A Note on the Compaction of long Training Sequences for Universal Classification -a Non-Probabilistic Approach

Jacob Ziv
Department of Electrical Engineering
Technion–Israel Institute of Technology
Haifa 32000, Israel

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Abstract

One of the central problems in the classification of individual test-sequences (e.g. genetic analysis), is that of checking for the similarity of a sample test sequence as compared with a very long training sequence that contains specific features that are sought in the test sequence. It should be noted that the storage of long training sequences is considered to be a serious bottleneck in the next generation sequencing for Genome analysis.

Some popular classification algorithms adopt a probabilistic approach, by assuming that the sequences are realizations of some variable-length Markov process or a hidden Markov process (HMM), thus enabling the imbedding of the training data onto a variable-length Suffix-tree, the size of which is usually linear in \( N \), the length of the test sequence.

Despite the fact that it is not assumed here that the sequences are realizations of probabilistic processes (an assumption that does not seem to be fully justified when dealing with biological data), it is demonstrated that any classifier may, without any loss in generality, always be based on a universal compaction of the training data that is contained in a (long) individual training sequence, onto a suffix-tree with no more than \( O(N) \) leaves, regardless of how long the training sequence is, at only a vanishing increase in the misclassification error rate.

Keywords: universal classification, universal compression, bio-informatics.
Introduction:

Upon observing an individual training $N'$-sequence $Y = (y_1, y_2, ..., y_{N'})$, a classifier searches for some typical features that may be imbedded in the training sequence and also appear in a test $N$-sequence $X = (x_1, x_2, ..., x_N)$.

One of the central problems in the classification of individual test-sequences (e.g., Genetic analysis) is that of checking the similarity of a sample test sequence against a training sequence (which in many cases is much longer than the test sequence) that contains specific features that are sought in the test sequence. Upon observing an individual training $N'$-sequence $Y = (y_1, y_2, ..., y_{N'})$, a classifier searches for some typical features that may also be imbedded in the training sequence and also appear in a test $N$-sequence $X = (x_1, x_2, ..., x_N)$.

It should be noted that data-storage is considered to be a serious bottleneck in the next generation sequencing for genome analysis” (quoting Prof. Stuart M. Brown, NYU Genome Center).

Some popular classification algorithms adopt a probabilistic approach, by assuming that the sequences are realizations of some variable-length Markov process or a hidden Markov process (HMM), thus enabling the imbedding of the training data in a variable-length Suffix-tree, the size of which is usually linear in $N$, the length of the test sequence[e.g. Bejerano et al, 2001, Giancarlo P. et al 2009, Reinert G. et al, 2009, Ulitsky I et al, 2009].

Despite the fact that the probabilistic approach is not theoretically justified, it apparently led to good empirical classification results.

In the case of data compression of long sequences, an alternative to the probabilistic approach was established: The stream of data to be compressed is assumed to be a non-probabilistic individual sequence.

The assumption that the compression is carried out via a universal Turing machine led to the notion of Kolmogorov complexity, which is the best asymptotic compression ratio that may be achieved for the individual sequence by any computer.
A more conceptually restricted, but practical approach was obtained by replacing the universal Turing machine model by a finite-state machine (FSM) model or a finite block-length compression model (LZ [Ziv, J. and Lempel, A 1977], Ziv, J. 2008, CTW [Willems, F.M.J. et al 1995, Weinberger, M. et al 1995]. and led to an associated suffix-tree data base with \( \mathcal{O}(N') \) leaves, where all leaves have about the same empirical probability of appearance, and where \( N' \) is the length of the sequence to be compressed.

It has been demonstrated that the common probabilistic modeling approach for prediction tasks may be replaced by an individual sequence approach as well. In this case too, organizing the data base in the form of a variable-length suffix-tree (context-tree) with leaves that have about the same empirical probability of appearance of suffixes, led to efficient on-line prediction [Ziv, J and Merhav, N. 2007]. A similar approach is adapted here, studying the performance of universal classification of an individual test sequence relative to a long individual training sequence.

Despite of the fact that it is not assumed that the sequences are realizations of a probabilistic process (an assumption that does not seem to be fully justified when dealing with biological data), it is demonstrated that optimal classification may be based on the compaction of the individual, long training sequence onto a suffix-tree with no more than \( \mathcal{O}(N) \) leaves (rather than \( \mathcal{O}(N') \) leaves as is in the data compression case), regardless of how long the training sequence is, at the cost of only a negligible increase in the misclassification error rate.

Furthermore, the generation algorithm of the suffix-tree from the training sequence is universal, since it does not depend on the specific features that are imbedded in the training sequence, thus yielding a formal justification for efficiency of classifiers that are associated with the compaction of the training data onto a suffix-tree data-base with an \( \mathcal{O}(N) \) storage complexity, without relying on any a-priori probabilistic assumptions.
Features and Similarity:

A feature is a distinct function of some substring \( Y_i(j) = (y_i, y_{i-1}, \ldots y_{i-j+1}); j \in [1, N - 1] \) of \( Y \). Not every substring of \( Y \) necessarily supports a feature, and no feature-supporting substring is a prefix of another longer feature-supporting substring.

Let \( F(Y) \) be a set of features that are imbedded in a (long) training sequence \( Y \) and are sought in the test sequence \( X \).

The discussion is restricted to the case where, given a collection of observed features of \( Y \) in \( X \), the classifier has to decide if \( X \) is similar enough to \( Y \), and should be declared to be acceptable. Also, given two test sequences \( X \) and \( X' \), decide which one is more similar (relative to some similarity measure) to \( Y \). Two tasks are typically considered:

Filtering:

Upon observing a collection of features of \( Y \) that appear in \( X \), decide if the test sequence \( X \) is similar enough (acceptable) (to \( Y \) relative to the training sequence \( Y \).

Clearly, a test sequence that contains no element of \( F(Y) \) should be declared by an effective classifier to be not – acceptable relative to \( Y \).

Sorting:

Sorting of test sequences \( X \) that passed the filtering stage, by their degree of ”similarity” to the training sequence \( Y \)

Example:

\( Y = A \ B \ A \ C \ D \ C \ B \ E \ D \ E \ D \ E \)
Features: A, BA, C, CD

\[ X = A A B D A D A D \]

Features in \( X \): A, A, BA, A, A

Consider, for example a version of Average Common Length (ACL) classification algorithm [Ulitsky, et al, 2006]:

Let the set of features \( F(Y) \) consist of distinct \( f(Y) \) substrings \( Y_i(j); 1 \leq j < L_{max} \) in \( Y \), that are leaves of a full tree, and where each being a prefix of some ”trimmed” suffix \( Y_i(j); 1 \leq j \leq i - 1; 1 \leq j < N' - 1 \) of \( Y \).

Let \( L(Y) \) denote the empirical average length of the elements of \( F(Y) \) when sliding along \( Y \).

Let \( L(X|Y) \) be the empirical average length of ”trimmed” suffixes \( X_i(j); j < L_{max} \) in \( X \) that are elements of \( F(Y) \).

Declare that \( X \) is similar to \( Y \) iff:

\[
D(X|Y) = \frac{L(X|Y) - L(Y)}{L_{max}} > T
\]

where \( T \) is a preset threshold. Here \( D(X|Y) \) is a measure of the similarity of \( X \) to \( Y \).

Observe that, given a particular set \( F(Y) \), then all it’s features may be mapped onto a suffix-tree with no more than \( f(Y) \) leaves. However, we are looking for universal compaction schemes, where the set of features \( F(Y) \) in \( Y \) is not known.

In the following it will be demonstrated that despite of the fact that the particular set of features \( F(Y) \) is not known (aside from it’s cardinality \( f(Y) \)), it is possible to universally compact \( Y \) onto a suffix-tree with no more than \( O(N) << N' \) leaves with only a negligible effect on the efficiency of any classifier.
**Definition: Classification Error**

A test sequence $X$ is *misclassified* if it is similar to $Y$, but is wrongly declared by the classifier to be *not similar* to $Y$, and therefore a *not-acceptable* one.

Traditionally, one assumes that the test sequences are realizations (of some probabilistic source (e.g. a hidden Markov process) and evaluate the performance of a given classifier via the corresponding probability of a misclassification event. In our case, no such probabilistic model exist, and the performance of a classifier is evaluated via the average error-rate of misclassification in a sliding window of length $N$ along the training sequence $Y$.

Let the fraction of substrings of $Y$ of length $N$ among the $N'-N$ such substrings in $Y$ that are similar to $Y$, be $q; 0 \leq q \leq 1$.

An efficient training sequence $Y$ for a given classifier $C(Y,X)$ is expected to have high values of $q$.

Given an individual training sequence $Y$ and a classifier $C(Y,X)$, the empirical classification efficiency may be evaluated by the following measure:

**Definition: Classification Error rate relative to Y.**

The *error-rate* $p_c(Y,X)$ of a classifier $C(Y,X)$ is the fraction $p(Y,X)$ among the $q(N'-N)$ substrings in $Y$ of length $N$, that should be declared to be *acceptable* by the classifier, but are rejected by it.

**Theorem 1** Assume that the number of (unknown a-priori) features in $Y$ is $f(Y)$. Let $\epsilon$ be an arbitrarily small positive number and consider the compaction of $Y$ onto a suffix-tree with at most $\frac{Nf(Y)}{\epsilon}$ leaves, which are the distinct substrings $Y_i(j); 1 \leq j < N$ in $Y$ with an empirical probability of appearance in $Y$ that is at least $\frac{\epsilon}{Nf(Y)}$.

Then, the error rate $p_c(Y)$ of $C(Y,X)$ might be increased by the compaction by no more than $\frac{\epsilon}{q}$, which vanishes with $\epsilon$. 
Proof of Theorem 1:

Let $F^*(Y)$ consist of all the substrings $Y_i(j); 1 \leq j < N$ in $Y$, with an empirical probability less than $\frac{\epsilon}{Nf(Y)}$.

Then, the average number of instances in a substring of length $N$ in $Y$ at which some element of $F^*(Y)$ appears is at most $\frac{Nf(Y)\epsilon}{Nf(Y)} = \epsilon$.

Therefore, by Chebyshev Inequality, the empirical probability of appearance of a suffix of length $N$ that contains one or more elements of $F^*(Y)$ is at most $\epsilon$ and the empirical probability that such an $N$-suffix will be one of the $q(N' - N)$ $N$-suffixes that should be accepted, but might be rejected due to the compaction is at most $\epsilon q^{-1}$.

Thus, as claimed above, it is possible to universally compact a very long training sequence $N' >> N$ onto a Suffix-tree with no more than $O(N)$ leaves that serves as an alternative data base to $Y$, with only a negligible effect on the classifiers performance.

Observe that a compaction of the training sequence $Y$ onto a Suffix-tree with $O(N)$ leaves is traditionally justified under a probabilistic HMM regime, by assuming that $N > 2^H(L_{max})$ where $L_{max}$ is the length of the longest feature-supporting suffix in $Y$, and $H$ is the entropy of the HMM process that generates $Y$, thus, by the Asymptotic Equipartition Property (AEP) of Information Theory, yielding a vanishing probability measure of $F^*(Y)$ as $L_{max}$ and $N'$ tend to infinity [e.g. Ulitsky T., et al, 2006], thus bridging the probabilistic approach with the non-probabilistic one that is presented here.

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