Large-scale Kernel Methods and Algorithms

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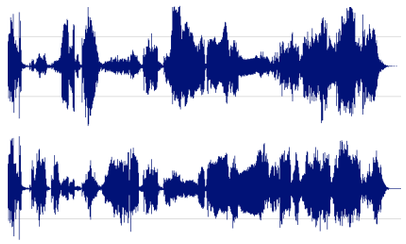
What are we after?

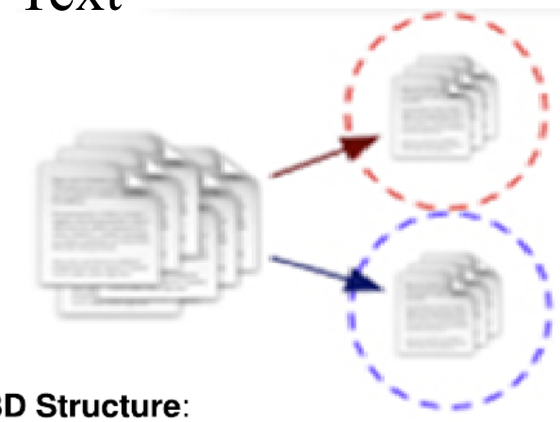
- Scalable methods for annotation, information extraction for structured/sequence data
  - sequence ID (classification): e.g. topic, genre, etc
  - sequence Labeling: e.g. entity tagging
  - information extraction: eg. entity relationships

Audio/Music



Music Genre
Artist
etc

Text



Bio-informatics

Sequence

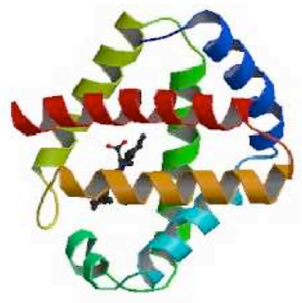
VDAAVAKVCGSEAIKANLRRSWGVLSADIEA
TGLMLMSNLFTLRPDTKTYFTRLGDVQKGK
ANSKLRGHAITLTYALNNFVDSLDDPSRLKC
VVEKFAVNHINRKISGDAFGAIVEPMKETLKA
RMGNYYSDDVAGAWAALVGVVQAAL

predict

Class:
Globin-like

Function:
Oxygen transport

3D Structure:



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- Scalable methods for annotation, information extraction for structured/sequence data
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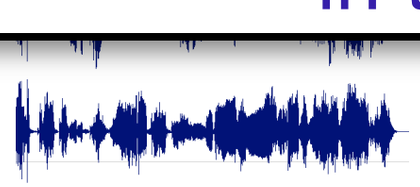
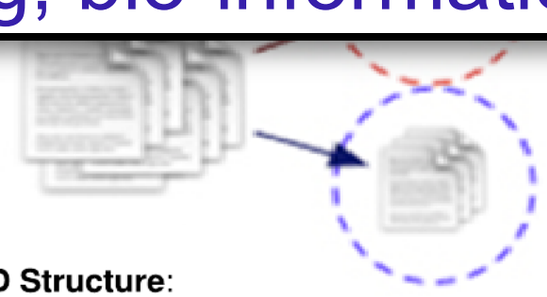
This talk: (1) New algorithmic framework for general kernel computation on sequence data
(2) Important and challenging practical problems in text, audio mining, bio-informatics



Artist
etc



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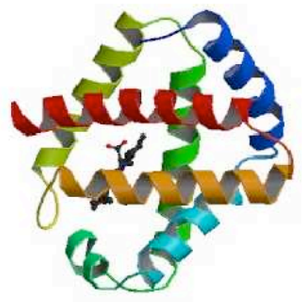
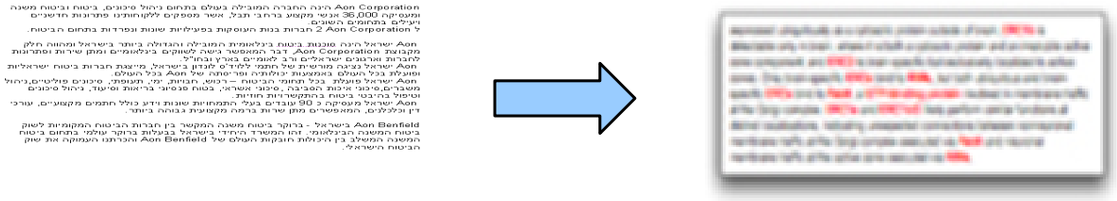
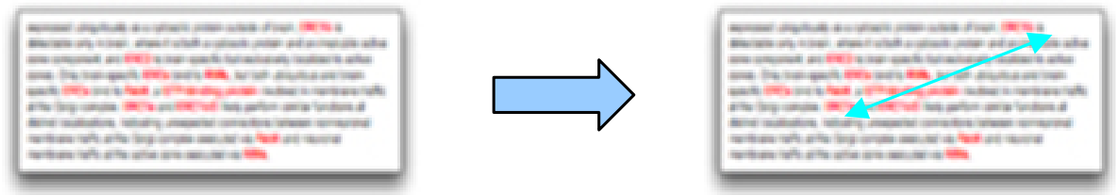


Case I: NLP

- Entity tagging



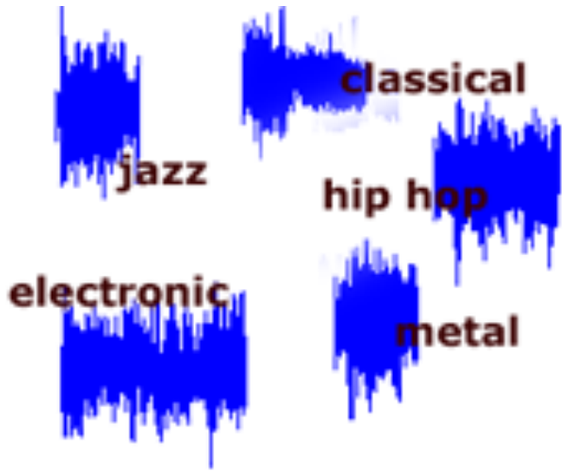
- Relationship extraction



- Relevant document retrieval

Case II: Music ID

- How to tell apart/predict music genre?
- How to tell apart/predict music artists?
- How to tell apart/predict mood or emotions in music?

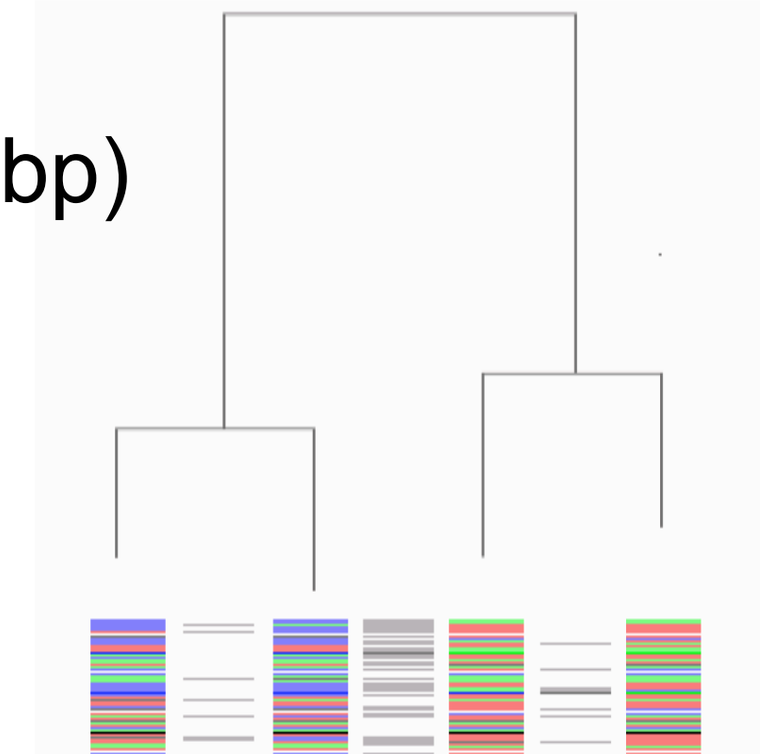


- Challenges:
  - what are important characteristics (features)?
  - great variability in content

Case III: DNA Barcoding

- DNA barcode: a “short” sequence (≈600bp) of mitochondrial DNA (CO1)
- Barcoding of Life:

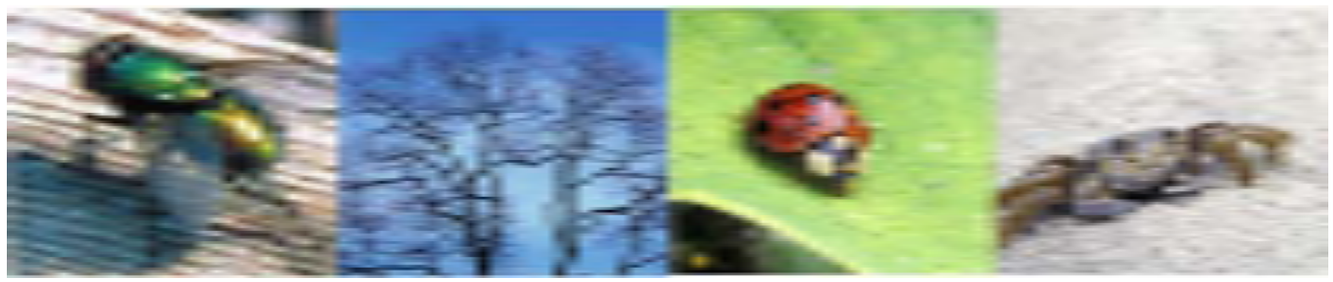
classification and identification of organisms using ‘DNA barcodes’

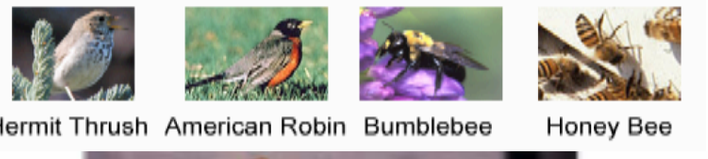


Inherently large-scale problem:

Known species:

>150,000	>250,000	>300,000	>30,000
flies, mosquitoes	flowering plants	beetles	crabs, lobsters

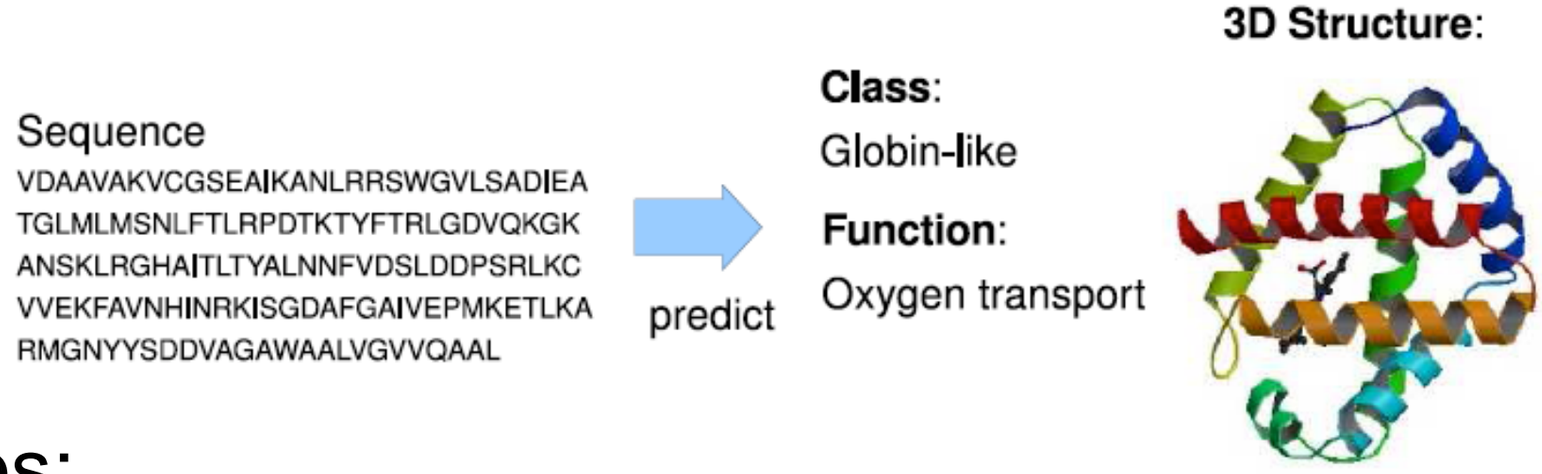




- Applications: taxonomy, biodiversity understanding, invasive species tracking, etc

Case IV: Protein Annotation

- Primary (amino-acid) sequence easy to obtain
- Structural/Functional information difficult to obtain
- **Goal**: predict structural/functional class from primary sequence



- Challenges:
  - Limited labeled data, highly diverse sequences
  - Millions of unannotated sequences, many classes

Solving Sequence ID Problems

Sequence X

GTATATGATCAGGACTAGTTGGTACAGCTCTTAGACTATTAATT
CGAGCTGAACTAGGCCAACCAGGAGCTCTTCTGGGGGATGA
TCAATTATATAATGTAATTGTAACCGCCCACGCTTTTGTTATAAT
TTTCTTTTTAGTAATACCTATAATGATTGGAGGATTTGGAAACT
GATTAGTTCCTTTAATACTAGGAGCCCCAGACATGGCATTCCC
ACGTCTAAATAATATAAGTTTCTGACTTCTTCCGCCTGCCCTT
CTACTACTCCTTTCTTCAGCAGCAGTCGAAAGTGGAGTTGGA
ACTGGATGAACCGTCTACCCTCCTTTAGCCGGAAACCTTGCT
CACGCATTGACAGACCGAAACTTTAACACCGCTTTCTTTGAT
CCAGCAGGAGGTGGAGA

?

Sequence Y

ATGGTTAAATTCTCCTCAGAACCACATTTGGCTCAGGTAGTC
GCAGAAGACCTTCTTTCTCCTAGCGTGGTGGATGTGGGTGA
CTTCACAATATCAATCAACGAGGGTCTCCCCTCTGGGGTGCC
CTGCACCTCCCAATGGAACTCCATCGCCCACTGGCTTCTCA
CTCTCTGTGCGCTCTCTGAAGTTACAAATCTGTCCCCTGACA
TCATACAGGCTAATTCCCTCTTCTCCTTCTATGG

- Pattern matching approach:
  - Compare sequence patterns (substrings, subsequences, other features)
  - Compute **similarity** based on pattern comparison

Similarity score: $K(X,Y) = \langle F(X), F(Y) \rangle$

String kernel

Fixed-length vector of features derived from sequence

String Kernel Concept

X

GGAATTTGAGCAGGACTAATTGGAACTTCTTTAAGATTACTTATTCGAACTGAATTAGGAACCCCAGGATCTTTAATTGGAGATGATCAAATTTATAATACAAT
TGTTACAGCTCATGCATTTATTATAATTTTTTTTATAGTTATACCTATTATAATCGGAGGATTTGGAAATTGACTAGTTCCATTAATAATAGGTGCCCCAGATATAG
CTTTCCCCCCGTATAAATAACATAAGATTTTGATTATTACCCCCATCTTTAACTTTATTAATTTCAAGAAGAATTGTTGAAAATGGGGCTGGTACAGGATGAACA
GTTTATCCCCCTCTTTCATCAAATATCGCCCATCAAGGAGCATCTGTTGATTTAGCAATTTTTTCCCTTCATCTTGCTGGTATTTCATCAATTCTTGGAGCTA
TTAATTTTATTACAACAATTATTAATATACGAATTAATAATTTATCTTTTGATCAAATACCATTATTTGTTTGAGCTGTAGGAATTACAGCATTATTATTATTACTTTC
ATTACCTGTTTTAGCAGGTGCTATTACTATATTATTAACAGATCGAAATTTAAATACTTCTTTTTTTGATCCTGCAGGAGGAGGAGATCCAATCTTATACCAACA
CTTATTT

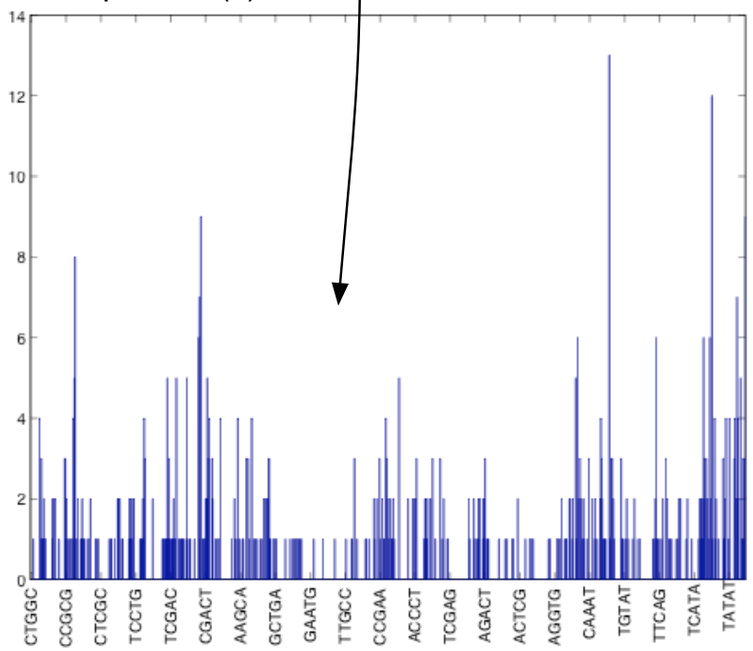
GGAAT

Length k=5

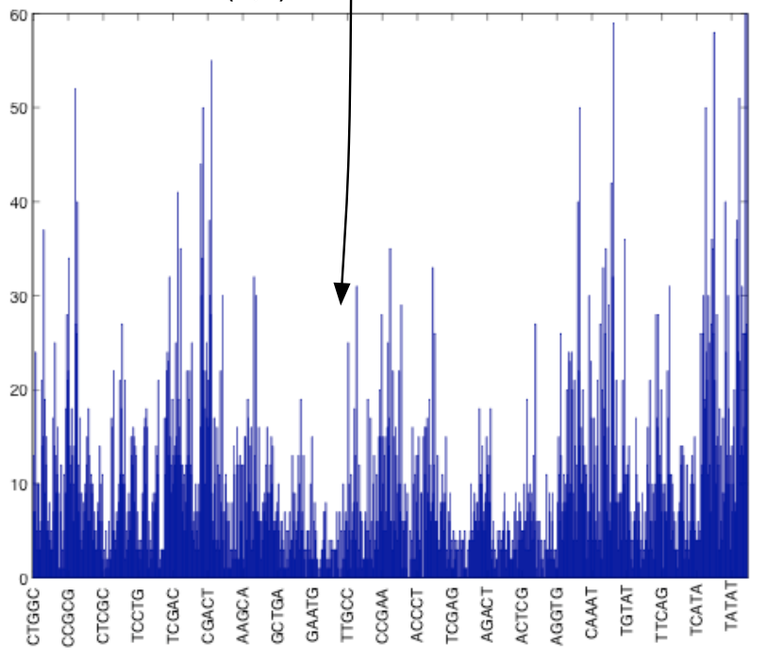
xGAAT
GxAAT
GGxAT
GGAxT
GGAAx

Up to m=1 mismatch

Spectrum(5)



Mismatch(5,1)



F(X)

Similar spectra ~ High Similarity

String Kernel Concept

x

GGAATTTGAGCAGGACTAATTGGAACTTCTTTAAGATTACTTATTCGAACTGAATTAGGAACCCCAGGATCTTTAATTGGAGATGATCAAATTTATAATACAAT
TGTTACAGCTCATGCATTTATTATAATTTTTTTTATAGTTATACCTATTATAATCGGAGGATTTGGAAATTGACTAGTTCCATTAATAATAGGTGCCCCAGATATAG
CTTTCCCCCCGTATAAATAACATAAGATTTTGATTATTACCCCCATCTTTAACTTTATTAATTTCAAGAAGAATTGTTGAAAATGGGGCTGGTACAGGATGAACA
GTTTATCCCCCTCTTTCATCAAATATCGCCCATCAAGGAGCATCTGTTGATTTAGCAATTTTTTCCCTTCATCTTGCTGGTATTTCATCAATTCTTGGAGCTA
TTAATTTTATTACAACAATTATTAATATACGAATTAATAATTTATCTTTTGATCAAATACCATTATTTGTTTGAGCTGTAGGAATTACAGCATTATTATTATTACTTTC
ATTACCTGTTTTAGCAGGTGCTATTACTATATTATTAACAGATCGAAATTTAAATACTTCTTTTTTTGATCCTGCAGGAGGAGGAGATCCAATCTTATACCAACA
CTTATTT

GGAAT

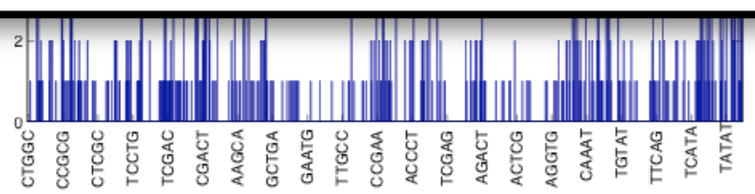
Length k=5

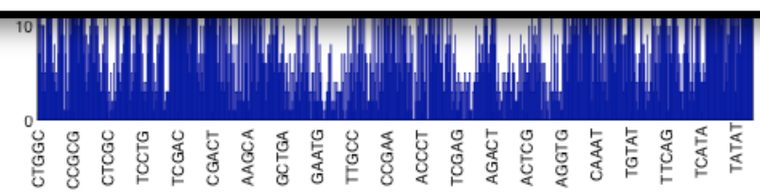
xGAAT
GxAAT
GGxAT
GGAxT

Up to m=1 mismatch

Two important questions:

1. What are the features (representation)?
2. How efficient is the similarity evaluation? (quadratic? linear?)





r(x)

Similar spectra ~ High Similarity

String Kernels

- Kernel functions *K(x,y)* on sequences from alphabet ∑
  - Pairwise-alignment algorithms (Needleman-Wunsch)
    Not Mercer kernels [Vert et al.'04]
  - Pair HMMs [Watkins'99], convolution kernels [Haussler'99], gappy n-gram kernels [Lodhi et al.'02], rational kernels [Cortes et al.'02]

    O(n²) complexity in sequence length ***n*** / pair
  - *Spectrum kernels* [Leslie'02], *mismatch kernels* [Leslie'04], substring kernels [Vishwanathan & Smola'02]

    O(n) complexity in sequence length ***n*** / pair

- *Accuracy & Algorithmic complexity still insufficient for large-scale sequence comparison / annotation*

Spectrum/Mismatch Kernels (I)

- Feature map ($|\Sigma|^k$-dim. representation) based on counts of k-length substrings

$$\Phi_{k,m}(\gamma|X) = \left(\sum_{\alpha \in X} I_m(\alpha, \gamma) \right)_{\gamma \in \Sigma^k}$$

substring length *k*

sequence

feature count for γ

$$I_m(\alpha, \gamma) = \begin{cases} 1, d(\alpha, \gamma) \leq m \\ 0, \text{otherwise} \end{cases}$$

indicator (matching) function

Hamming distance

Example: k-mer feature space for DNA ($|\Sigma|$=4)

AA	AC	AG	...	TT
1	2	3	...	$\|\Sigma\|^k$

feature count

Very important in practice!

exact (m=0) or approximate/smoothed (m>0)

Spectrum kernels (2)

- Spectrum kernel function K(X,Y)

  cumulative pairwise comparison of all substrings *a* and *b* contained in X and Y

$$K(X,Y|k,m) = \sum_{\gamma\in\Sigma^k} \Phi_{k,m}(\gamma|X)\Phi_{k,m}(\gamma|Y).$$

$$= \sum_{\alpha\in X}\sum_{\beta\in Y}\sum_{\gamma\in\Sigma^k} I_m(\alpha,\gamma)I_m(\beta,\gamma)$$

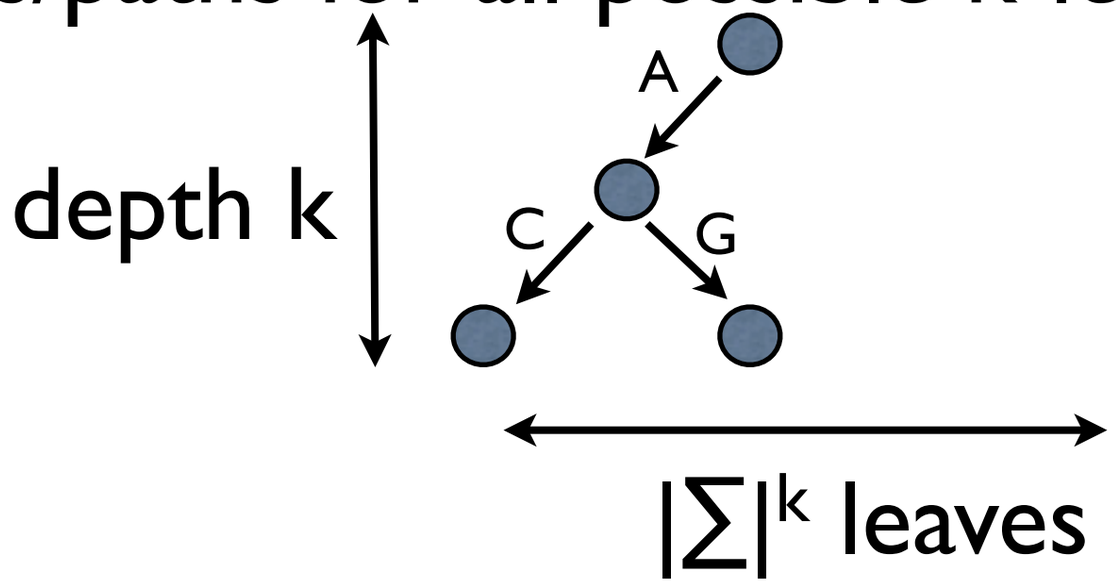
number of similar substrings shared by(a,b)

What are the best algorithms for string kernels?

- Suffix trees (Vishwanathan & Smola, 2002)
  - linear-time all-substring kernel
- (Sparse) dynamic programming (Rousu, 2005)
  - gapped kernel
- ***Mismatch trie*** (Leslie, 2004)
  - applies to mismatch, spectrum, gapped kernels, etc (*inexact matching!!!*)
  - Complexity $O(k^{m+1}|\Sigma|^m(|X| + |Y|))$
    - limits applicability to small k,m,|∑|

Mismatch Trie Algorithm

- Depth-first search over complete tree with leaves/paths for all possible k-length substrings



- each node has a list of substrings that match node's prefix
- branches correspond to all discrete alphabet symbols

- Applies to spectrum, mismatch, gapped, etc kernel computation $O(k^{m+1}|\Sigma|^m(|X| + |Y|))$

- Problematic for large-Σ inputs and relaxed matching (larger m)

Want to address this

Our Results

- New *sufficient-statistic* based algorithms for kernel computation
  - Improve *complexity* bounds over existing algorithms, *removes dependency on the alphabet size*

$$O(k^m|\Sigma|^m n) \Rightarrow O(c_{k,m} n)$$

- Several *orders-of-magnitude* speed-up ⇒

  can now be applied to large-alphabet inputs (music, text, time series, etc)

- Enhance performance: more complex kernels improve predictive accuracy

Our approach: Sufficient Statistics

Evaluation of string kernel functions using *Sufficient Statistics*

Two steps

- (I) Exact spectrum computation with counting sort
- (2) *Sufficient statistics* for string kernels and their computation using (1) as sub-algorithm

(I) Exact Spectrum computation with counting sort

Input sequences

X1: GGAA

X2: TTTGAA

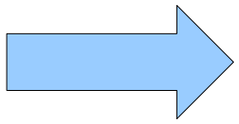
X3: GGAAT

substring kernel

k=3,m=0

Features:	Seq. Index:
GGA	1
GAA	1
TTT	2
TTG	2
TGA	2
GAA	2
GGA	3
GAA	3
AAT	3

Counting sort



AAT	3	Seq. index: 3, Counts: 1
GAA	1	Seq. index: 1 2 3, Counts: 1 1 1
GAA	2	
GAA	3	
GGA	1	Seq. index: 1 3, Counts: 1 1
GGA	3	
TTA	2	...
TTG	2	
TTT	2	Seq. index: 2, Counts: 1

Counting sort:
O(kn) evaluation for exact spectrum

Kernel updates (per *substring*):

$K(J,J) = K(J,J) + cc^T$

c - feature counts, J - sequence index

How does this extend to *inexact matching* (m>0)?

Mismatch Kernel

Main issue: *denser* substring spectrum, many more features due to approximate counts (m>0)

I: $$K(X,Y|k,m) = \sum_{\gamma\in\Sigma^k} \Phi_{k,m}(\gamma|X)\Phi_{k,m}(\gamma|Y).$$

$$= \sum_{\alpha\in X}\sum_{\beta\in Y}\sum_{\gamma\in\Sigma^k} I_m(\alpha,\gamma)I_m(\beta,\gamma)$$

$$I_m(\alpha,\gamma) = \begin{cases} 1, d(\alpha,\gamma)\leq m \\ 0, \text{otherwise} \end{cases}$$

introduces for every *a* mismatch neighborhood *N*(*a*,*m*) of size $O(k^m|\Sigma|^m)$

II: $$K(X,Y|k,m) = \sum_{i_x=1}^{n_x-k+1}\sum_{i_y=1}^{n_y-k+1}\sum_{a\in\Sigma^k} I_m(a, x_{i_x:i_x+k-1})I_m(a, y_{i_y:i_y+k-1})$$

$$= \sum_{i_x=1}^{n_x-k+1}\sum_{i_y=1}^{n_y-k+1} |(N(x_{i_x:i_x+k-1},m)\cap N(y_{i_y:i_y+k-1},m)|$$

$$= \sum_{i_x=1}^{n_x-k+1}\sum_{i_y=1}^{n_y-k+1} \mathcal{I}(x_{i_x:i_x+k-1}, y_{i_y:i_y+k-1})$$

intersection size for two mismatch neighborhoods

Observation I: number of substrings within distance *m* from both *a* and *b* is *independent* of *a* and *b*

I: Intersection Algorithm

Algorithm 1. (Hamming-Mismatch) Mismatch algorithm based on Hamming distance

Input: strings $X, Y, |X| = n_x, |Y| = n_y$, parameters k, m, lookup table $\mathcal{I}$ for intersection sizes
Evaluate kernel using Equation 5:
$K(X, Y|k, m) = \sum_{i_x=1}^{n_x-k+1} \sum_{i_y=1}^{n_y-k+1} \mathcal{I}(d(x_{i_x:i_x+k-1}, y_{i_y:i_y+k-1})|k, m)$
where $\mathcal{I}(d)$ is the intersection size for distance d
Output: Mismatch kernel value $K(X, Y|k, m)$

- *Independent* of alphabet size ∑ and mismatch degree *m*
- *In-place* (only uses $\min(2m,k)+1$ extra space for an auxiliary look-up table)
- Only linear in k (not k^m)
- Quadratic O(|X||Y|) in sequence length
- Can be used with other kernels given corresponding lookup table

Sufficient Statistics for String Kernels

Observation II: kernel is incremented only by min(2m,k)+1 distinct values

$$K(X,Y|m,k) = \sum_{i_x=1}^{n_x-k+1} \sum_{i_y=1}^{n_y-k+1} \mathcal{I}(x_{i_x:i_x+k-1}, y_{i_y:i_y+k-1}) = \sum_{i=0}^{\min(2m,k)} M_i \mathcal{I}_i$$

Matching (sufficient) statistics:
M_i = number of pairs of substrings (a,b) at Hamming distance d(a,b)=i

How to compute matching statistics M_i efficiently?

- Problem: direct computation of M_i is still *quadratic*!

Auxiliary problem

Mismatch Statistic Counting: Given a set of n k-mers from two strings X and Y, for each Hamming distance $i = 0, 1, ..., \min(2m, k)$, output the number of k-mer pairs $(a, b), a \in X, b \in Y$ with $d(a, b) = i$.

- Efficient direct computation of the *number* of substring pairs (a,b) at distance *i* (M_i) is difficult (requires *quadratic* time!)
- Avoiding *quadratic* time:
  - compute *inexact*(!) statistics C_i first (in *linear* time)
  - then obtain exact matching statistics M_i in *closed form* from the set of inexact statistics

Computing matching statistics

- Instead of Mi first compute *approximate* (with over-counting) number of pairs C_i at distance *at most i*

- *Algorithm*: iteratively remove *i* positions, sort and compute spectrum kernel for (*k-i*)-length substrings

$$d(a', b') = 0 \Rightarrow d(a, b) \leq i$$

- Inexact matching statistics C_i:

$$C_i = M_i + \Sigma_{j=0}^{j=i-1} \binom{k-j}{i-j} M_j$$

II: Sufficient Statistic (SS) algorithm

Algorithm. **(Mismatch-SS) Mismatch kernel algorithm based on Sufficient Statistics**
Input: strings X, Y, parameters k,m, $\mathfrak{I}_i$
1. Compute min(2m,k) *cumulative* matching statistics, C_i, using counting sort
2. Compute *exact* matching statistics, M_i

$$M_i = C_i - \Sigma_{j=0}^{i-1} \binom{k-j}{i-j} M_j, \quad i = 0,\ldots, min(min(2\mathrm{m}, k), k-1)$$

$$M_k = T - \Sigma_{j=0} k-1 M_j$$

3. Evaluate kernel using :

$$K(X, Y \mid m, k) = \Sigma_{i=0}^{min(2\mathrm{m},k)} M_i \mathfrak{I}_i$$

Output: Mismatch kernel value K(X,Y|k,m)

$$O(k^{m+1} |\Sigma|^m n) \quad \Rightarrow \quad O(c_{k,m} n), \; c_{k,m} = \Sigma_{i=0}^{2\mathrm{m}} \binom{k}{i} (k-i)$$

original complexity (trie-based)

Sufficient-statistic based

Using Sufficient Statistics to compute String Kernel Functions

- Spectrum kernels (Leslie, 2002)

$$K(X,Y) = M_0$$

- Gapped kernels (Leslie, 2004; Rousu, 2005)

$$K(X,Y) = \Sigma_{i=0}^{i=m} C_i'$$

- Spatial kernels (Kuksa, 2008)

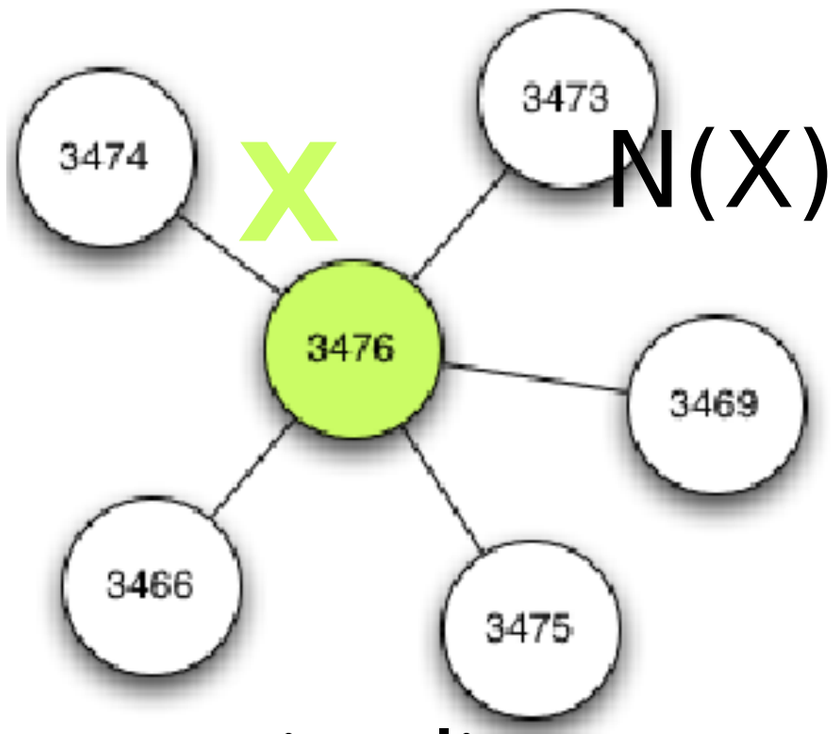
$$K(X,Y) = \Sigma_{\boldsymbol{d}=(d_1, d_2, .., d_{t-1})} C_{\boldsymbol{d}}$$

- Reduce computation to multiple rounds of exact spectrum kernel computation (counting sort)
- Extends to *semi-supervised settings: (I) cluster kernels (Weston, 2005)*, (II) abstraction kernels (*Kuksa, 2010*)

Neighborhood Kernels

$$K(X,Y) = \sum_{x \in N(X)} \sum_{y \in N(Y)} K(x,y)$$

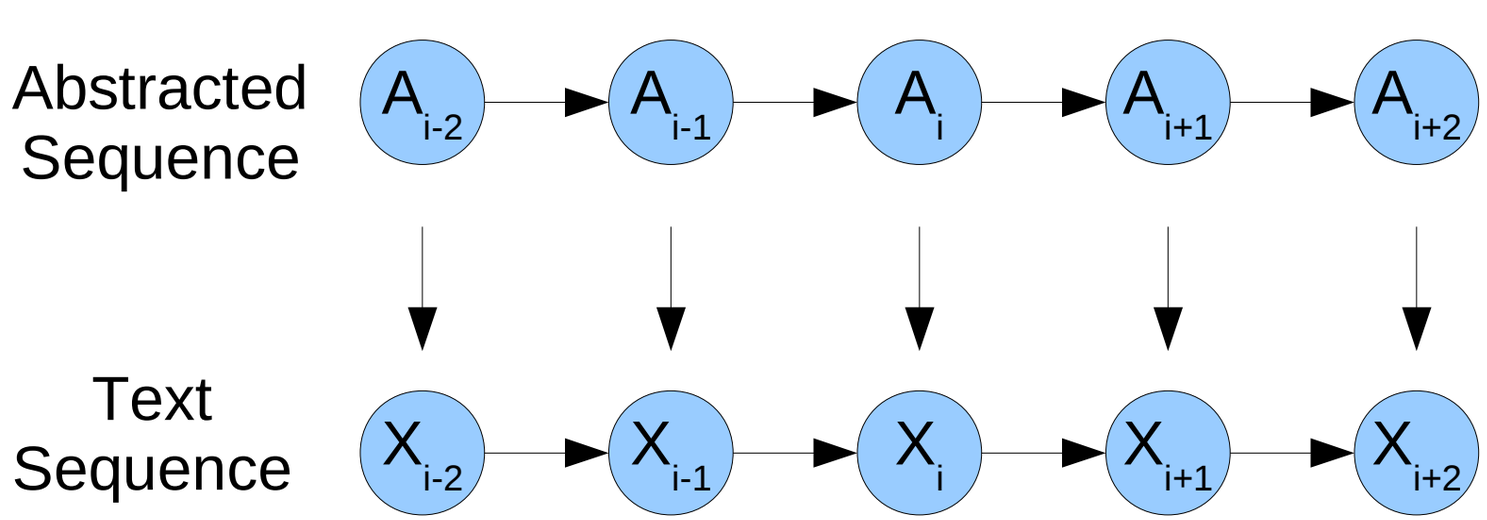
(Weston, 2005)



- N(X) - set of sequences neighboring X
- Can be labeled or unlabeled
  (semi-supervised learning)
- Direct evaluation is quadratic!
- Can extend our approach and make computation linear
  - Jointly sort N(X), N(Y)
  - Apply desired similarity measure (mismatch, spectrum, gapped, etc)
  - Works with millions of sequences

Abstraction-augmented kernels

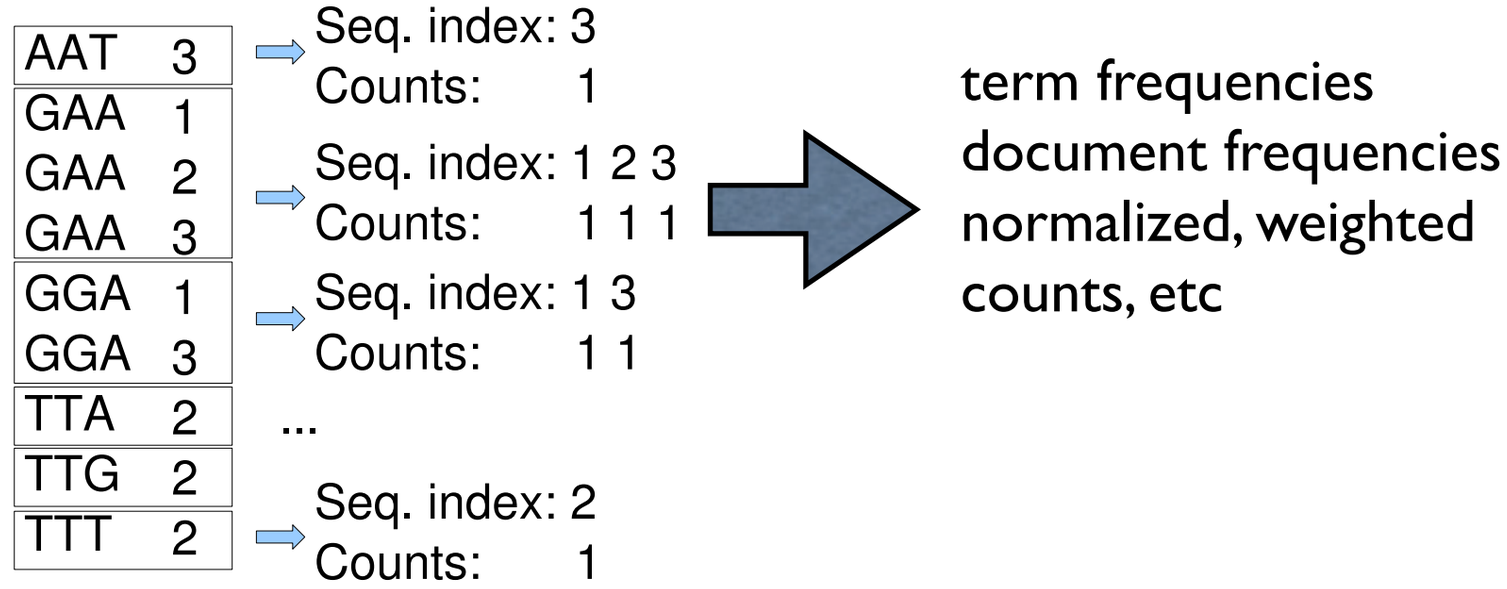
- Learn word abstractions using unsupervised (or semi-supervised) embedding and clustering (ECML 2010)



- Apply kernel to both original sequence X

Weighted Kernels

- Can use with weighted embeddings
  - Multinomial Manifold Kernels (Zhang, SIGIR 2005), geodesic distance kernels
  - TF-IDF embedding, L1, L2 normalization
  - Gap-weighted kernels, etc



Summary

- New family of algorithms based on *sufficient statistics* and counting sort for string kernels
  - unified approach
  - improves complexity bounds over existing algorithms
  - reduces computation to exact spectrum kernel computation

Evaluation I:

time efficiency

Running time (I)

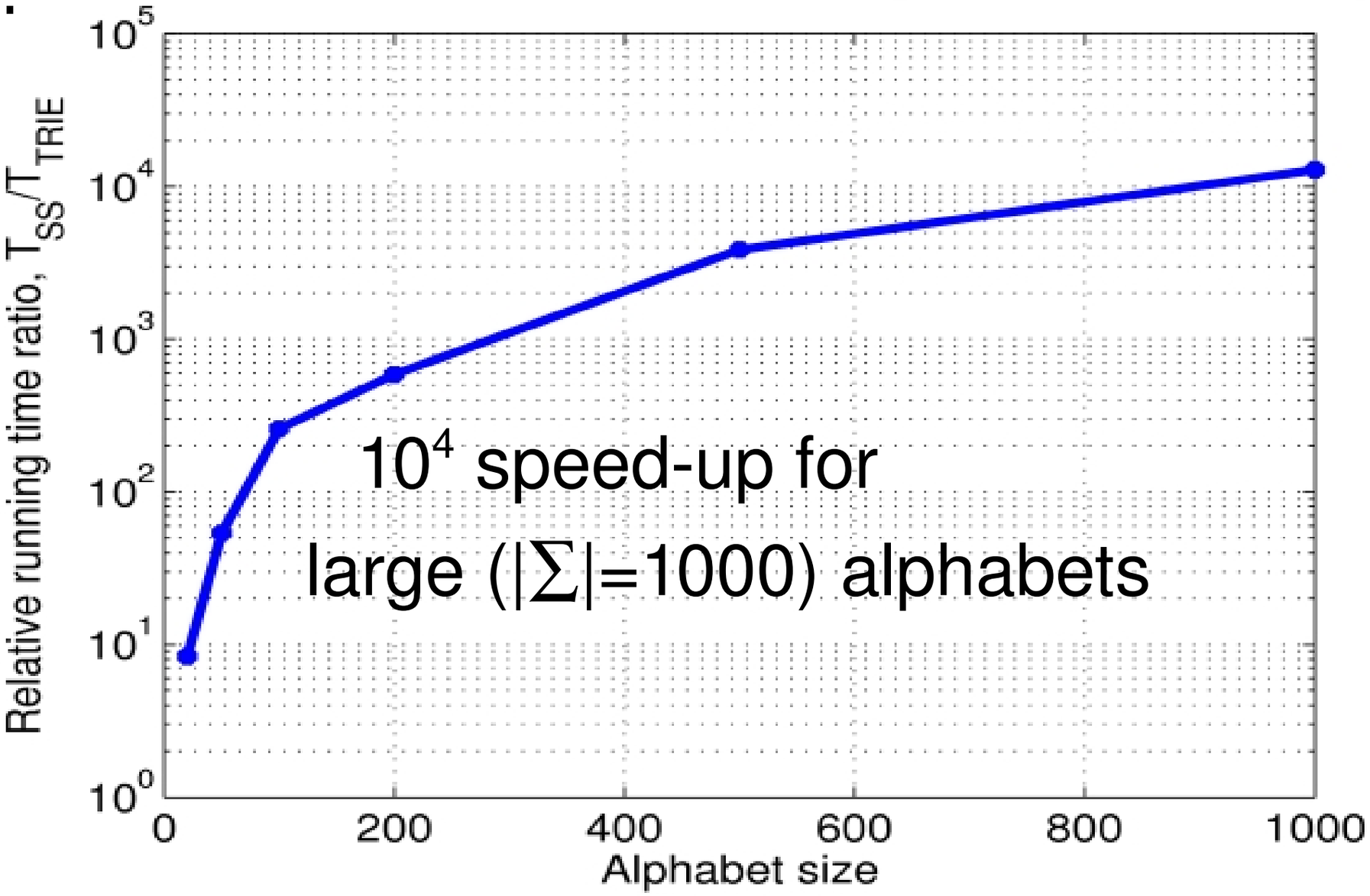


Figure 1: Relative running time vs. alphabet size

Settings: seq. length = 10K, k=5, m=1

Speed-up

Protein	100
Music	~10^4
Text	~10^6

Running time (2)

Kernel computation K(X,Y), real data

Running time, (s)

	long protein	protein	dna	text	music
n	36672	116	570	242	6892
$\|\Sigma\|$	20	20	4	29224	1024
(5,1)-trie	1.6268	0.0212	0.0260	20398	526.8
(5,1)-ss	0.1987	0.0052	0.0054	0.0178	0.0331
time ratio	8	4	5	10^6	16,000
(5,2)-trie	31.5519	0.2918	0.4800	-	-
(5,2)-ss	0.2957	0.0067	0.0064	0.0649	0.0941
time ratio	100	44	75	-	-

Evaluation II:

- Text
- Relation extraction
- Music
- Bio-informatics:
  - DNA Barcoding
  - Protein structural annotation

Relevant Document Detection

- BioCreativeII competition data: detect PPI relevant documents from their abstracts
  - ~5K abstracts, ~1.2M words
  - unlabeled: 1.4M abstracts, 1.3G words

Method	**F1**
Semi-supervised Abstraction Kernel (Kuksa et al, 2010)	80.11
Baseline I: BioCreativeII competition (best)	78.00
Baseline II: TF-IDF	73.98

Relation Extraction

Example:

The protein product of **c-cbl** proto-oncogene is known to interact with several proteins, including **Grb2**, **Crk**, and **PI3 kinase**, and to regulate signaling …

Interacting pairs: (c-cbl, Grb2), (c-cbl, Crk), etc.

- PPI Relation extraction (sentence-level), ~4K sentences, F1 scores (AIMED dataset)

Method	**F1**
Mismatch	**64.48**
Baseline I: Multiple kernel, multiple parser (Makoto et al, 2008)	**61.4**
Baseline II: Dependency and deep parsers (Miyao et all, 2008)	**59.5**

Text classification

- Reuters, test F1 scores, |∑|=29,224

Comparison with state-of-the-art

Class	TF-IDF	KSG	Double	SS-4†	NG-4‡
Acq	97.11	96.8	**97.72**	88.0	93.20
Crude	87.71	89.4	**90.11**	84.0	84.80
Earn	98.70	98.3	**99.02**	97.0	98.40
Grain	**93.29**	92.5	90.18	84.0	84.0
Interest	71.80	81.5	**81.63**	66.0	71.90
Money	77.61	**84.0**	82.66	76.0	75.70
Ship	72.97	81.9	**85.56**	65.0	62.60
Trade	84.26	90.2	**93.47**	73.0	77.90
Mean (macro-average)	85.43	89.33	**90.05**	79.13	81.06
Mean (micro-average)	93.18	93.9	**94.51**	-	-

SS = subsequence kernel
NG = n-gram kernel
KSG = key-substring-group method
TF-IDF = tf-idf kernel

Music Genre Prediction

- 10 genres, ~30s of audio per song
- VQ with $|\Sigma|=1024$ codewords (MFCC feat.), seq. length ~7000

Method	**Error**
Mismatch kernel	35.6
Spatial kernel	29.4
Baseline 1: DWCH (Daubechies Wavelet), Li et al	41.6

Music Artist Recognition

- Album-wise cross-validation over 20 artists (120 albums)
- VQ with $|\Sigma|=1024$ codewords

Method	**Error**
Mismatch kernel	44.66
Spatial kernel	32.50
Baseline 1: GMM	44.0

DNA Barcoding (1)

Dataset	# species	# barcodes
ACG	573	4267
Hesperiidae	364	2185
Astraptes	12	465
Bats of Guyana	96	840
Birds of North America	656	2589
Fish of Australia	211	754
Fish larvae	7	35

- Task: assign DNA barcode to its species group
- Large number of classes (species), limited labeled data

DNA Barcoding (2)

cross-validation error:

	Mismatch	Hamming	Kimura	Smith-Waterman
ACG	**2.37±0.81**	11.44 ± 1.52	5.51 ± 0.86	3.66 ± 0.66
Hesperiidae	**3.48±1.02**	14.49 ± 2.36	3.81 ± 1.26	5.45 ± 1.20
Astraptes	**1.07±1.81**	3.61 ± 2.77	1.71 ± 1.96	1.64 ± 1.03
Bats Guyana	**1.63±1.22**	2.72 ± 1.83	**1.63 ± 1.22**	**1.63 ± 1.22**
Birds of North America	**6.10±1.52**	18.38 ± 2.05	**6.02 ± 1.36**	8.20 ± 1.53
Fish Australia	**5.35±3.36**	5.87 ± 4.01	**5.35 ± 3.36**	5.35 ± 3.36
Fish larvae†	**2.86**	11.43	8.57	5.71

Linear time

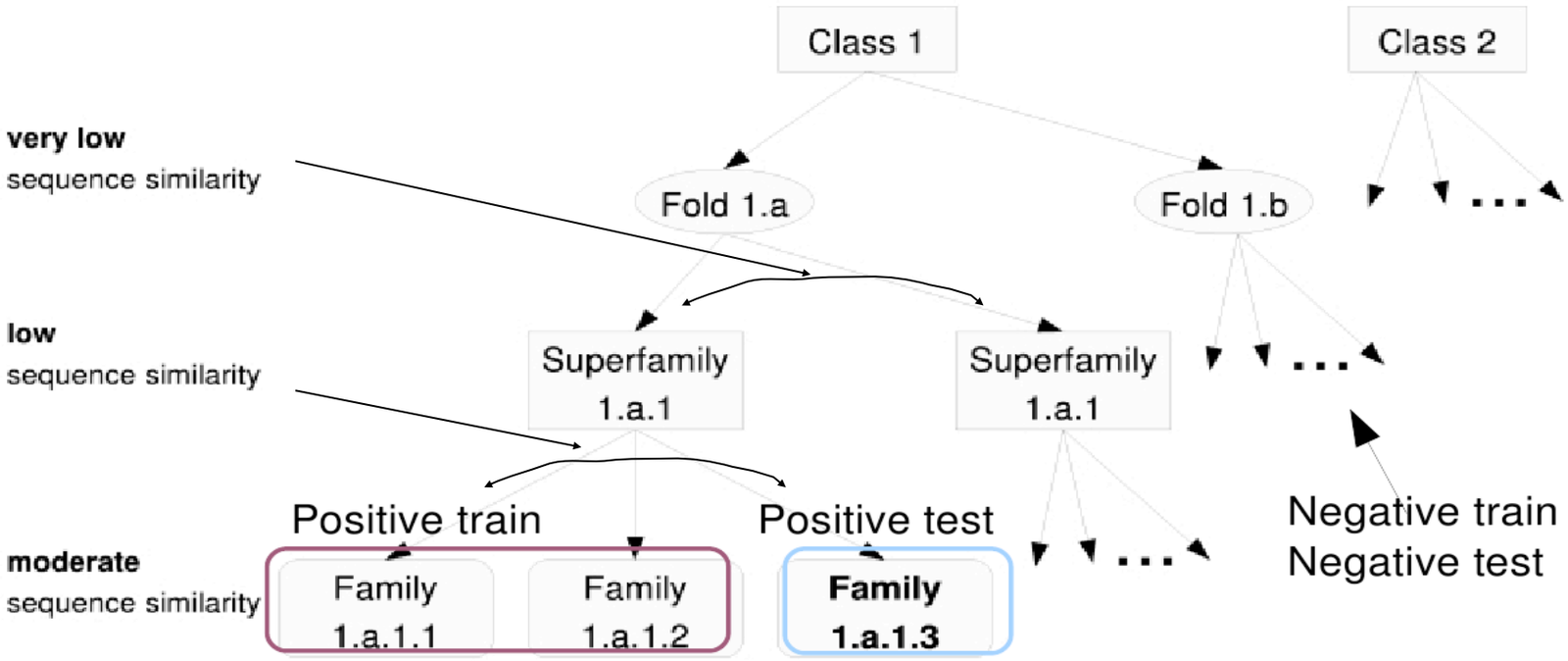
Quadratic

Large-scale protein annotation

- Semi-supervised setting:
  - 2862 labeled sequences (SCOP)
  - 1M unlabeled sequences (NR dataset)

Method	Multi-class fold prediction (27 classes)	Remote homology prediction (54 superfam)
SSSK (triple)	**77.62**	**89.44**
State-of-the-art: profile kernel	67.83	81.51

Structural classification of proteins (SCOP)



Summary

- New string kernel methods and algorithms
- **Benefit I** (complexity): fast, alphabet-free sequence matching based on sufficient statistics
- **Benefit II** (accuracy): enhances performance on many practical tasks (text, music, bio-informatics)
- Extends to richer semi-supervised settings
  - neighborhood kernels
  - abstraction-based kernels
- Outlook
  - Sequence modeling challenge: continuous and no-word-boundary sequences
  - Similarity search: efficient indexing & retrieval algorithms
  - Web applications

Thank you!

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