

Protein Sequence Classification Using Feature Hashing

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Abstract—Recent advances in next-generation sequencing technologies have resulted in an exponential increase in the rate at which protein sequence data are being acquired. The k -gram feature representation, commonly used for protein sequence classification, usually results in *prohibitively* high dimensional input spaces, for large values of k . Applying data mining algorithms to these input spaces may be intractable due to the large number of dimensions. Hence, using dimensionality reduction techniques can be crucial for the performance and the complexity of the learning algorithms. In this paper, we study the applicability of a recently introduced feature hashing technique to protein sequence classification, where the original high-dimensional space is “reduced” by *hashing* the features, using a hash function, into a lower-dimensional space, i.e., mapping features to hash keys, where multiple features can be mapped (at random) to the same hash key, and “aggregating” their counts. We compare feature hashing with the “bag of k -grams” and feature selection approaches. Our results show that feature hashing is an effective approach to reducing dimensionality on protein sequence classification tasks.

Keywords-feature hashing; variable length k -grams; dimensionality reduction.

I. INTRODUCTION

Many problems in computational biology, e.g., protein function prediction, subcellular localization prediction, etc., can be formulated as sequence classification tasks [1], where the amino acid sequence of a protein is used to classify the protein in functional and localization classes.

Protein sequence data contain intrinsic dependencies between their constituent elements. Given a protein sequence $\mathbf{x} = x_0, \dots, x_{n-1}$ over the amino acid alphabet, the dependencies between neighboring elements can be modeled by generating all the contiguous (potentially overlapping) sub-sequences of a certain length k , x_{i-k}, \dots, x_{i-1} , $i = k, \dots, n$, called k -grams, or *sequence motifs*. Because the protein sequence motifs may have variable lengths, generating the k -grams can be done by sliding a window of length k over the sequence \mathbf{x} , for various values of k .

Exploiting dependencies in the data increases the richness of the representation. However, the fixed or variable length k -gram feature representations, used for protein sequence classification, usually results in *prohibitively* high dimensional input spaces, for large values of k . Applying data mining algorithms to these input spaces may be intractable

due to the large number of dimensions. Hence, using dimensionality reduction techniques can be crucial for the performance and the complexity of the learning algorithms.

Models such as Principal Component Analysis [2], Latent Dirichlet Allocation [3] and Probabilistic Latent Semantic Analysis [4] are widely used to perform dimensionality reduction. Unfortunately, for very high-dimensional data, with hundreds of thousands of dimensions (e.g., 160,000 4-grams), processing data instances into feature vectors at run time, using these models, is computationally expensive, e.g., due to *inference* at runtime in the case of LDA.

A less expensive approach to dimensionality reduction is feature selection [5], [6], which reduces the number of features by selecting a subset of the available features based on some chosen criteria. In particular, feature selection by average mutual information [7] selects the top features that have the highest average mutual information with the class. The main disadvantages of feature selection are: (i) feature selection requires storing in memory the vocabularies of k -grams, which can become difficult given today’s very large collections of protein sequences, resulted due to progress on sequencing technologies [8]; and (ii) it does not allow for learning online features.

Recently, a new approach to dimensionality reduction, called feature hashing has been introduced for text classification [9], [10], [11], [12], which offers a very inexpensive, yet effective, approach to reducing the number of features provided as input to a learning algorithm, and overcomes the disadvantages of feature selection. Feature hashing allows random collisions into the latent factors. Specifically, the original high-dimensional space is “reduced” by *hashing* the features, using a hash function, into a lower-dimensional space, i.e., mapping features to hash keys, where multiple features can be mapped (at random) to the same hash key, and “aggregating” their counts. Figure 1 shows the application of feature hashing on sparse high-dimensional feature spaces. Although very effective for reducing the number of features from very high dimensions (e.g., 2^{22}) to mid-size dimensions (e.g., 2^{16}), feature hashing can result in significant loss of information, especially when hash collisions occur between highly frequent features, with significantly different class distributions.

In this paper, we study the applicability of feature hashing

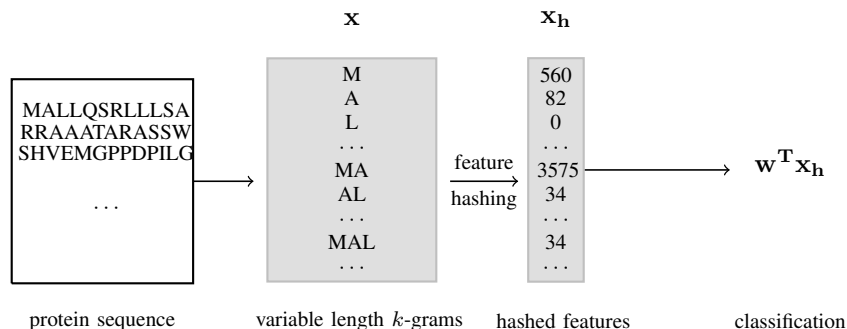


Figure 1: Feature hashing on sparse high-dimensional feature spaces. Hashing is performed to reduce very high dimensions to mid-size dimensions, which does not significantly distort the data.

to protein sequence classification and address three main questions: (i) What is the influence of the hash size on the performance of protein sequence classifiers that use hash features, and what is the hash size at which the performance starts degrading, due to hash collisions? (ii) How effective is feature hashing on prohibitively high dimensional k -gram representations? (iii) How does the performance of feature hashing compare to that of feature selection by average mutual information?

The results of our experiments on the three protein sub-cellular localization data sets show that feature hashing is an effective approach to reducing dimensionality on protein sequence classification tasks.

The paper is organized as follows. In Section 2, we discuss the related work. We then provide background on feature selection and feature hashing in Section 3. Section 4 presents experiments and results, and Section 5 concludes the paper.

II. RELATED WORK

Feature Selection. Feature selection [5], [13], [7], is a dimensionality reduction technique, which attempts to remove redundant or irrelevant features in order to improve classification performance of learning algorithms. Feature selection methods have been widely used in Bioinformatics for tasks such as sequence analysis, e.g., prediction of protein function from sequence, gene prediction, where the features could be the amino acids or k -grams; microarray analysis; mass spectra analysis; and single nucleotide polymorphisms (SNPs) analysis, among others (see [14] for a review and the citations therein).

Topic models. Topic models, such as Latent Dirichlet Allocation (LDA) [3], Probabilistic Latent Semantic Analysis (PLSA) [4], and Latent Semantic Indexing (LSI) [15] are dimensionality reduction models, designed to uncover hidden *topics*, i.e., clusters of semantically related words that co-occur in the documents. LSI uses singular value decomposition to identify topics, which are then used to represent documents in a low dimensional “topic” space. LDA models each document as a mixture of topics (drawn

from a conjugate Dirichlet prior), and each topic as a distribution over the words in the vocabulary.

LDA has recently emerged as an important tool for modeling protein data. For example, Airoidi et al. [16] proposed the mixed membership stochastic block models to learn hidden protein interaction patterns. Pan et al. [17] used LDA to discover latent topic features, which correspond to hidden structures in the protein data, and input these features to random forest classifiers to predict protein interactions. However, topic models are computationally expensive, for example, LDA requires *inference* at runtime to estimate the topic distribution.

Feature Abstraction. Feature abstraction methods [18], [19] are data organization techniques, designed to reduce a model input size by grouping “similar” features into clusters of features. Specifically, it learns an abstraction hierarchy over the set of features using hierarchical agglomerative clustering, based on the Jensen-Shannon divergence. A *cut* through the resulting abstraction hierarchy specifies a compressed model, where the nodes (or abstractions) on the cut are used as “features” in the classification model. Baker and McCallum [18] applied feature abstraction to reduce the dimensionality of the feature space for document classification tasks. Silvescu et al. [19] used it to simplify the data representation provided to a learner on biological sequence classification tasks.

Feature Hashing. Shi et al. [9] and Weinberger et al. [10] presented hash kernels to map the high dimensional input spaces into lower dimensional spaces for large scale classification and large scale multitask learning (i.e., personalized spam filtering for hundreds of thousands of users), respectively. Ganchev and Dredze [20] empirically showed that hash features can produce accurate results on various NLP applications. Forman and Kirshenbaum [11] proposed a fast feature extraction approach by combining parsing and hashing for text classification and indexing.

Hashing techniques have been also used in Bioinformatics. For example, Wesselink et al. [21] applied hashing to find the shortest contiguous subsequence that uniquely iden-

tifies a DNA sequence from a collection of DNA sequences. Buhler and Tompa [22] applied Locality-Sensitive Hashing (LSH) [23], a random hashing/projection technique, to discover transcriptional regulatory motifs in eukaryotes and ribosome binding sites in prokaryotes. Furthermore, Buhler [24] applied LSH to find short ungapped local alignments on a genome-wide scale. Shi et al. [9] used hashing to compare all subgraph pairs on biological graphs.

In contrast to the approaches above, we used feature hashing, a very inexpensive approach, to reduce dimensionality on protein sequence classification tasks, and compared it with feature selection by average mutual information.

Markov models. In the context of protein sequence classification, it is worth mentioning the fixed and variable-order Markov models (MMs), which capture dependencies between neighboring sequence elements. MMs are among the most widely used generative models of sequence data [25]. In a k^{th} order MM, the sequence elements satisfy the *Markov property*: each element is independent of the rest given the k preceding elements. One main disadvantages of MMs in practice is that the number of parameters increases exponentially with the range k of direct dependencies, thereby increasing the risk of *overfitting*. Begleiter et al. [26] (and papers cited therein) have examined methods for prediction using variable order MMs, including probabilistic suffix trees, which can be viewed as variants of abstraction wherein the abstractions are constrained to share suffixes.

III. METHODS

The traditional k -gram approaches construct a vocabulary of size d , which contains all k -grams in a protein data set. A protein sequence is represented as a vector \mathbf{x} with as many entries as the number of k -grams in the vocabulary. For a protein sequence, an entry i in \mathbf{x} can record the frequency of k -gram i in the sequence, denoted by x_i . Because only a small number of k -grams (compared to the vocabulary size) occur in a particular sequence, the representation of \mathbf{x} is very sparse, i.e., only a small number of entries of \mathbf{x} are non-zero. However, storing the parameter vectors in the original input space requires $O(d)$ numbers, which can become difficult given today’s very large collections of protein and DNA sequence data.

Feature selection reduces the size of the parameter vectors by selecting a subset of features from the original features, but still requires a mapping from strings to integers. Feature hashing eliminates the need for such a requirement by implicitly encoding the mapping into a hash function.

Next, we briefly overview feature selection and feature hashing.

A. Feature Selection by Average Mutual Information

Feature selection can be used to perform dimensionality reduction by selecting a subset \mathcal{F} of features from the set of k -grams (of size d) such that $|\mathcal{F}| = b$. The features are

Algorithm 1 Feature Hashing

Input: Protein sequence \mathbf{x} ; hash functions h and ξ , $h : \mathcal{S} \rightarrow \{0, \dots, b-1\}$, $\xi : \mathcal{S} \rightarrow \{\pm 1\}$.
Output: Hashed feature vector \mathbf{x}^h .
 $\mathbf{x}^h := [0, \dots, 0]$;
for all k -gram $\in \mathbf{x}$ **do**
 $i = h(k\text{-gram}) \% b$; // Places k -grams into hash bins, from 0 to $b-1$.
 $x_i^h = x_i^h + \xi(k\text{-gram})$; // Updates the i^{th} hash feature value.
end for
return \mathbf{x}^h // Records values of hash features.

ranked according to a scoring function and the top m best ranked features are selected.

As the scoring function, we used the average mutual information [27] between the class variable Y and the random variable over the absence or presence of a feature x_i in a document, denoted by X_i , which takes values 0 or 1, respectively. The average mutual information is defined as follows:

$$\begin{aligned} I(Y, X_i) &= H(Y) - H(Y|X_i) \\ &= \sum_{Y \in \{y_i\}} \sum_{X_i \in \{0,1\}} p(Y, X_i) \log \frac{p(Y, X_i)}{p(Y)p(X_i)} \end{aligned} \quad (1)$$

where $H(Y)$ is the entropy of the class variable, and $H(Y|X_i)$ is the entropy of the class variable conditioned on the absence or presence of feature x_i . The probability $p(Y, X_i)$ is estimated from counts gathered from \mathcal{D} , and $p(Y)$ and $p(X_i)$ are obtained by marginalizing $p(Y, X_i)$.

The feature selection representation. Let (\mathbf{x}, y) be an instance in \mathcal{D} . The “bag of k -grams” representation of (\mathbf{x}, y) is given by: $(\#x_1, \dots, \#x_d, y)$, where $\#x_i$, $i = 1, \dots, d$, represents the frequency counts of the k -gram x_i in the protein sequence \mathbf{x} . Given the selected set of features $\mathcal{F} = \{x_{i_1}, \dots, x_{i_b}\}$, the instance (\mathbf{x}, y) is transformed into $(\#x_{i_1}, \dots, \#x_{i_b}, y)$ (see Figure 2a).

B. Feature Hashing

Feature hashing [9], [10], [11], [12] is a dimensionality reduction technique, in which high-dimensional input vectors \mathbf{x} of size d are *hashed* into lower-dimensional feature vectors \mathbf{x}^h of size b . The procedure for hashing a protein sequence \mathbf{x} is shown in Algorithm 1 (see also Figure 1). Let \mathcal{S} denote the set of all possible strings (or k -grams) and h and ξ be two hash functions, such that $h : \mathcal{S} \rightarrow \{0, \dots, b-1\}$ and $\xi : \mathcal{S} \rightarrow \{\pm 1\}$, respectively. For a protein sequence \mathbf{x} , each k -gram in \mathbf{x} is directly mapped, using h^1 , into a hash key, which represents the index of the k -gram in the feature vector \mathbf{x}^h , such that the hash key is a number between 0 and $b-1$. Each index in \mathbf{x}^h stores the value

¹Note that h can be any hash function, e.g. `hashCode()` of the `java String` class, or `murmurHash` function available online at <http://sites.google.com/site/murmurhash/>.

(“frequency counts”) of the corresponding hash feature. The hash function ξ indicates whether to increment or decrement the hash dimension of the k -gram, which renders the hash feature vector \mathbf{x}^h to be unbiased (see [10] for more details).

Thus, an entry i in \mathbf{x}^h records the “frequency counts” of k -grams that are hashed together into the same hash key i . That is,

$$x_i^h = \sum_{k:h(k)=i} \xi(k)x_k, \quad (2)$$

for $k = 0, \dots, d - 1$ and $i = 0, \dots, b - 1$. Note that in the trivial case of $\xi \equiv 1$, x_i^h represents the actual frequency counts (see Figure 2b).

As can be seen, multiple k -grams can be mapped, through h , into the same hash key. According to Birthday Paradox, if there are at least \sqrt{b} features, then collisions are likely to happen [9], and hence, useful information for high accuracy classification could be lost through feature hashing. The k -grams in a collection of protein sequences typically follow a Zipf distribution, i.e., only very few k -grams occur with high frequency, whereas the majority of them occur very rarely (see Figure 3). Because hash collisions are independent of k -gram frequencies, most collisions are likely to happen between infrequent k -grams. Weinberger et al. [10] have proven that, for a feature vector \mathbf{x} such that $\|\mathbf{x}\|_2 = 1$, the length of \mathbf{x} is preserved with high probability, for sufficiently large dimension (or hash size) b and sufficiently small magnitude of \mathbf{x} , i.e., $\|\mathbf{x}\|_\infty$ (lower and upper bounds are theoretically derived).

However, for many practical applications, the value of b can be smaller than the theoretical lower bound. This may be problematic as the smaller the size of the hash vector \mathbf{x}^h becomes, the more collisions occur in the data. Even a single collision of very high frequency words with different class distributions, can result in significant loss of information.

IV. EXPERIMENTS AND RESULTS

In this section, we empirically study the applicability of feature hashing on three protein subcellular localization data sets: **psortNeg**² introduced in [28], **plant**, and **non-plant**³ introduced in [29].

The **psortNeg** data set is extracted from PSORTdb v.2.0 Gram-negative sequences, which contains experimentally verified localization sites. Our data set consists of all proteins that belong to exactly one of the following five classes: *cytoplasm* (278), *cytoplasmic membrane* (309), *periplasm* (276), *outer membrane* (391) and *extracellular* (190). The total number of examples (proteins) in this data set is 1444.

The **plant** data set contains 940 examples belonging to one of the following four classes: *chloroplast* (141), *mitochondrial* (368), *secretory pathway/signal peptide* (269)

and *other* (consisting of 54 examples with label nuclear and 108 examples with label cytosolic).

The **non-plant** data set contains 2738 examples, each in one of the following three classes: *mitochondrial* (361), *secretory pathway/signal peptide* (715) and *other* (consisting of 1224 examples labeled nuclear and 438 examples labeled cytosolic).

A. Experimental Design

Our experiments are designed to explore the following questions: (i) What is the influence of the hash size on the performance of biological sequence classifiers that use hash features, and what is the hash size at which the performance starts degrading, due to hash collisions? (ii) How effective is feature hashing on prohibitively high dimensional k -gram representations? (iii) How does the performance of feature hashing compare to that of feature selection by average mutual information?

To answer these questions, we proceed with the following steps. We first preprocess the data by generating all the k -grams from each collection of sequences, i.e., generating all the contiguous (potentially overlapping) sub-sequences of length k , for various values of k . This is done by sliding a window of length k over sequences in each data set. Note that if a k -gram does not appear in the data, it is not considered as a feature⁴.

Given a protein sequence \mathbf{x} , we apply feature hashing in two settings as follows: (i) We first generate all the k -grams of a fixed length k , i.e., $k = 3$. Each such k -gram is then *hashed* into a hash key. We refer to this setting as the fixed-length k -grams; (ii) We then generate all the k -grams of various lengths k , for values of $k = 1, 2, 3$, and 4. Thus, this setting uses the union of k -grams, for values of k from 1 to 4. Each such k -gram, i.e., unigram, 2-gram, 3-gram, or 4-gram, is *hashed* into a hash key. We refer to this setting as the variable-length k -grams.

We train Support Vector Machine (SVM) classifiers [30] on hash features, in both settings, fixed-length and variable-length k -grams, and investigate the influence of the hash size on the performance of the classifiers. Specifically, we train SVM classifiers for values of the hash size ranging from a 1 bit hash to a 22 bit hash, in steps of 1, and compare their performance.

Furthermore, we apply feature hashing to the sparse high dimensional variable-length k -gram representations to reduce the dimensionality to a mid-size b -dimensional space, e.g., $b = 2^{16}$ or $b = 2^{14}$, and compare the performance of SVM classifiers trained using hashed features with that of their corresponding counterparts trained using feature selection.

⁴The number of unique k -grams is exponential in k . However, for large values of k , many of the k -grams may not appear in the data (and, consequently, their frequency counts are zero). Note that the number of unique k -grams is bounded by the cardinality of the *multiset* of k -grams.

²www.psort.org/dataset/datasetv2.html

³www.cbs.dtu.dk/services/TargetP/datasets/datasets.php

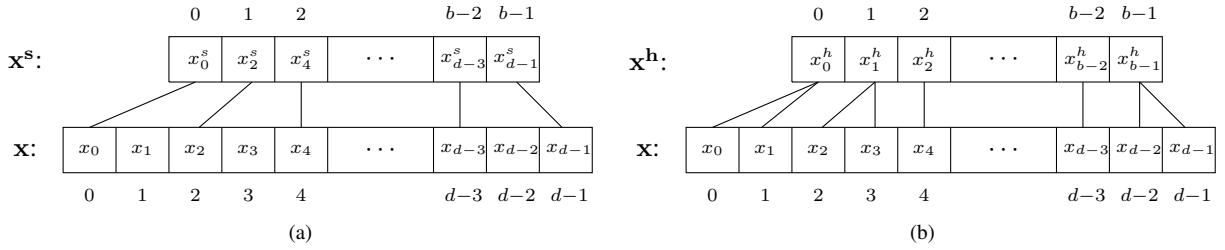


Figure 2: The transformation of “bag of k -grams” into: (a) feature selection, and (b) feature hashing representations.

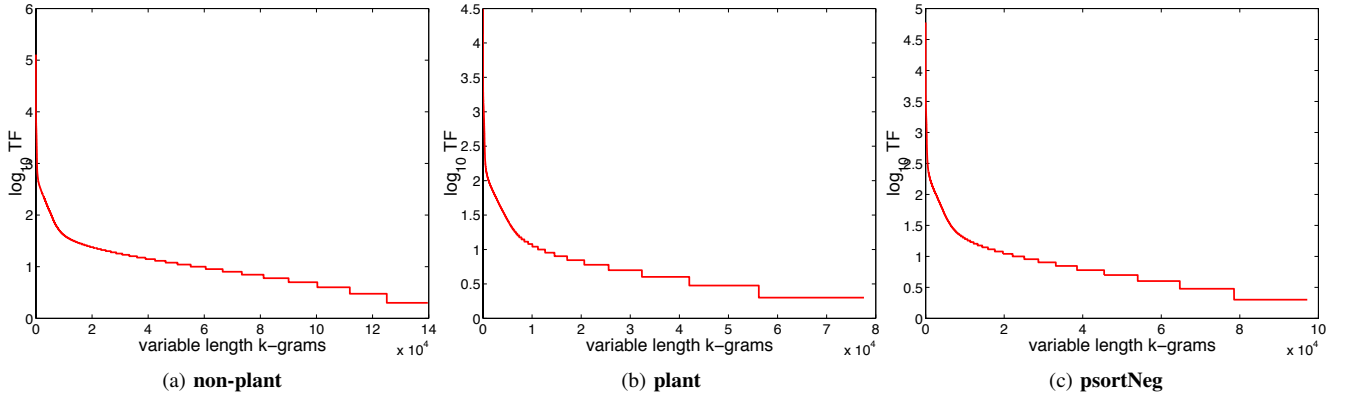


Figure 3: The variable length k -grams in each protein data set: (a) **non-plant**, (b) **plant**, and (c) **psortNeg**, follow a Zipf distribution, i.e., only very few k -grams occur with high frequency, whereas the majority of them occur very rarely.

Specifically, the feature representations used in each case are the following:

- a bag of b variable-length k -grams chosen from all d variable-length k -grams, using feature selection by average mutual information (See Section III.C for details). This experiment is denoted by FS.
- a bag of b hash features obtained using feature hashing over all d variable-length k -grams, i.e., for each k -gram, feature hashing produces an index i such that $i = h(k\text{-gram}) \% b$. This experiment is denoted by FH.

In our experiments, for SVM, we used the LibLinear implementation⁵. As for the hash function, we experimented with both the `hashCode` of the Java `String` class, and `murmurHash`. We found that the results are not significantly different from one another in terms of the number of hash collisions and classification accuracy. We also experimented with both $\xi : S \rightarrow \{\pm 1\}$ and $\xi \equiv 1$ - actual counts, and found that the results were not significantly different. The results shown in the next subsection use the `hashCode` function and $\xi \equiv 1$.

On all data sets, we report the average classification accuracy obtained in a 5-fold cross validation experiment. The results are statistically significant ($p < 0.05$). The

Bag of fixed or variable length k -grams	non-plant	
	Accuracy %	# features
1-grams	71.21	20
2-grams	70.85	400
3-grams	79.80	7999
4-grams	79.03	146598
(1-2)-grams	70.56	420
(1-3)-grams	79.69	8419
(1-4)-grams	82.83	155017
(1-5)-grams	80.09	950849

Table I: The performance of SVM classifiers trained using feature hashing on fixed length, 1-, 2-, 3-, 4-gram representations, as well as variable length, (1-2)-, (1-3)-, (1-4)-, (1-5)-grams representations, where the hash size is set to 2^{22} , on the **non-plant** data set.

classification accuracy is shown as a function of the number of features. The x axis of all figures in the next subsection shows the number of features on a \log_2 scale (i.e., number of bits in the hash-table).

B. Results

Comparison of fixed length k -gram representations with variable length k -gram representations. Table I shows, on the **non-plant** data set, the performance of SVM classifiers trained using feature hashing on fixed length

⁵Available at <http://www.csie.ntu.edu.tw/~cjlin/liblinear/>

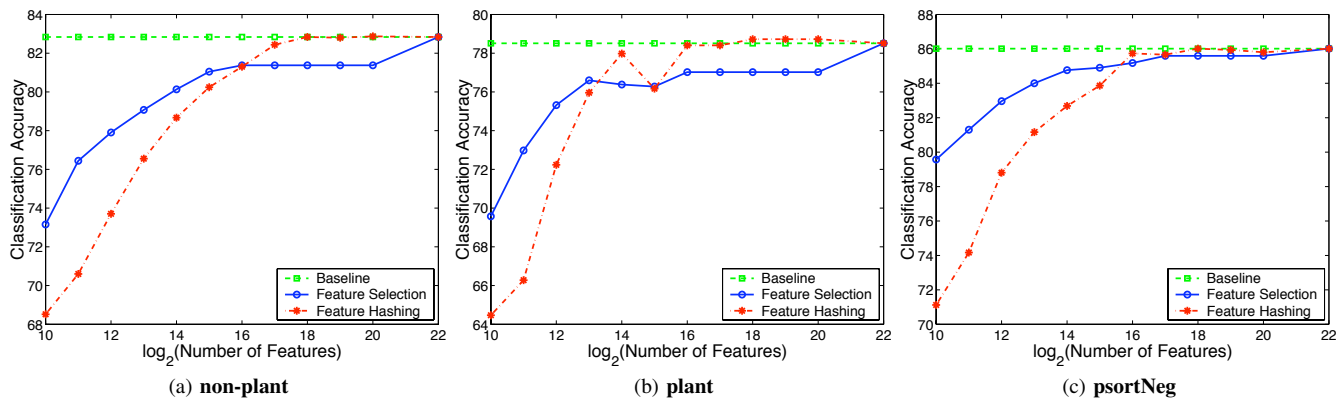


Figure 4: Comparison of feature hashing with the “bag of variable length k -grams” approach, referred as *baseline*, and feature selection on the protein data sets: (a) **non-plant**, (b) **plant**, and (c) **psortNeg**, respectively, using (1-4)-grams representations.

as well as variable length k -gram representations, where the hash size is set to 2^{22} . As seen in the table, the performance of SVMs trained on fixed length k -gram representations is worse than that of SVM classifiers trained using variable length k -gram representations, with (1-4)-grams representation (i.e., k ranging from 1 to 4), resulting in the highest performance. This is expected as the protein sequence motifs, i.e., k -grams, have variable length. Hence, the performance of SVM classifiers trained using variable length k -gram representations increases as we add more dependencies in the data (i.e., larger values of k), but starts decreasing as k becomes greater than or equal to 5, due to *overfitting*.

The number of variable length k -grams, for k ranging from 1 to 4, is 155,017. Feature hashing eliminates the need for storing the vocabularies in memory by implicitly encoding the mapping from strings to integers into a hash function, and at the same time, allows for learning new online features. Similar results are obtained for the **plant** and **psortNeg** data sets (data not shown).

We conclude that feature hashing is very effective on prohibitively high-dimensional n -gram representations, which would otherwise be impractical to use, resulting in memory-efficiency.

Because (1-4)-grams representation results in the highest performance, we used it for subsequent experiments.

The influence of hash sizes on classifiers’ performance. Figures 4a, 4b, and 4c show the influence of the hash size b on the performance of the SVM classifiers, trained using variable-length k -grams as feature representations, on the three protein data sets used in this study, **non-plant**, **plant**, and **psortNeg**, respectively. The values of b range from 2^{10} to 2^{22} .

As can be seen in the figures, as the hash size b increases from 2^{10} to 2^{22} , the performance of SVM classifiers increases as well, due to a smaller rate of hash collisions

for larger values of b . Table II shows, on all three data sets used, the number of unique features and the percentage of collisions for various hash sizes. The number of unique features is calculated as the number of non-empty entries in the hash vector, and the number of collisions as the number of entries with at least one collision. Note that the percentage of collisions below 2^{14} is 100%.

As the hash size increases beyond 2^{16} , the performance of SVM classifiers does not change substantially, and, eventually, converges. For example, on the **non-plant** data set, with 2^{16} hash size, SVM achieves 81.3% accuracy, whereas with 2^{22} hash size, SVM achieves an accuracy of 82.83% (Figure 4a). On the **plant** data set, SVMs achieve 78.4% and 78.51% accuracy, with 2^{16} and 2^{22} hash sizes, respectively (Figure 4b). Furthermore, as the hash size increases beyond 2^{16} , the percentage of hash collisions decreases until no collisions occur (Table II). For all three data sets, with 2^{22} hash size, there are no hash collisions. The performance of SVMs trained on hash features in the 2^{22} dimensional space is matched by that of SVMs trained on hash features in the 2^{18} dimensional space, suggesting that the hash collisions beyond 2^{18} does not significantly distort the data.

Because 2^{22} ($= 4, 194, 304$) highly exceeds the number of unique features, and the rate of hash collisions becomes zero, this can be regarded as equivalent to the classifiers trained without hashing, which require storing the vocabularies in memory, referred as *baseline* (Figure 4). Moreover, we considered 2^{16} as the point where the performance starts degrading. Note that the vocabulary sizes, i.e., the number of unique variable length k -grams, for **non-plant**, **plant**, and **psortNeg**, are 155,017, 111,544, and 124,389, respectively.

We conclude that, if feature hashing is used to reduce dimensionality from very large dimensions, e.g., 2^{22} to mid-size dimensions, e.g., 2^{16} , the hash collisions do not substantially hurt the classification accuracy, whereas if it is used to reduce dimensionality from mid-size dimensions to

Value of b	non-plant		plant		psortNeg	
	# features	Collisions %	# features	Collisions %	# features	Collisions %
2^{22}	155017	0	111544	0	124389	0
2^{20}	153166	1.21	110236	1.18	122894	1.22
2^{19}	147223	5.29	107299	3.95	118871	4.64
2^{18}	132754	16.30	99913	11.43	109535	13.22
2^{17}	99764	45.04	82141	31.38	87618	35.66
2^{16}	59358	78.53	53616	64.29	55555	68.85
2^{15}	32474	95.80	31788	89.56	32075	92.02
2^{14}	16384	100	16384	100	16384	100

Table II: The number of unique features (denoted as # features) as well as the rate of collisions on **non-plant**, **plant**, and **psortNeg** data sets, respectively, for variable length k -gram representations, where k varies from 1 to 4.

smaller dimensions, e.g., 2^{10} , the hash collision significantly distort the data, and the corresponding SVM classifiers result in poor performance.

Comparison of feature hashing with baseline and feature selection. Figures 4a, 4b, and 4c also show the results of the comparison of feature hashing (FH) with *baseline*, i.e., the “bag of k -grams”, and feature selection (FS) on the three protein data sets, **non-plant**, **plant**, and **psortNeg**, respectively, for (1-4)-grams representations.

As can be seen in the figures, feature hashing makes it possible to train SVM classifiers that use substantially smaller number of dimensions compared to the *baseline*, for a small or no drop in accuracy, for hash sizes between 2^{16} and 2^{22} . Furthermore, the performance of SVM classifiers trained using feature hashing is similar or slightly better compared to that of SVMs trained using feature selection, for hash sizes greater than 2^{16} . For example, for 2^{18} on **non-plant**, the SVM trained using feature hashing achieves an accuracy of 82.83%, whereas the SVM trained using feature selection, for the same hash size, achieves an accuracy of 81.37%. This can be due to removal of important sequence patterns, i.e., *motifs*, during the selection process. As the hash size decreases below 2^{16} (and the hash collisions significantly distort the data), feature selection significantly outperforms feature hashing, for the same choice of the hash size. For example, for 2^{14} , on **non-plant**, the SVMs trained using feature hashing and feature selection achieve an accuracy of 78.67% and 80.13%, respectively. However, for different choices of the hash size, the performance of feature selection is smaller than that of feature hashing, e.g., on the **non-plant** data set, with 2^{14} , the accuracy of feature selection is 80.13%, whereas on the same data set, with 2^{18} , the accuracy of feature hashing is 82.83%.

We conclude that feature hashing results in slightly more accurate models compared to feature selection, for relatively large hash sizes. As the hash size decreases, feature selection significantly outperforms feature hashing, for the same choice of the hash size. However, similar to the *baseline*, feature selection requires storing the vocabularies in memory, and does not allow for learning new, online features.

V. CONCLUSION

We presented an application of feature hashing to reduce dimensionality of very high-dimensional feature vectors to mid-size feature vectors on protein sequence data. We compared feature hashing with feature selection, which is another dimensionality reduction technique.

The results of our experiments on three protein subcellular localization data sets show that feature hashing is an effective approach to dealing with prohibitively high-dimensional variable length k -gram representations. Feature hashing makes it possible to train SVM classifiers that use substantially smaller number of features compared to the approach which requires storing the vocabularies in memory, i.e., the “bag of k -grams” approach, while resulting in a small or no decrease in classification performance. Moreover, feature hashing results in slightly more accurate models compared to feature selection, for relatively large hash sizes. As the hash size decreases, feature selection significantly outperforms feature hashing. However, feature hashing has two main advantages over the “bag of k -grams” approach and feature selections, which are as follows: (i) does not require storing the vocabularies in memory, and (ii) allows for learning new, online features at runtime.

Because recent advances in sequencing technologies have resulted in an exponential increase in the rate at which DNA and protein sequence data are being acquired [8], the application of feature hashing on biological sequence data advances the current state of the art in terms of algorithms that can efficiently process high-dimensional data into low-dimensional feature vectors at runtime.

In the future, it would be interesting to investigate how the performance of hash kernels compares to that of histogram-based motif kernels for protein sequences, introduced by Ong and Zien [31], and the mismatch string kernels for SVM protein classification introduced by Lesli et al. [32]. Along the lines of dimensionality reduction, it would be interesting to compare the performance of feature hashing with that of feature abstraction [19] on protein sequence classification tasks. Furthermore, another direction is to apply feature hashing to other types of biological sequence data, e.g., DNA data, and other tasks, e.g., protein function prediction.

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