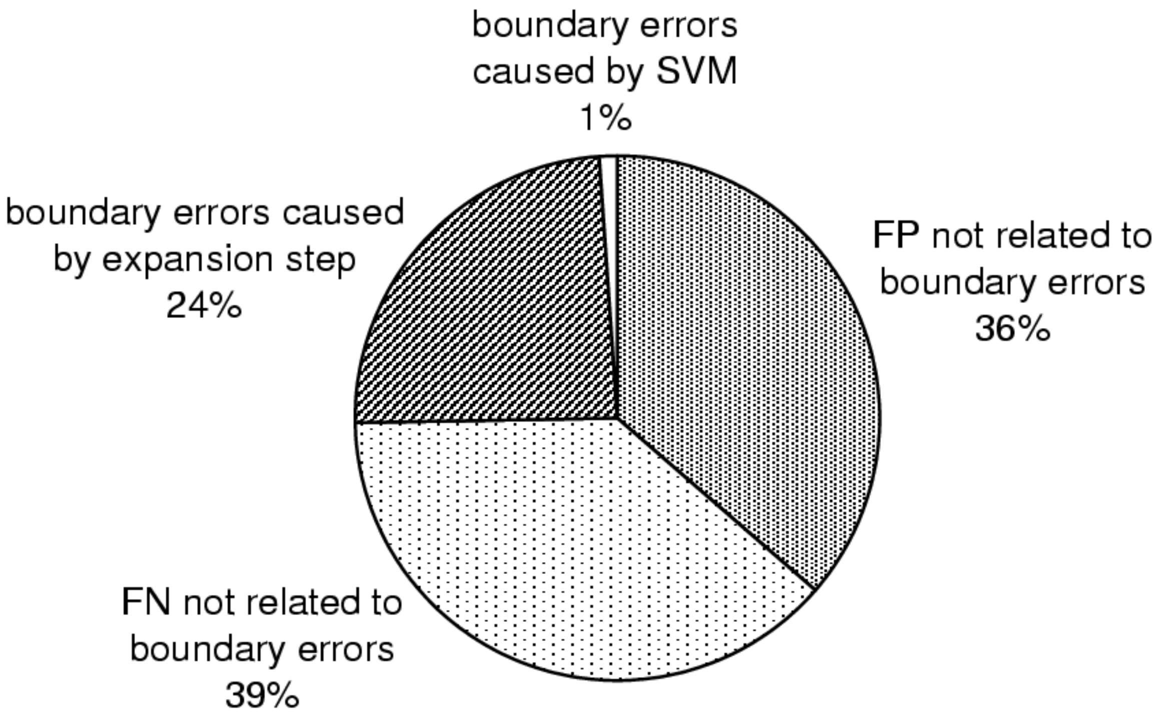
GENE NN*	→	GENE GENE
NN* GENE	→	GENE GENE
GENE (NN)	→	GENE (GENE)
GENE protein	→	GENE GENE
GENE ADJ GENE	→	GENE GENE GENE

Performance



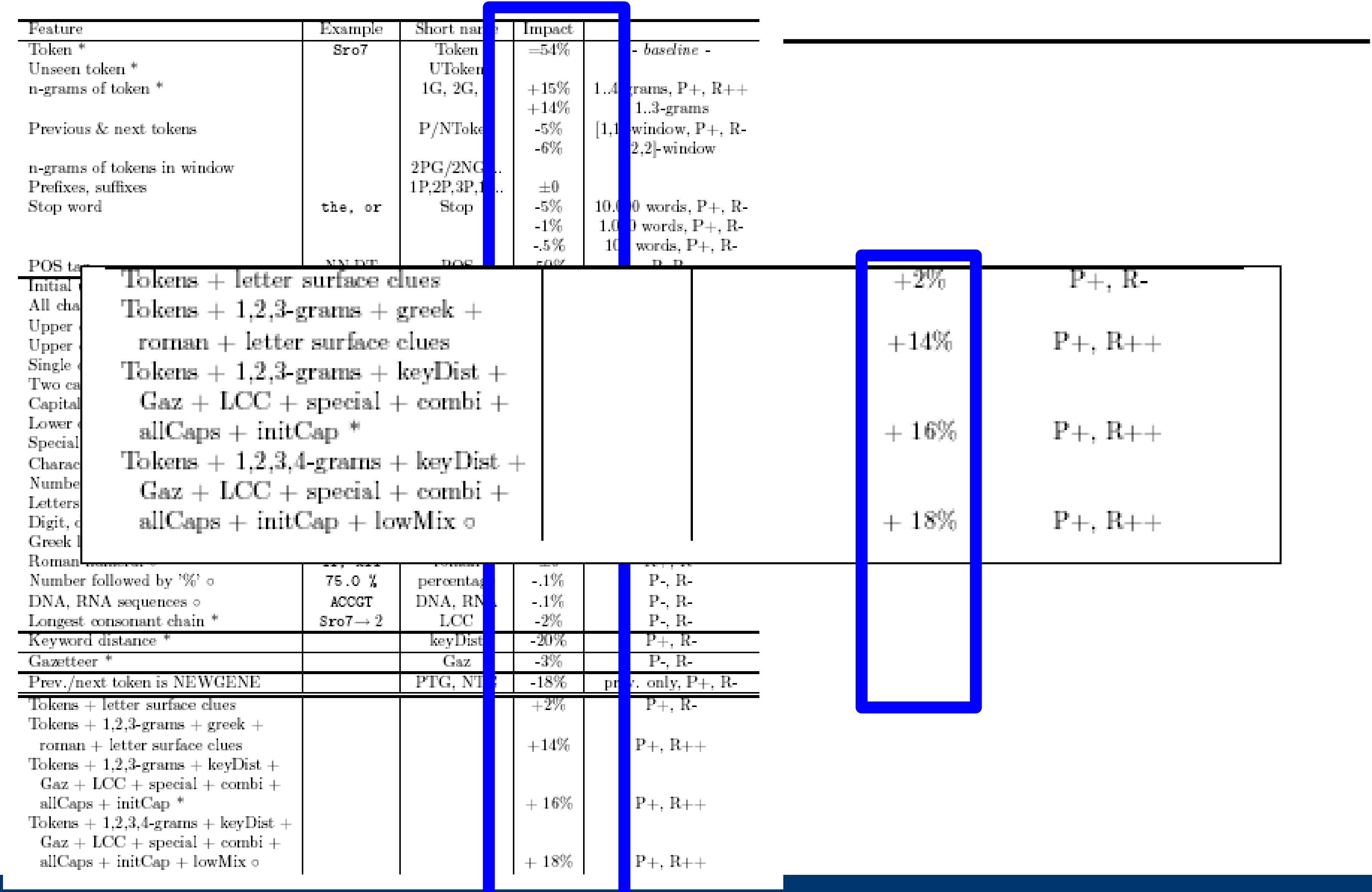
- Best result for BioCreative Cup: 73 F-measure
  - 12 percentage point increase by post-processing only
- Raises from 73 to 83 for loose evaluation

Where did we Fail?



- „Boundary error“ – problems with multi-word phrases
- >70% of errors are token classification errors from SVM

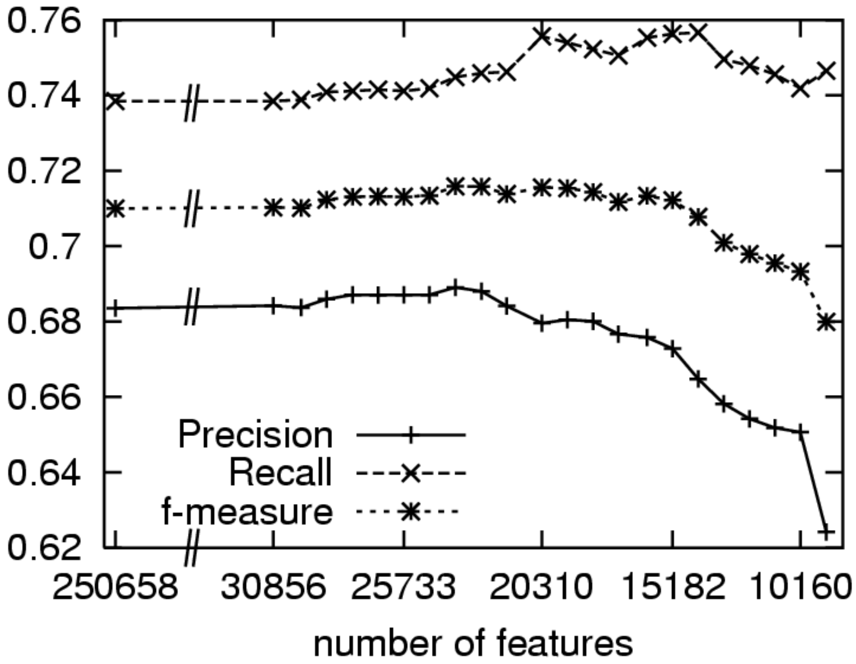
Impact of Feature Classes



Feature	Example	Short nar	Impact	
Token *	`Sro7`	Token	=54%	- *baseline* -
Unseen token *		UToken		
n-grams of token *		1G, 2G,	+15% +14%	1..4 grams, P+, R++ 1..3-grams
Previous & next tokens		P/NToke	-5% -6%	[1,1 window, P+, R- 2,2]-window
n-grams of tokens in window		2PG/2NG ..		
Prefixes, suffixes		1P,2P,3P,1 ..	±0	
Stop word	`the, or`	Stop	-5% -1% -.5%	10.0 0 words, P+, R- 1.0 0 words, P+, R- 10 words, P+, R-
POS ta				
Initial				
All cha				
Upper				
Upper				
Single				
Two ca				
Capital				
Lower				
Special				
Charac				
Numbe				
Letters				
Digit, c				
Greek l				
Roman				
Number followed by '%' ○	`75.0 %`	percentag	-.1%	P-, R-
DNA, RNA sequences ○	`ACCGT`	DNA, RN	-.1%	P-, R-
Longest consonant chain *	`Sro7`→ 2	LCC	-2%	P-, R-
Keyword distance *		keyDist	-20%	P+, R-
Gazetteer *		Gaz	-3%	P-, R-
Prev./next token is NEWGENE		PTG, NT	-18%	pr . only, P+, R-
Tokens + letter surface clues			+2%	P+, R-
Tokens + 1,2,3-grams + greek + roman + letter surface clues			+14%	P+, R++
Tokens + 1,2,3-grams + keyDist + Gaz + LCC + special + combi + allCaps + initCap *			+ 16%	P+, R++
Tokens + 1,2,3,4-grams + keyDist + Gaz + LCC + special + combi + allCaps + initCap + lowMix ○			+ 18%	P+, R++

Tokens + letter surface clues			+2%	P+, R-
Tokens + 1,2,3-grams + greek + roman + letter surface clues			+14%	P+, R++
Tokens + 1,2,3-grams + keyDist + Gaz + LCC + special + combi + allCaps + initCap *			+ 16%	P+, R++
Tokens + 1,2,3,4-grams + keyDist + Gaz + LCC + special + combi + allCaps + initCap + lowMix ○			+ 18%	P+, R++

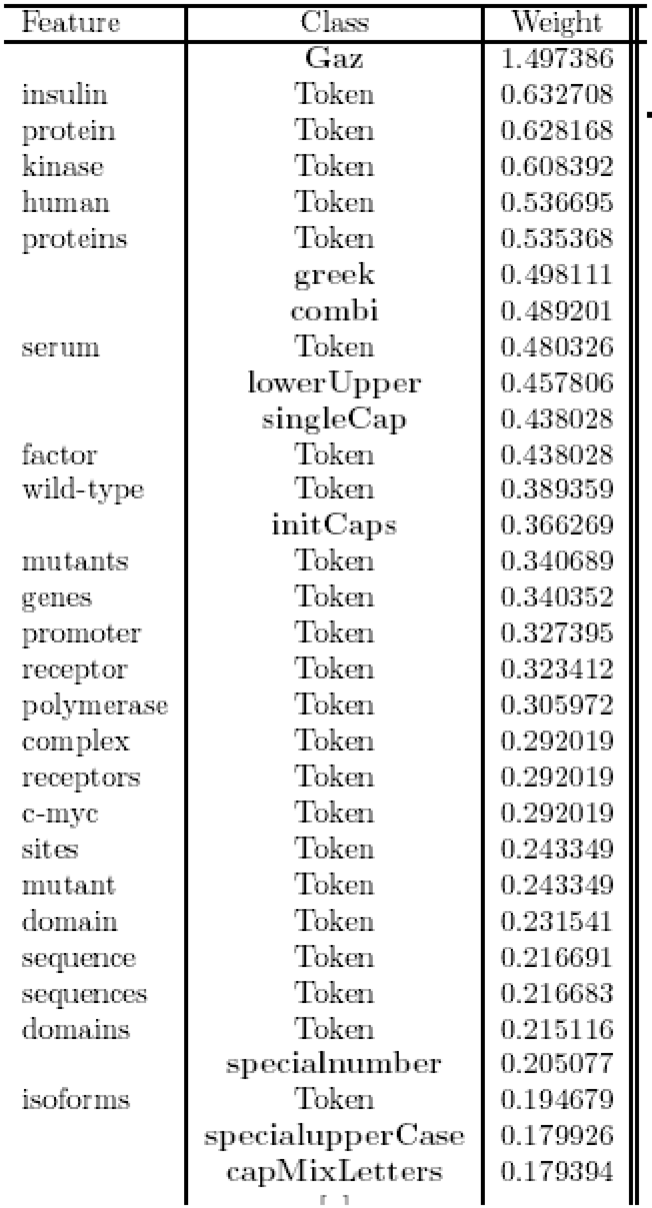
Do we need them all?



- Repeated elimination of 5% least discriminating features
- Eliminating 95% of features costs only 2% F-Measure

Which Ones?

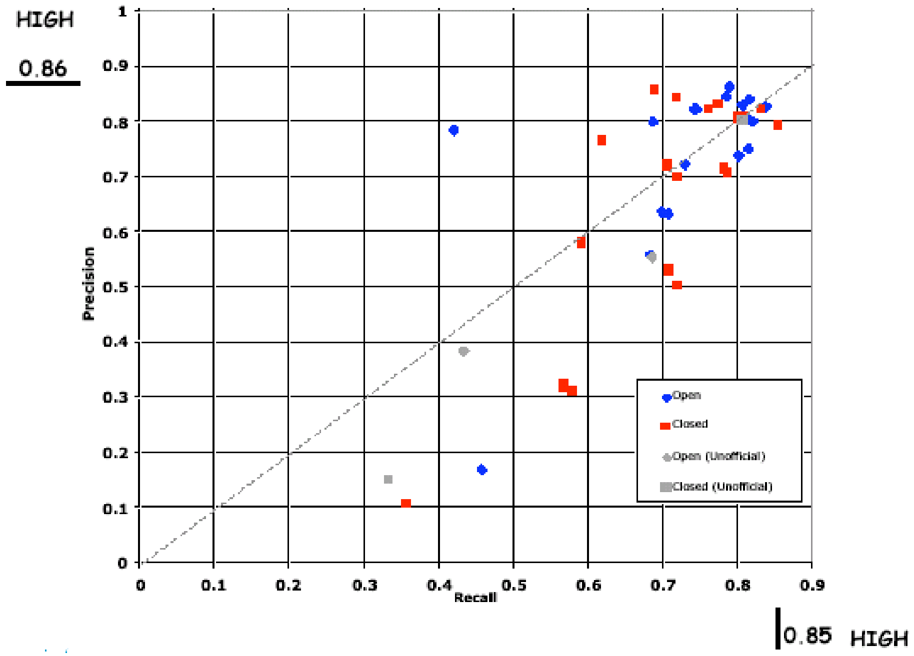
- Single features from different classes are among the most important ones
- Difficult to remove entire classes of features



Feature	Class	Weight
	Gaz	1.497386
insulin	Token	0.632708
protein	Token	0.628168
kinase	Token	0.608392
human	Token	0.536695
proteins	Token	0.535368
	greek	0.498111
	combi	0.489201
serum	Token	0.480326
	lowerUpper	0.457806
	singleCap	0.438028
factor	Token	0.438028
wild-type	Token	0.389359
	initCaps	0.366269
mutants	Token	0.340689
genes	Token	0.340352
promoter	Token	0.327395
receptor	Token	0.323412
polymerase	Token	0.305972
complex	Token	0.292019
receptors	Token	0.292019
c-myc	Token	0.292019
sites	Token	0.243349
mutant	Token	0.243349
domain	Token	0.231541
sequence	Token	0.216691
sequences	Token	0.216683
domains	Token	0.215116
	specialnumber	0.205077
isoforms	Token	0.194679
	specialupperCase	0.179926
	capMixLetters	0.179394

Other Systems

- Best: MMEM or CRF
- Much larger feature sets
- Use of ensembles trained on different corpora
- Current state-of-the-art
  - F-measure ~85%
  - Strongly dependent on eval corpus
  - Inter-annotator agreement assumed at ~90%
  - Loose evaluation reaches >90%
  - Still less than MUC results



Gene-NER: Why is it hard?

- „Scientists would rather share each other‘s underwear than use each other‘s nomenclature“ [Keith Yamamoto]
- Ambiguous gene names and high number of acronyms
  - The, white, ACL, ...
- Small training and eval corpora, mostly only abstracts
- Strict vs. loose matching (up to 20% in F1 difference)
- Generally little agreement on gene names (low IAA)
- Cross-corpus performance
  - All corpora differ in scope and size
    - Method trained on corpus A performs bad on corpus B
  - Domain Adaptation Problem

Content of this Lecture

- Named Entity Recognition
- Dictionary-based approaches
- Rule-based approaches
- ML-based approached
- Case studies
  - BioCreative
  - MUC conferences

Message Understanding Conferences (MUC)

- Large conferences and competitions (1987 – 1998)
- Initiated and funded by DARPA (among other)
- Similar to TREC, but focusing on information extraction / named entity recognition
- Tasks including co-reference resolution
- Template filling / “model-based” IE

Mr. John Smith was appointed CEO of ACME last December 31.

Name:	John Smith
Post:	CEO
Company:	ACME
Date:	December 31

Corpora

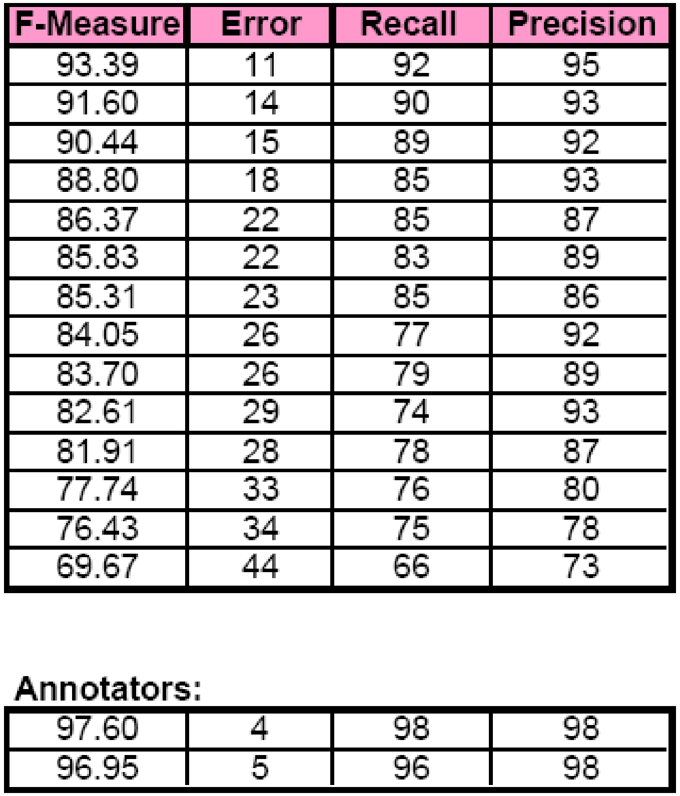
Year	**Conference**	**Domain**
1987	MUC-I	Navy messages
1989	MUC-II	Navy messages
1991	MUC-3	News about terrorist attacks
1992	MUC-4	News about terrorist attacks
1993	MUC-5	Company news (joint-ventures, micro-electronics production)
1995	MUC-6	Company news (management succession)
1998	MUC-7	Airline company orders

Source: Boullosa, NER

Results (MUC-7, 1998)

Task	Recall (%)	Precision (%)
Named Entity (NE)	92	95
Coreference	63	72
Scenario Template (complete events)	47	70

Systems (MUC-7, 1998)

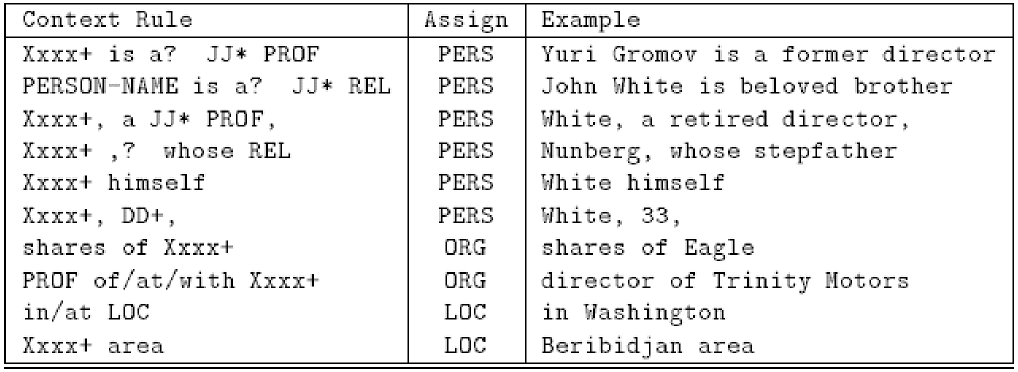


F-Measure	Error	Recall	Precision
93.39	11	92	95
91.60	14	90	93
90.44	15	89	92
88.80	18	85	93
86.37	22	85	87
85.83	22	83	89
85.31	23	85	86
84.05	26	77	92
83.70	26	79	89
82.61	29	74	93
81.91	28	78	87
77.74	33	76	80
76.43	34	75	78
69.67	44	66	73

Annotators:

97.60	4	98	98
96.95	5	96	98

- Best system is a hybrid between an extensive set of rules and a ME classifier



Context Rule	Assign	Example
Xxxx+ is a? JJ* PROF	PERS	Yuri Gromov is a former director
PERSON-NAME is a? JJ* REL	PERS	John White is beloved brother
Xxxx+, a JJ* PROF,	PERS	White, a retired director,
Xxxx+ ,? whose REL	PERS	Nunberg, whose stepfather
Xxxx+ himself	PERS	White himself
Xxxx+, DD+,	PERS	White, 33,
shares of Xxxx+	ORG	shares of Eagle
PROF of/at/with Xxxx+	ORG	director of Trinity Motors
in/at LOC	LOC	in Washington
Xxxx+ area	LOC	Beribidjan area

Source: Mikheev, Grover, Moens, „DESCRIPTION OF THE LTG SYSTEM USED FOR MUC-7“