

Explainable Machine Learning Models for Structured Data

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Overview

- **Structured Data**
 - Symbolic Sequences (e.g., DNA, malware)
 - Numeric Sequences (e.g., time series)
- **Explainable Learning Models**
 - Black-Box vs Linear Models with Rich Features
- **SEQL: Sequence Learning with All-Subsequences**
 - Framework for Sequence Classification & Regression

Structured Data: Sequences & Time Series

Many Applications:

- **DNA**

Value	Data points
290.507	AGGGCATCATGGAGCTGTCCAG
679.305	ATCACAATTTTGCCGAGAGCGA
1998.715	GTACACCCCGTTTCGGCGGCCCA
447.803	CCTTTAGCCCATCGTTGGCCAA

Byte sequence

- **Malware**

Class	Data points
+1	C7 01 24 04 5F 0E EA DC 00 E9 D6 4A 00 0C 66 89
+1	74 13 BA EF 01 00 06 68 95 14 88 B7 00 0F 0E EA
-1	08 F9 C8 1A 80 C1 8B 48 40 00 89 51 10 B8 04 00
-1	B8 00 00 00 00 50 E8 D8 00 00 00 83 C4 04 53 FF

- **Sensors**

0	-0.26927	-0.26927	-0.26927	-0.26927	-0.26927
1	-0.46887	2.748	1.6263	-0.46887	-0.46887
0	2.2429	-0.39296	-0.39296	-0.39296	-0.39296
0	-0.45836	2.4229	-0.45836	2.5162	1.9876
0	-0.58609	-0.58609	-0.58609	-0.58609	-0.58609
0	1.8657	-0.44769	-0.44769	-0.44769	1.7914
0	1.3541	1.9638	-0.53962	-0.53962	-0.53962

Explainable Machine Learning Models

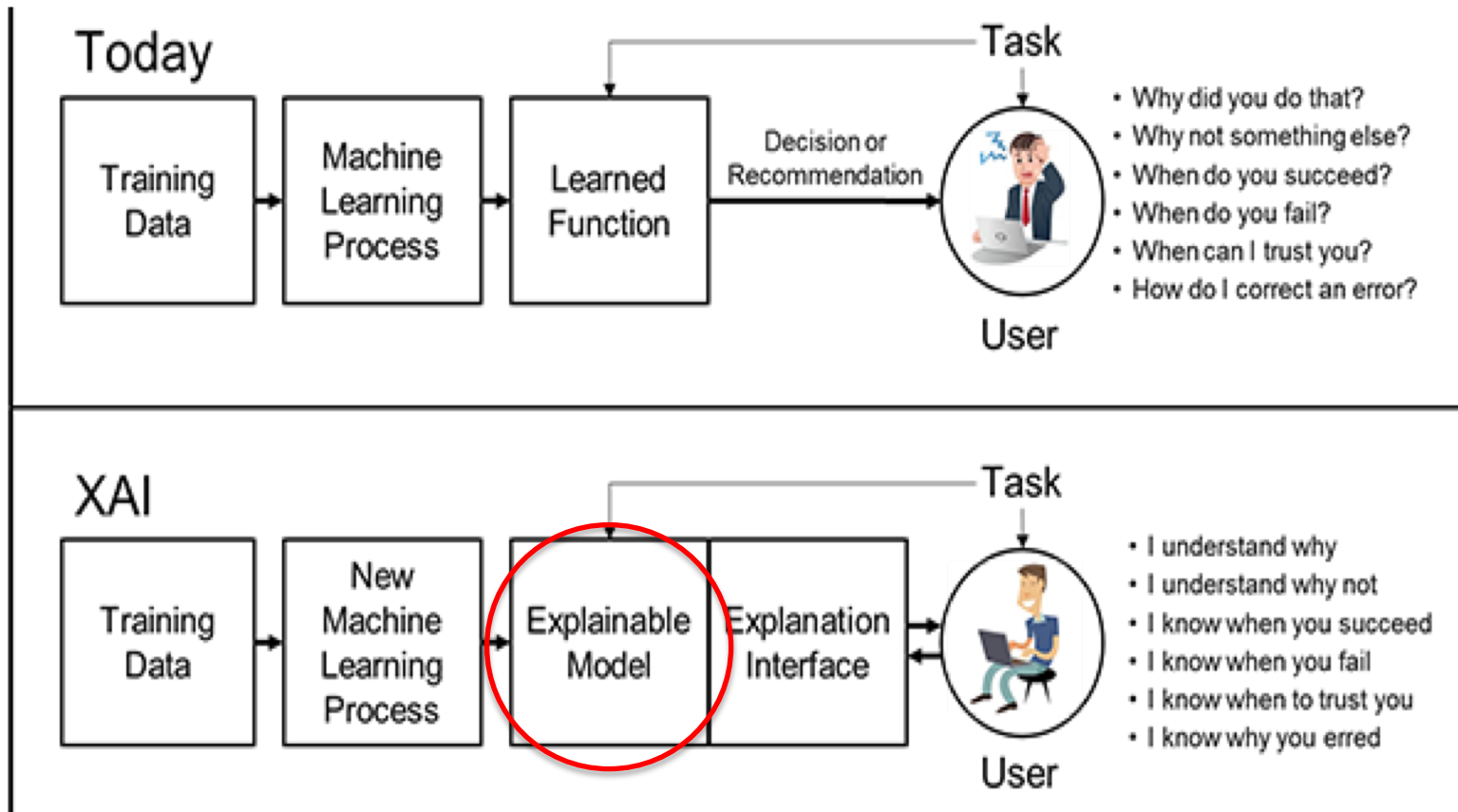
- **Accuracy & Efficiency:**

- Many accurate algorithms: e.g., ensembles (Random Forest), Deep Neural Networks; but hard to interpret big, complex models
- Large volumes of data, need efficient models

- **Interpretability:**

- White box (linear models) vs black box (deep nets)
- Interpretable AI is a big deal: Darpa Explainable AI (XAI; 2016), EU GDPR legislation (May 2018)

Darpa Explainable AI (XAI)



[Source: <http://www.darpa.mil/program/explainable-artificial-intelligence>]

SEQL: Sequence Learning with All-Subsequences

Key Idea: **Linear Models with Rich Features are Accurate and Interpretable**

- Linear models are **interpretable and well understood** (linear regression, logistic regression).
- Linear models with rich features are **accurate** (similar accuracy to ensembles, kernel-SVM, deep nets).
- **Efficiently optimize linear models:** We exploit the structure of a massive feature space (all-subsequences) to quickly select good features.

SEQL: Linear Models for Symbolic Sequences

Solution Approach **SEQL:** all-subsequences are candidate features;
focus on selecting good features quickly

Score	Sequence
290.5	AGTC CACAA GGCTAGGATAGCTAT TCCG GATCGA
315.1	TATCCTGCAGTACAAG TCCG TAATT CACAA TCCA
805.6	AGTCCGCT TAGGCT AGGATAGCTAGCCCGATCGA
799.7	AGCCAAGACCTGAAAT TAGGCT CCTGAGATACAG
???	CGGGTCGTAT TCCG CACTGAATATCT TAGGCT TACG

SEQL Model:

Weight	k-mer
796.6	TAGGCT
402.5	CACAA
-125.3	TCCG

Goal is to learn a mapping:

$$f: S \rightarrow \mathbb{R}$$

Linear model (weighted sum of features):

$f(x) = \beta^t x$, with β the feature weights and x the feature vector

SEQL: Linear Models for Symbolic Sequences

Add features iteratively with greedy coordinate descent + branch-and-bound (bound the search for the best feature)

Algorithm 1 Coordinate Descent with Gauss Southwell Selection

- 1: Set $\beta^{(0)} = 0$
 - 2: **while** termination condition not met **do**
 - 3: Calculate objective function $L(\beta^{(t)})$
 - 4: **Find coordinate j_t with maximum gradient value**
 - 5: Find optimal step size η_{j_t}
 - 6: Update $\beta^{(t)} = \beta^{(t-1)} - \eta_{j_t} \frac{\partial L}{\partial \beta_{j_t}}(\beta^{(t-1)}) e_{j_t}$
 - 7: Add corresponding feature to feature set
 - 8: **end while**
-

Key Ideas

Bound gradient of k-mer using only information about its sub-k-mers.

Example

Given: $s_p = \text{"ACT"}$

Calculate bound: $\mu(s_p)$

$s_1 = \text{"ACTC"}$ $\rightarrow \text{gradient}(s_1) \leq \mu(s_p)$

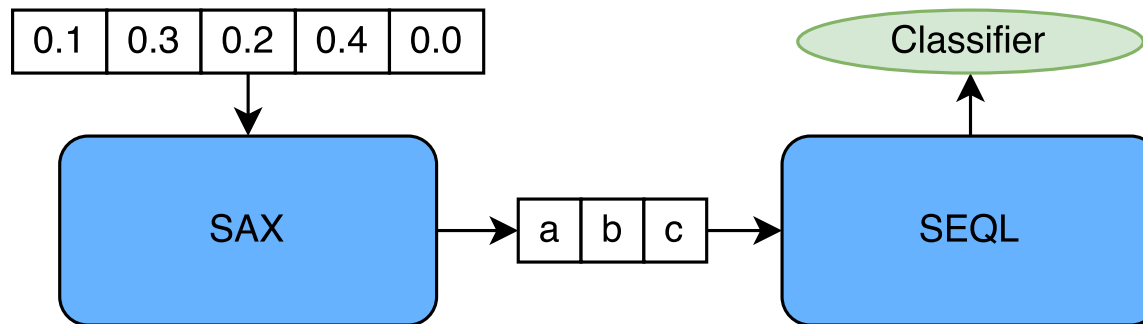
$s_2 = \text{"AACT"}$ $\rightarrow \text{gradient}(s_2) \leq \mu(s_p)$

$s_3 = \text{"TACTG"}$ $\rightarrow \text{gradient}(s_3) \leq \mu(s_p)$

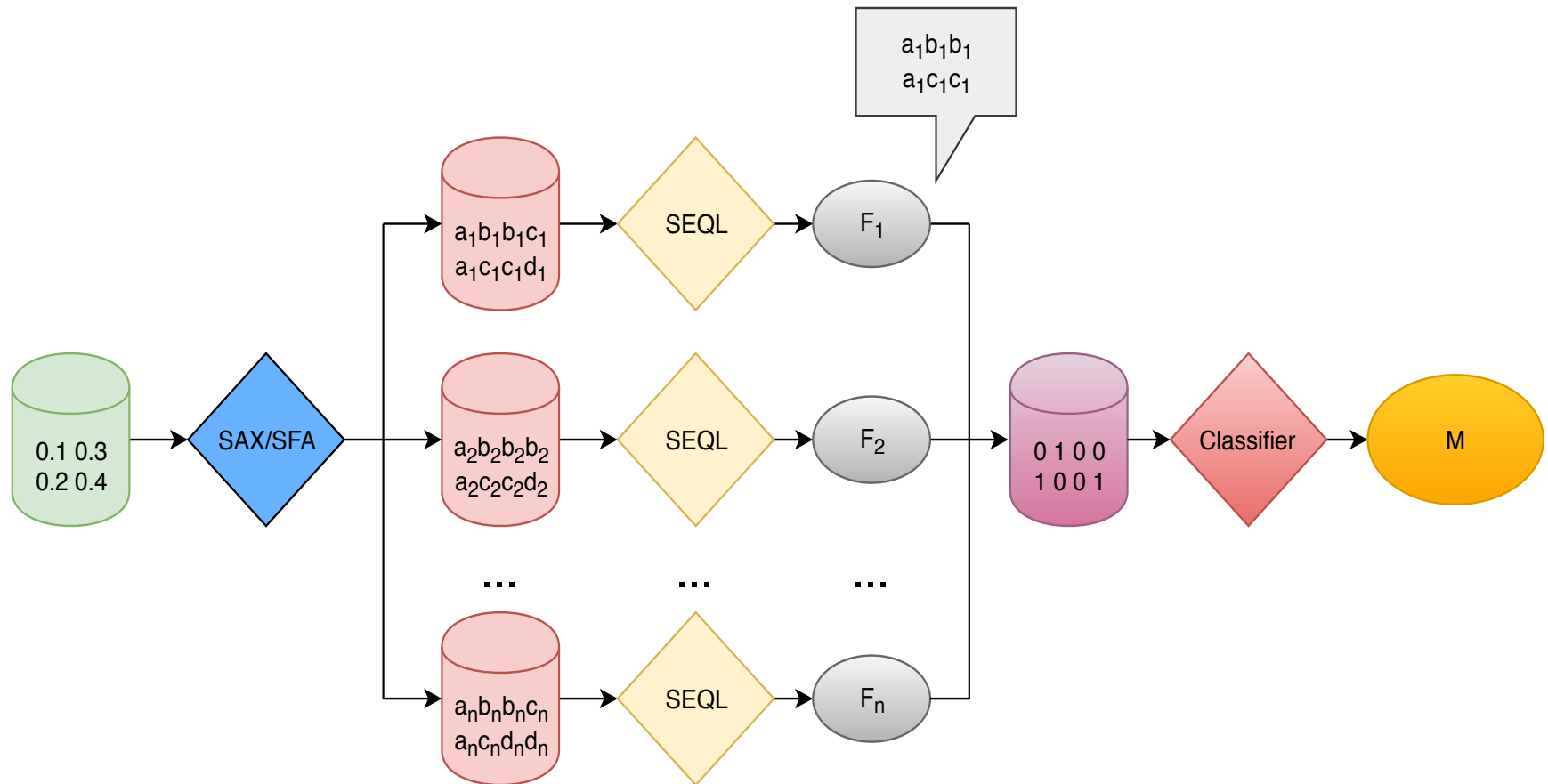
How do we find coordinate j_t efficiently?

SEQL for Time Series Classification

Time Series → Discretisation (SAX, SFA) → Symbolic Sequence → Sequence Learner (SEQL)



SEQL for Time Series Classification



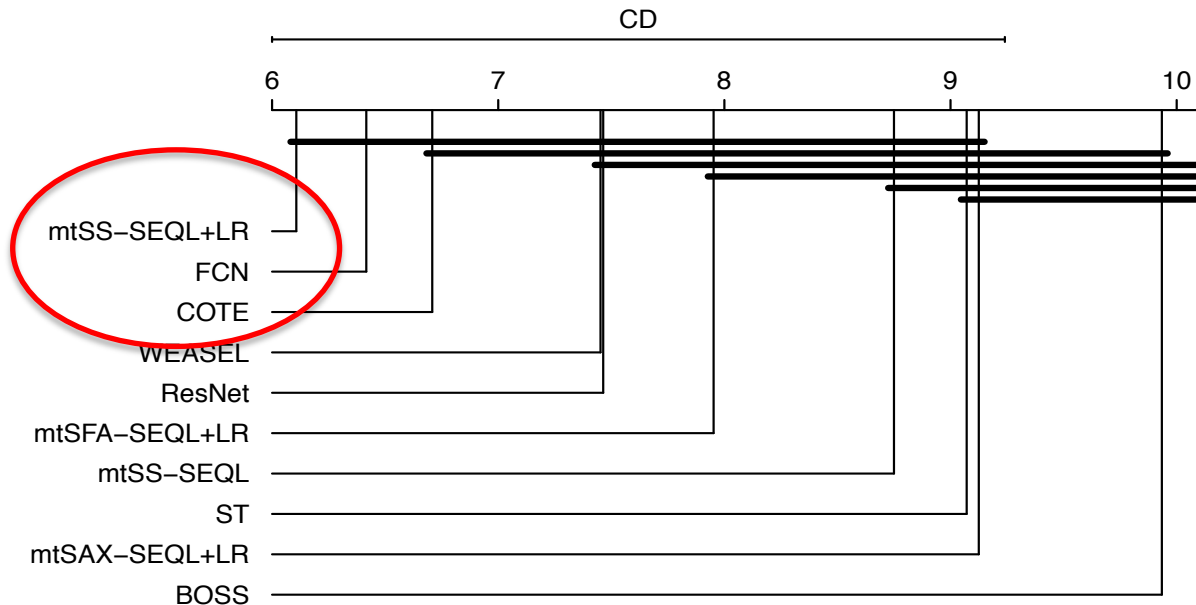
Evaluation on Time Series Classification

Ranking of learning algorithms by Accuracy

UCR Archive (85 TSC datasets: sensors, images, ECG)

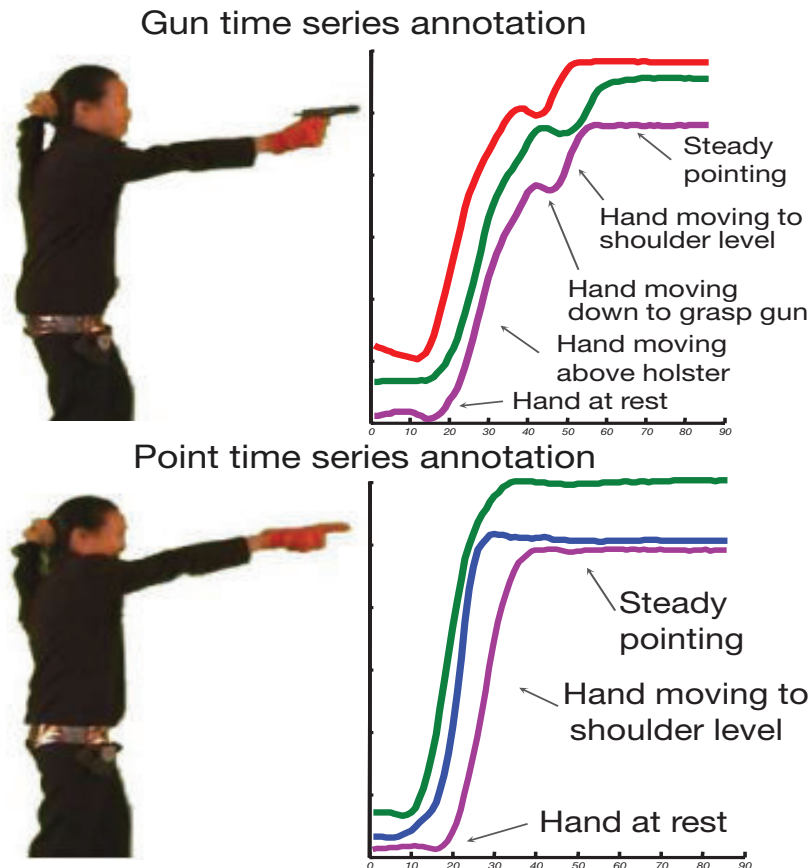
Top-3 models:

1. mtSS-SEQL+LR (our method, a linear model)
2. FCN (deep neural network)
3. COTE (ensemble of 35 classifiers)



Interpretability

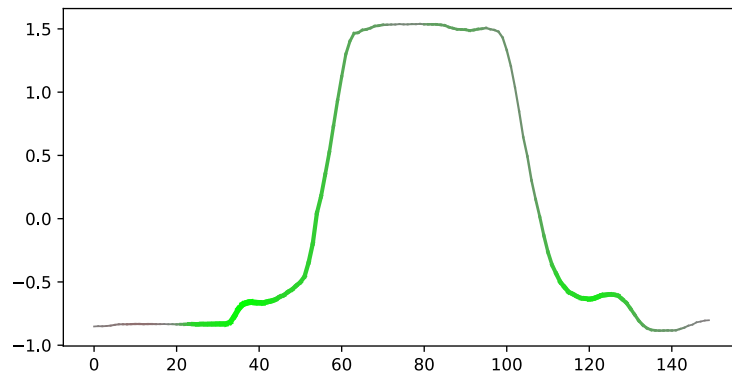
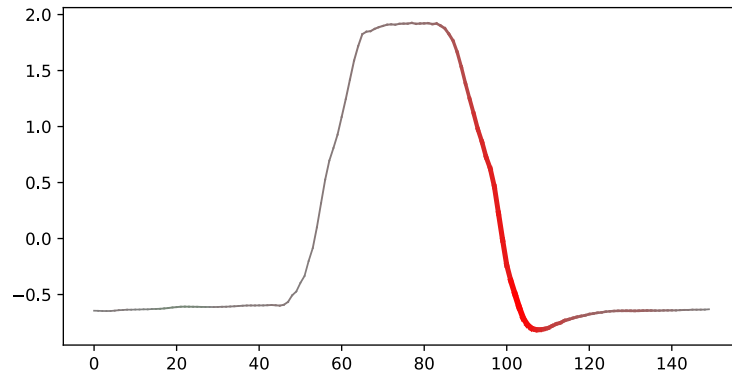
- GunPoint dataset tracking hand movement w/o Gun



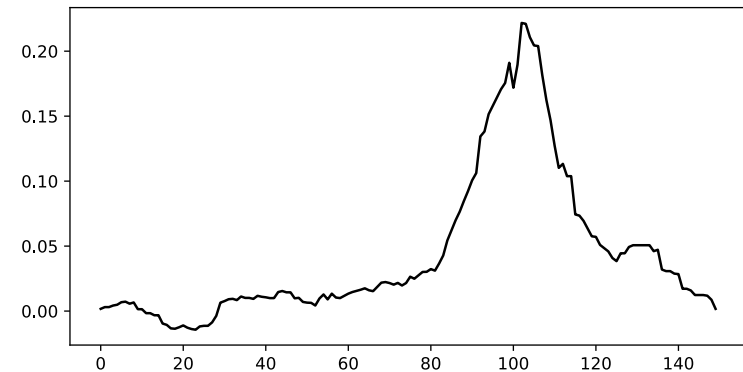
Interpretability

Coefficients	Subsequences
0.065 84	cbaab
0.062 47	db
0.062 23	ddddb
0.062 00	da
0.059 72	bbbbbbbbbbcbddd
-0.053 72	aaaaaabbabb
-0.054 39	bbbbaaaaa
.....	

Point (top) and Gun (bottom)



Salient Region for Classification Decision



Github code for our work: <https://github.com/heerme?tab=repositories>

Recap SEQL

- Family of machine learning algorithms to train/predict (with) linear models for sequences
- Coordinate descent with Gauss-Southwell feature selection + Branch-and-bound for efficient feature search
- **Sequence Classification** (KDD08, KDD11): Logistic loss, l2-SVM loss
- **Sequence Regression** (ECMLPKDD17): Least-squares loss
- **Time Series Classification** (ICDE17): SEQL + SAX discretization
- Future Work:
 - Multi-dimensional Sequences

References

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- **[ECMLPKDD17]** S Gsponer,, B Smyth, G Ifrim. **Efficient Sequence Regression by Learning Linear Models in All-Subsequence Space**, ECML-PKDD, 2017.
- **[ICDE17]** T Le Nguyen, S Gsponer, G Ifrim, **Time Series Classification by Sequence Learning in All-Subsequence Space**, ICDE, 2017.
- **[PlosOne14]** BP Pedersen, G Ifrim, P Liboriussen, KB Axelsen, MG Palmgren, P Nissen, C. Wiuf, C. Pedersen, **Large scale identification and categorization of protein sequences using structured logistic regression**, PloS one 9 (1), 2014.
- **[KDD11]** G Ifrim, C Wiuf, **Bounded coordinate-descent for biological sequence classification in high dimensional predictor space**, KDD, 2011.
- **[KDD08]** G. Ifrim, G. Bakir, and G. Weikum, **Fast logistic regression for text categorization with variable-length n-grams**, KDD, 2008.