Bioinformatics and handwriting/speech recognition: unconventional applications of similarity search tools

Kyle Jensen and Gregory Stephanopoulos
Department of Chemical Engineering, Massachusetts Institute of Technology

***Abstract*—**
This work introduces two unconventional applications for sequence alignment algorithms outside the domain of bioinformatics: handwriting recognition and speech recognition. In each application we treated data samples, such as the path of a handwritten pen stroke, as a protein sequence and use the FastA sequence alignment tool to classify unknown data samples, such as a written character. That is, we handle the handwriting and speech recognition problems like the protein annotation problem: given a sequence of unknown function, we annotate the sequence via sequence alignment. This approach achieves classification rates of 99.65% and 93.84% for the handwriting and speech recognition respectively. In addition, we provide a framework for applying sequence alignment to a variety of other non–traditional problems.

***Index Terms*— Machine learning, bioinformatics, amino acids, protein sequences, sequence alignment, FastA, handwriting, voice, dynamic programming**

INTRODUCTION

Bioinformatics has benefited immensely from tools and techniques imported from other disciplines. Markov models used for gene–finding have their origin in information science, neural networks are imported from machine learning, and the countless clustering methods used for analyzing microarray data are from a wide variety of fields.

Sequence alignment tools are no exception to this trend; however, within bioinformatics, they have reached new levels of speed and sophistication. Tools, such as Blast [1], [2] and FastA [3], are used routinely to search through a database for sequences (DNA or protein) that are similar to a query sequence. Over the years, these tools have been optimized for speed by employing a number of heuristic shortcuts to the dynamic programming algorithms on which they are based. Even searches in very large databases, such as Swiss–Prot/TrEMBL [4] or GenBank [5], take only a few seconds for queries of small to moderate size. This is substantially faster than the time required for a rigorous Smith–Waterman search [6]. In light of the remarkably speed and accuracy that characterize these algorithms, it is intriguing to investigate other applications where similarity search tools might be of material importance. In this work, we present two alternative applications of these fast sequence alignment tools outside the domain of bioinformatics: handwriting recognition and speech recognition.

The dynamic handwriting recognition problem is to recognize handwriting from a touch tablet as found on personal digital assistants (PDAs), for example Palm Pilots, or tablet PCs [7]. These writing tablets sample the position of a pen as a function of time to produce a series of (x, y) points that are used by handwriting recognition algorithms to determine which character was written. An excellent review of the most common algorithms is available from Plamodon and Srihari, 2000. These include feature analysis, curve matching, Markov models, and elastic matching, the last of which is based on dynamic programming and is related to both Blast and FastA.

To apply similarity search concepts to the handwriting recognition problem, we represented the path of a PDA pen as a protein sequence by translating the (x, y) points into a string of amino acids. Using the protein representation of handwriting samples, we were able to classify unknown samples with FastA. This is analogous to the problem of protein annotation using similarity searching: given a protein (a written character) of unknown function, we annotated the protein by searching for similar sequences (characters with similar (x, y) paths).

We applied the same sequence alignment approach to speech recognition. Automated phone services, security checkpoints, and computer dictation software employ some form of speech recognition. Common speech recognition methods include feature recognition, neural networks, hidden Markov models, dynamic programming [8] and a variety of other statistical and signal processing algorithms. A good review of these techniques and more is available from Juang & Furui, 2000. For this problem, we represented digital speech recordings as sequences of amino acids, and used a database of annotated recordings to classify unknown recordings.

In the following section, we describe the data sets used for the handwriting recognition and speech recognition problems. Then, we detail how these data were represented using strings of amino acids and how we used FastA to annotate unknown samples in four handwriting and speech recognition experiments. We compare our results to more traditional methods of handwriting and speech recognition and, finally, we discuss ways of improving upon the results and extending sequence alignment to other classification problems.

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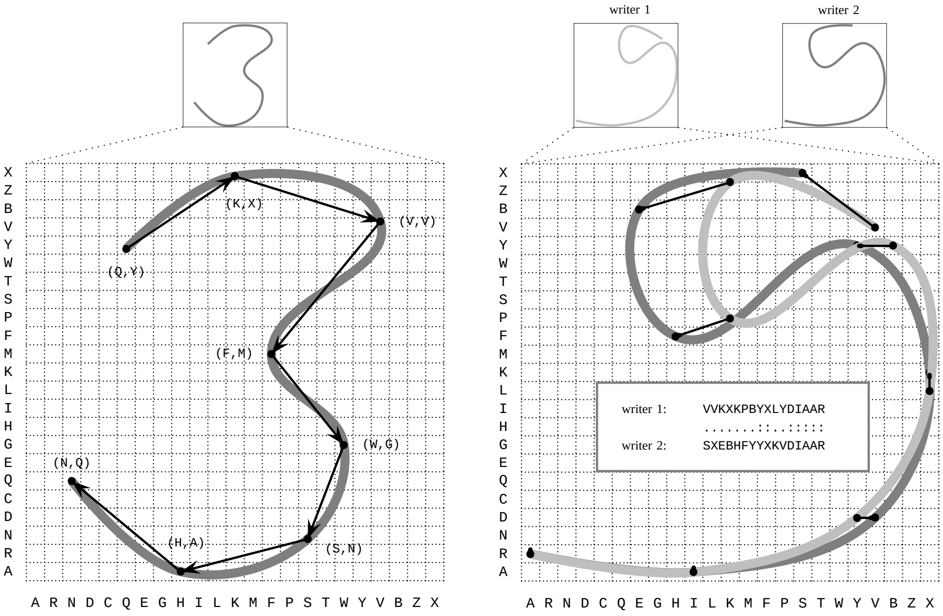
writer 1
writer 2
X Z B V Y W T S P F M K L I H G E Q C D N R A
A R N D C Q E G H I L K M F P S T W Y V B Z X
(Q,Y)
(K,X)
(V,V)
(F,M)
(W,G)
(N,Q)
(H,A)
(S,N)

```
writer 1:   VVKXKPBYXLYDIAAR
            .......::..:::::
writer 2:   SXEBHFYYXKVDIAAR
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(a) Projection of a digit written with a PDA stylus into protein space. Concatenating the set of points gives a protein sequence representative of the digit. In this case, the sequence is QYKXVVFMWGSNHANQ.

(b) An alignment of nines from two different writers. The boxes at the top show the input from each writer and the large grid show the superposition of the two handwritten digits. The FastA alignment between the protein representations of the two digits is shown in the center.

Fig. 1. Two visualizations of the handwriting recognition problem. In both cases the x and y axes are divided into 23 parts corresponding to the columns and rows in an amino acid scoring matrix. The eight sampled points from the digit are cast from x, y space into protein space by assigning amino acid coordinates to each point.

TABLE I

RESULTS FOR THE HANDWRITING AND SPEECH RECOGNITION PROBLEMS DESCRIBED IN THE TEXT. FOR EACH EXPERIMENT, THE MISCLASSIFICATION IS THE PERCENT OF SEQUENCES IN THE UNKNOWN SET FOR WHICH THE DIGIT OR LETTER WAS NOT PREDICTED CORRECTLY.

Experiment	Classification	Classification in Alimoglu & Alpaydin, 1996
1	97.34%	97.80%
2	99.64%	n/a

(a) Handwriting recognition results.

Experiment	Classification	Classification with clustering	Classification in Dietterich & Bakiri, 1995
1	93.84%	98.91%	96.73%
2	92.61%	98.61%	n/a

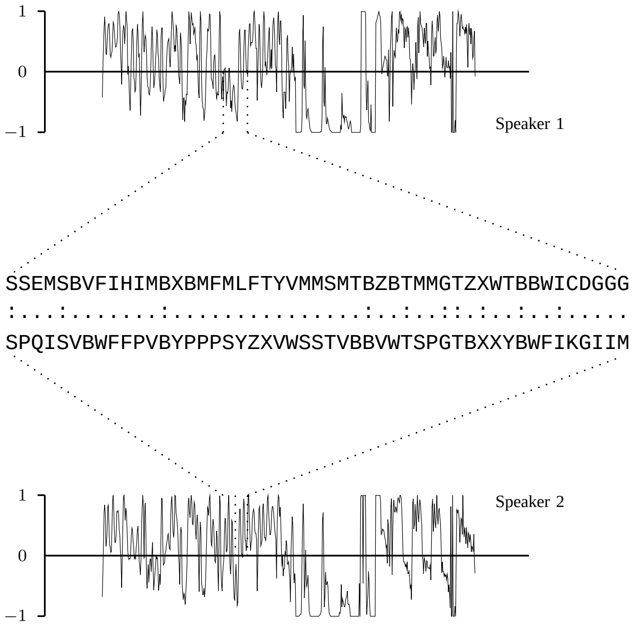
(b) Speech recognition results. The second column shows the misclassification using the clustering of all /ee/ sounding letters as described in the text.

SYSTEM AND METHODS

Handwriting Recognition

For our handwriting recognition experiments, we used data from Alimoglu and Alpaydin, 1996, available in the University of California Irvine repository of machine learning databases [12]. These data comprised of 10992 handwritten digits between *0* and *9*, written by 44 writers with each writer submitting 250 digits (8 samples were discarded by the original authors).

Each digit was written with a stylus pen on a touch tablet, which recorded the x and y coordinates of the pen as a function of time. These data were re-sampled such that each written digit was represented by a series of eight (x, y) points, spaced out by a constant arc length over the path of the digit. Then, for each digit, the set of (x, y) points were scaled such that the largest axis, usually the y axis, ranged from 0 to 1. By dividing the number line $[0, 1]$ into 23 "bins" we translated each of these



```
SSEMSBVFIHIMBXBMFMLFTYVMMSMTBZBTMMGTZXWTBBWICDGGG
:...:.......:...............:..:..::.:..:..:.....
SPQISVBWFFPVBYPPPSYZXVWSSTVBBVWTSPGTBXXYBWFIKGIIM
```

Fig. 2. An alignment of the spoken–letter "X" recorded from two different speakers. The plots at the top and bottom are recordings for first and second speakers, respectively. The breakout in the center shows a section of the protein projection of each recording and the alignment generated using FastA as described in the text. This example was taken from the first speech recognition experiment. In this case, the bottom recording was the top scoring alignment against the top recording.

coordinates into a pair of amino acids as shown in Figure 1. We concatenated these amino acid pairs to obtain a protein sequence representation of each digit: a "digit–protein."

Speech Recognition

For our speech recognition experiments, we used data from Deitterich and Bakiri, 1995, available in the University of California Irvine repository of machine learning databases [12]. This data set consisted of 7797 recordings of individuals speaking one of the letters *A–Z*. A total of 150 speakers each said every letter *A–Z* twice (three recordings were discarded by the original authors). Then, each recording was processed into a set of 617 real–valued attributes in the range $[-1, 1]$. A more detailed description of the database is available from Dietterich & Bakiri, 1995.

By dividing the number line $[-1, 1]$ into 23 bins we translated these real numbers into a series of amino acids. For example, the series "-1.0,-0.55, 0.11, 0.65" was translated to "AQKY". We concatenated these amino acids to make a protein representation of each recording: a "voice–protein".

TABLE II

THE SCORING MATRIX USED FOR THE HANDWRITING AND SPEECH RECOGNITION FASTA ALIGNMENTS. EACH ENTRY OF THE SCORING MATRIX, s_{ij}, IS GIVEN BY $s_{ij} = 10 - (|i - j|)$. THAT IS, MATCHING AMINO ACIDS ARE GIVEN 10 "POINTS", AMINO ACIDS THAT ARE ONE OFF ARE GIVEN 9 POINTS, AND SO ON. THIS MATRIX WAS USED IN PLACE OF THE DEFAULT SCORING MATRIX, BLOSUM50 [9], FOR FASTA. THE SCORING MATRIX WAS FOUND HEURISTICALLY. ALSO, A FEW EXPERIMENTS INDICATED THAT THE ALIGNMENTS ARE RELATIVELY INSENSITIVE TO PERMUTATIONS ABOUT THE FORM OF s_{ij} GIVEN ABOVE.

	A	R	N	D	C	Q	E	G	H	I	L	K	M	F	P	S	T	W	Y	V	B	Z	X
A	10	9	8	7	6	5	4	3	2	1	0	-1	-2	-3	-4	-5	-6	-7	-8	-9	-10	-11	-12
R	9	10	9	8	7	6	5	4	3	2	1	0	-1	-2	-3	-4	-5	-6	-7	-8	-9	-10	-11
N	8	9	10	9	8	7	6	5	4	3	2	1	0	-1	-2	-3	-4	-5	-6	-7	-8	-9	-10
D	7	8	9	10	9	8	7	6	5	4	3	2	1	0	-1	-2	-3	-4	-5	-6	-7	-8	-9
C	6	7	8	9	10	9	8	7	6	5	4	3	2	1	0	-1	-2	-3	-4	-5	-6	-7	-8
Q	5	6	7	8	9	10	9	8	7	6	5	4	3	2	1	0	-1	-2	-3	-4	-5	-6	-7
E	4	5	6	7	8	9	10	9	8	7	6	5	4	3	2	1	0	-1	-2	-3	-4	-5	-6
G	3	4	5	6	7	8	9	10	9	8	7	6	5	4	3	2	1	0	-1	-2	-3	-4	-5
H	2	3	4	5	6	7	8	9	10	9	8	7	6	5	4	3	2	1	0	-1	-2	-3	-4
I	1	2	3	4	5	6	7	8	9	10	9	8	7	6	5	4	3	2	1	0	-1	-2	-3
L	0	1	2	3	4	5	6	7	8	9	10	9	8	7	6	5	4	3	2	1	0	-1	-2
K	-1	0	1	2	3	4	5	6	7	8	9	10	9	8	7	6	5	4	3	2	1	0	-1
M	-2	-1	0	1	2	3	4	5	6	7	8	9	10	9	8	7	6	5	4	3	2	1	0
F	-3	-2	-1	0	1	2	3	4	5	6	7	8	9	10	9	8	7	6	5	4	3	2	1
P	-4	-3	-2	-1	0	1	2	3	4	5	6	7	8	9	10	9	8	7	6	5	4	3	2
S	-5	-4	-3	-2	-1	0	1	2	3	4	5	6	7	8	9	10	9	8	7	6	5	4	3
T	-6	-5	-4	-3	-2	-1	0	1	2	3	4	5	6	7	8	9	10	9	8	7	6	5	4
W	-7	-6	-5	-4	-3	-2	-1	0	1	2	3	4	5	6	7	8	9	10	9	8	7	6	5
Y	-8	-7	-6	-5	-4	-3	-2	-1	0	1	2	3	4	5	6	7	8	9	10	9	8	7	6
V	-9	-8	-7	-6	-5	-4	-3	-2	-1	0	1	2	3	4	5	6	7	8	9	10	9	8	7
B	-10	-9	-8	-7	-6	-5	-4	-3	-2	-1	0	1	2	3	4	5	6	7	8	9	10	9	8
Z	-11	-10	-9	-8	-7	-6	-5	-4	-3	-2	-1	0	1	2	3	4	5	6	7	8	9	10	9
X	-12	-11	-10	-9	-8	-7	-6	-5	-4	-3	-2	-1	0	1	2	3	4	5	6	7	8	9	10

Results

Handwriting Recognition

We conducted two handwriting recognition experiments. In both experiments part of the digit–protein database was assumed to contain a “known” set of digits that was subsequently used to annotate, or classify, the remaining “unknown” digits. For our first experiment, we used for the known database containing the writing of 30 persons (7494 digits) and an unknown database with the writing of the remaining 14 persons (3498 digits). Using FastA, we searched each sequence from the unknown set in the known set and used the top scoring hits to annotate the unknown digits. Searches were carried out using the scoring matrix shown in Table II with FastA version 3.4t11 using the default gap open and extension penalties, and the following options: `-p -Q -d0 -f-8 -g-1 -H -E1000 -b1`. An example alignment of two handwritten nines from different writers is shown in Figure 1.

For our second experiment, we used 25% (2748 digits) of our digit–protein database, selected randomly, as the unknown set and the remaining 75% (8244 digits) as our known set. Alignments and annotations using FastA were performed as in the first experiment.

The results of the two handwriting recognition experiments are shown in Table I. In experiment 1, our results are about the same as the best k–means clustering results of Alimoglu and Alpaydin [13], [14]. This experiment simulates the user–independent handwriting recognition problem: the handwriting of one group of writers was used to classify digits from a different group. In the user–dependent problem, experiment 2, the database of known handwritten digits contains samples from all the writers, on average. Thus, for every unknown handwriting sample, there is often a close match in the database of known samples. As such, the results of experiment 2 are significantly better than those of experiment 1 as shown in Table I.

In experiment 1, the average time for each alignment was 0.117 seconds per unknown sequence on a 1 gHz Pentium III processor. This is much shorter than the time required to write the digits. Thus sequence alignment could be used as a “real–time” method for handwriting recognition. This high speed, together with the high accuracy for user–dependent recognition makes sequence alignment good candidate for use on a Tablet PCs, or even PDAs.

Speech Recognition

Using the voice–protein database, we conducted two experiments, analogous to the two handwriting recognition experiments described previously. First, we used a known set consisting of 6238 recordings from 120 speakers and an unknown set with 1559 recordings from the remaining 30 speakers. Second, we used 25% (1949 recordings) of the voice–protein database, selected randomly, as the unknown set and the remaining 75% (5848 recordings) as the known set. Each of the speech recognition alignments was performed using the same scoring matrix and FastA parameters as the handwriting recognition experiments. An example alignment of two voice–proteins is shown in Figure 2.

The results of the two speech recognition experiments are shown in Table I. Experiment 1 is compared to the best Error Correcting Output Code (ECOC) results of Deitterich and Bakiri, but there was no comparison available for experiment 2. The misclassification for experiment 1 was 6.16%, higher than the ECOC result of 3.27%. However, we observed that most of the errors were due to rhyming letters, and in particular all of the /ee/ sounding characters [*B, C, D, E, G, P, T, V, Z*]. This indicated that these characters were similar on a sequence level, so we constructed a phylogenetic tree of the sequences to study their relationship.

A phylogenetic tree of 26 voice–proteins from a single speaker is shown in Figure 3. As the figure shows, the protein projections of phonetically similar letters tend to be

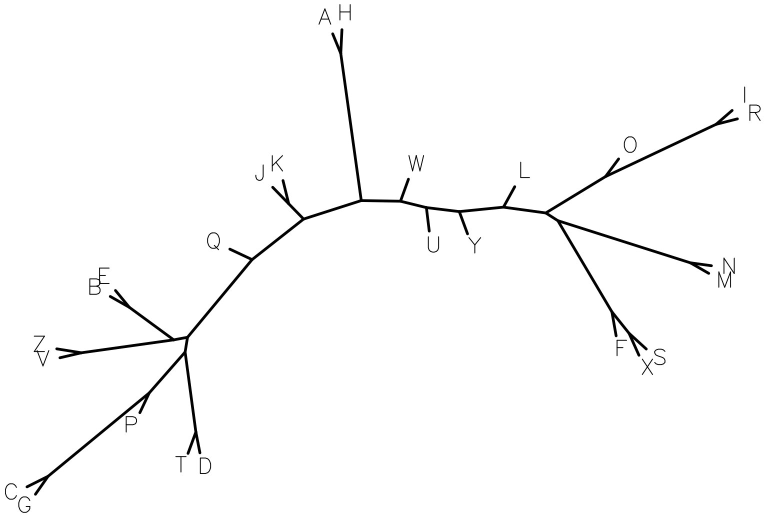


Fig. 3. A phylogenetic tree of voice–proteins. This tree was created using the Phylip [10] tree drawing program from a multiple sequence alignment of all 26 voice–proteins from a single speaker. The multiple sequence alignment was made using the ClustalW [11] alignment tool, with the scoring matrix in Table II. In the tree, similar sounding (homologous) letters are grouped near each other. For example, all the letters containing the /ee/ sound [*B, C, D, E, G, P, T, V, Z*] are clustered on the left side of the tree.

homologous. Furthermore, letters such as *A* and *H*, which have the /ay/ sound at the beginning, are more closely related to each other than they are to *J* and *K*, which have the /ay/ sound at the end. Because the /ee/ sounding letters all have /ee/ at the end, they are particularly difficult to distinguish from each other. These letters account for a disproportionate majority of the errors in our two experiments. By clustering these letters together such that they are considered the same for classification purposes, the error in experiment 1 was reduced to 1.09%. If the original error was evenly distributed between the classes, the error would have been reduced only to about 5.5%. This suggests that, although string alignment performs poorly for /ee/ sounding characters, it performs well for all other characters.

Conclusions

This work showed that sequence alignment can be a powerful classification tool for problems outside the domain of bioinformatics. In both the handwriting and speech recognition problems, we projected real–valued data into strings of amino acids and used FastA as a classification tool, in a manner analogous to protein annotation. In the case of handwriting recognition, we showed that sequence alignment is a viable alternative to traditional methods, such as k–means clustering, and is fast enough to be used as a real–time recognition method.

There are many ways to improve upon the results we presented here. First, we did not have any explicit training phase for either set of experiments. However, there are at least two sequence alignment parameters which can be trained: the gap open and extension penalties, and the scoring matrix. The optimization of these parameters for protein annotation is well documented [9], [15]–[19] and would be similar for alternative sequence alignment applications such as handwriting recognition. Second, intelligent projection of data into strings can greatly improve results. Here, we used bins of equal size to partition the real–valued data into amino acids; however, bins of unequal size may improve the resolution between closely related sequences and improve classification. Finally, more customizable sequence alignment tools would be very useful. These tools should take an arbitrary alphabet (Blast and FastA are restricted to 23 amino acids) and a user–defined scoring matrix (FastA allows user–defined matrices, but Blast does not).

The potential applications of sequence alignment tools outside of bioinformatics are boundless. Tools such as Blast and FastA can be used to quickly classify or search through any data that can be projected into a string of characters. Of course, these methods will work best with data that is of a low dimension. Our experiments with more complex data data, such as color images, suggest that how the data are projected into a string is very important with large number of dimensions. However, for simple types of data, such as customer purchase histories, black and white images, or Internet chat transcripts, we have been able to use sequence alignment as a quick and effective classification tool.

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