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A Smith-Waterman Local Alignment Approach for Spatial Activity Recognition

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Abstract

In this paper we address the spatial activity recognition problem with an algorithm based on Smith-Waterman (SW) local alignment. The proposed SW approach utilises dynamic programming with two dimensional spatial data to quantify sequence similarity. SW is well suited for spatial activity recognition as the approach is robust to noise and can accommodate gaps, resulting from tracking system errors. Unlike other approaches SW is able to locate and quantify activities embedded within extraneous spatial data. Through experimentation with a three class data set, we show that the proposed SW algorithm is capable of recognising accurately and inaccurately segmented spatial sequences. To benchmark the techniques classification performance we compare it to the discrete hidden markov model (HMM). Results show that SW exhibits higher accuracy than the HMM, and also maintains higher classification accuracy with smaller training set sizes. We also confirm the robust property of the SW approach via evaluation with sequences containing artificially introduced noise.

1. Introduction

Automatic human activity recognition is essential to the development of carer systems to support the elderly and to monitor pedestrian behaviour in public areas such as airports and railway stations. In this paper we recognise spatial activities, modelled on the elderly, in a mock smart home environment. Therefore, sequences are assumed to be spatially consistent across the same activity and of a similar duration. We refer to this type of matching as spatial activity recognition, in contrast to trajectory recognition, as spatial sequences corresponding to a specific activity are typically unique in relation to other activities and thus can be used for activity identification.

Much research has been done in the area of human activity recognition over the last decade indicating the increasing importance of this field. The different methodologies

can be classified in a myriad of different ways. For instance, in his review [1] classified existing approaches into two types: state-space models and template matching techniques. State-space models attempt to capture the statistical variation in spatial sequences. These approaches include neural networks [8, 12], HMMs [20] and extensions to the HMM [3, 11]. The HMM and multi-layer variants have been used successfully in dealing with uncertainty, yet typically suffer from high training complexity. Template matching approaches such as [2, 7] compare extracted features to pre-stored patterns or templates, but have issues with high runtime complexity, noise intolerance, spatial activity variation, and/or viewpoint specificity.

Robust approaches are necessary for determining the similarity of sequences obtained through non-invasive video tracking, as resulting spatial sequences can contain gaps and significant noise. The gaps and incorporated noise are caused by existing video tracking systems failing to consistently and accurately track people as a result of occlusions, lighting variation, foreground and background modelling limitations and/or geometrical constraints placed on the tracked objects. We address the accuracy and robustness issues apparent in spatial activity recognition with a bioinformatics inspired sequence alignment approach. Sequence alignment techniques, such as Smith-Waterman (SW)[16], have traditionally been used for identification of DNA, RNA and protein sequences. Recently the techniques have been applied in alternate pattern recognition domains such as speech recognition [14], string matching [15] and recently in recognising object trajectories from video surveillance data [17, 18, 5, 4, 6].

To address the gap and noise issues in spatial activity recognition we modify the traditional SW algorithm and introduce an euclidean matching function between trajectories, a matching threshold and a real non-matching penalty based on the euclidean distance. These modifications allow for direct application of SW to two dimensional spatial sequences without the need for symbolic mapping of trajectories. Through retaining the characteristics of SW in the proposed two dimensional SW algorithm, we are able

to find and quantify embedded activity sequences without the need for accurate activity sequence segmentation. This is highly advantageous if one wishes to accurately identify embedded activity sequences in online recognition systems, as techniques like DTW and the HMM are highly sensitive to the window sizes used in the sliding window approaches.

The layout of this paper is as follows. Related work is presented in section 2 and an overview of the proposed SW algorithm and HMM models are provided in sections 3 and 4, respectively. Data collection and experimental methodology are presented in section 5. In section 6 we evaluate SW with a three activity data set and contrast the results to the HMM as a benchmark. Lastly, a conclusion is given in section 7.

2. Related Work

Recent research on spatial activity recognition has utilised dynamic programming (DP) based methods for quantifying spatial sequence similarity and distance. DP alignment approaches are favoured as they provide accurate and robust recognition of spatial activity sequences containing significant outliers. In the following we provide a discussion of similar DP based approaches, including the LCSS based methods of [17, 18] and edit distance based techniques of [5, 4, 6].

The longest common subsequence (LCSS) algorithm is adopted in the development of similar non-metric algorithms for trajectory comparison by [17, 18]. In [17] the authors present an LCSS algorithm that aligns sequences spatially and temporally according to spatial and temporal thresholds. An approximate similarity function is also proposed that finds spatial sequences with the highest similarity, given a set of transformations. To alleviate the issue of choosing the thresholds with LCSS, [18] incorporated a sigmoidal matching function with a parameter to control the matching weight.

LCSS based techniques, such as those by [17] and [18], exhibit robust characteristics, but do so by ignoring all regions of dissimilarity between sequences. We argue that quantifying sequence dissimilarity is important as different sequences can have similar matching regions, but vastly different regions of dissimilarity. For example, if one measures the LCSS between a known 1D sequence $\mathbf{a} = [1234]$ and two observed sequences $\mathbf{b} = [1254]$ and $\mathbf{c} = [12744]$, both \mathbf{b} and \mathbf{c} would produce an LCSS of three, indicating that both are equally similar to \mathbf{a} . However, by visual inspection, one would say that \mathbf{b} is more similar to \mathbf{a} . Additionally, LCSS based methods use simple scoring schemes which do not provide for good discrimination, particularly with short sequences.

In [5, 4, 6], the authors propose the *global* alignment approaches, edit distance on real sequence (EDR) and edit

distance with real penalty (ERP), which align sequences across their entirety. To reduce dimensionality and computational complexity of the algorithms, trajectory sequences are mapped to movement pattern strings (MPSs). To quantify the MPSs a modified frequency distance is also given. Like the LCSS based techniques, EDRs discriminatory capability is reduced through use of a simple scoring scheme. This is addressed in the ERP algorithm, which uses a scoring scheme based on the local euclidean distance between trajectories. Unfortunately, ERP doesn't have the ability to control the degree of allowed deviation between sequences.

Throughout the paper we use the following notation. A symbol a_i or b_j represents a trajectory tuple (x, y) , where x and y denote the position within a two dimensional tracking space. The sequences \mathbf{a} and \mathbf{b} with lengths $|\mathbf{a}|$ and $|\mathbf{b}|$ are composed of symbols organised in time sequential order, where i and j ($1 \leq i \leq |\mathbf{a}|$ and $1 \leq j \leq |\mathbf{b}|$) determine the position within that corresponding sequence. Thus, a sequence of symbols $\mathbf{a} = [a_1, a_2, \dots, a_{|\mathbf{a}|}]$ can also be represented as a sequence of tuples $\mathbf{a} = [(x_1, y_1), (x_2, y_2), \dots, (x_{|\mathbf{a}|}, y_{|\mathbf{a}|})]$ and in combination as in $\mathbf{a} = [(a_1^x, a_1^y), (a_2^x, a_2^y), \dots, (a_{|\mathbf{a}|}^x, a_{|\mathbf{a}|}^y)]$. To simplify the notation we will predominately be using the symbol form.

3. Smith-Waterman Local Alignment

The Smith-Waterman (SW) local alignment approach [16] was originally developed and applied in bioinformatics to optimally locate biological sequence patterns within known database sequences. The original algorithm is similar to Needleman-Wunsch global alignment [9] but includes an extra zero, that prevents calculation of negative similarity. The extra zero allows termination of subsequence alignments that perform poorly and is thus able to find optimal *local* alignments between two sequences. Unlike other DP based similarity methods SW has no distance counterpart [19]. This is because the algorithm uses negative similarity to terminate poorly matching subsequence alignments, which can't be mimicked in a distance based approach.

We use the one dimensional SW local alignment technique as a basis to optimally locate patterns within observed two dimensional spatial sequences, that is in relation to the given match cost α , mismatch penalty $-d(a_i, b_j)$ and indel (insertion/deletion) penalty γ . By modifying the original one dimensional SW algorithm to incorporate an euclidean matching function between spatial symbols, a matching threshold and a real penalty, we improve the discrimination performance of the approach for spatial activity recognition, yet still retain the local alignment, high accuracy and robust characteristics of the original algorithm.

Our proposed SW algorithm utilises a stepwise similarity function $s(a_i, b_j)$ to differentiate between matches and non-

matches. The euclidean distance function (1) is used for the trajectory matching criteria in conjunction with a matching threshold θ .

$$d(a_i, b_j) = \sqrt{(a_i^x - b_j^x)^2 + (a_i^y - b_j^y)^2} \quad (1)$$

When the euclidean distance between the symbols a_i and b_j is less than the matching threshold θ a match occurs and a positive score is attributed, that is $s(a_i, b_j) = \alpha$. If the euclidean distance is equal to or larger than the matching threshold θ , reflecting a non-matching state, we assign the penalty $-d(a_i, b_j)$. For dealing with indels, a linear gap model with a gap penalty γ associated with each indel is adopted. If γ is larger in relation to the mismatch penalty, mismatches are favoured over gaps, producing shorter overall alignments. The opposite occurs when γ is larger than the mismatch penalty.

To calculate the similarity of two spatial sequences \mathbf{a} and \mathbf{b} using the proposed SW based approach one simply applies (3)-(5) to the DP matrix C (2) for $i = 0, 1, \dots, |\mathbf{a}|$ and $j = 0, 1, \dots, |\mathbf{b}|$ and finds the maximum value in C .

$$\begin{bmatrix} C(0, 0) & \dots & C(0, |\mathbf{b}|) \\ \vdots & \ddots & \vdots \\ C(|\mathbf{a}|, 0) & \dots & C(|\mathbf{a}|, |\mathbf{b}|) \end{bmatrix} \quad (2)$$

At each $C(i, j)$ where $i, j \neq 0$, four choices (match or mismatch, gap in \mathbf{a} , gap in \mathbf{b} and start a new subsequence) are evaluated with the choice corresponding to the maximum similarity value being selected for each $C(i, j)$. The match or mismatch score at each $C(i, j)$ is derived using $s(a_i, b_j)$ as previously described, while the gap scores for the sequences are derived using the linear gap model. If a negative similarity score results, then the fourth option of starting a new subsequence, represented by zero, is selected.

$$C(i, 0) = 0, \quad 0 \leq i \leq |\mathbf{a}| \quad (3)$$

$$C(0, j) = 0, \quad 0 \leq j \leq |\mathbf{b}| \quad (4)$$

$$C(i, j) = \max\{C(i-1, j-1) + s(a_i, b_j), \\ C(i-1, j) - \gamma, \\ C(i, j-1) - \gamma, 0\} \quad (5)$$

$$\text{where, } s(a_i, b_j) = \begin{cases} \alpha & d(a_i, b_j) < \theta \\ -d(a_i, b_j) & d(a_i, b_j) \geq \theta \end{cases}$$

4. Hidden Markov Model

The Hidden Markov Model (HMM) is a stochastic state transition model, capable of dealing with time sequential data [13]. It was first applied in the activity recognition domain, by [20], where mesh features were extracted from

time sequential images of tennis strokes and used in training and evaluation of the discrete model. Since then the HMM has been utilised extensively in activity recognition research, particularly through the multi-layer and hierarchical forms.

In this study, we utilise the discrete HMM to recognise spatial activity sequences. A discrete HMM is characterised by a number of hidden states N , distinct observation symbols per state M , state transition probability matrix A ($A = \{a_{ij}\}$), observation symbol probability distribution matrix B ($B = \{b_j(k)\}$) and the initial state distribution vector π . A derived HMM λ is typically represented by the following three parameters $\{\pi, A, B\}$. For further information on parameter estimation and inferencing refer to [13].

5. Data Collection and Methodology

The spatial activity sequences for evaluation are collected in a mock smart house environment using the multiple camera, QOS-based tracking system of [10]. The data set comprises three accurately segmented, spatially similar activities (variations of having breakfast) of ninety seconds in length, with twenty sequences per activity. Video sequences are captured at ten frames per second and then processed to obtain two dimensional trajectories for each frame. To obtain symbolised one dimensional sequences for the discrete HMM, the smart house environment is discretised into one square metre grids with each activity sequence, composed of x, y trajectories, being mapped to a sequence of unique integers u , where $u \in U$ and $U = 1, 2, 3, \dots, 156$.

Each data set is separated into training and testing sets prior to evaluation. By training set we refer to a database of spatial sequences from which optimal algorithm parameters are empirically determined. To quantify the recognition performance of the algorithms with the testing sets, we adopt a cross-validation methodology. In this approach each experiment uses thirty randomly generated training sets from which we take the mean of the individual test results. Cross-validation is preferred as it provides a more realistic picture of the true accuracy of the evaluated techniques.

6. Experimental Results

Experimental results that justify our claims of high accuracy and robustness with the proposed SW algorithm are provided in this section. The approaches used in the following experiments are developed in Matlab and C according to the specifications in Section 3 and 4. Optimal algorithm parameters were empirically derived from the training data as shown in Section 6.1 and used to evaluate the proposed SW algorithm in relation to accuracy and robustness. The results are then contrasted to the HMM as a benchmark.

6.1. Parameter Selection

An empirical approach is adopted in this study to determine the optimal sequence alignment parameters in relation to accuracy, with the exception of the matching threshold parameter θ . We believe that θ should be specified according to the desired recognition task. For instance, if the recognition task requires observed patterns to be strictly matched to those used in the training set, one would set θ to a small value. On the other hand if the matching constraint is relaxed and θ is set to a larger value, then we can expect to match more patterns and possibly obtain a higher proportion of misclassifications. In the following experimentation, we use $\theta = 1.0m$ to coincide with the size of the states used in symbolic mapping.

With a fixed θ , we first address the issue of selecting an appropriate value for the linear gap penalty γ . The effect of α in SW is minimised by setting it to a constant during the γ evaluation. To empirically find the optimum γ for the given data sets, we utilised values of γ from 0.5 to 10.0 and performed a cross-validation study using accurately segmented sequences (10 training and 10 testing). For the given dataset, $\gamma = 1.0$ provided the maximum classification accuracy and thus was used in further experimentation.

Following derivation of an empirically optimum value for γ we wished to find a optimum value for α , the match score for the proposed SW algorithm. Typically, one doesn't want α to be too large in relation to γ and the mismatch penalty, otherwise the algorithm behaves similarly to LCSS. In our case, we evaluated values of α from 0.5 to 10.0, with $\alpha = 2.0$ producing the highest accuracies across the data set. With the different values of α and γ it appears that the resulting recognition performance isn't highly sensitive to the parameter values as only a marginal 3% decrease in performance was observed over the evaluated ranges.

For the discrete HMM, a fixed number of symbols $M = 156$ was used with ten accurately segmented sequences for training. Consequent HMMs were built for each activity and trained using Baum-Welch parameter estimation, where the number of iterations was controlled by the convergence of the ratio of the average of the log-likelihoods between the current and previous iterations (< 0.001). In order to determine the optimal number of hidden states N to maximise discrimination performance, models were generated using $N = 5$ to $N = 15$ hidden states and evaluated with the accurately segmented testing sequences. The models with $N = 5$ and $N = 10$ produced similar maximum results; however, we selected $N = 5$ due to its lower runtime complexity.

6.2. Recognition Performance with Accurate Sequence Segmentation

The recognition performance of the proposed SW alignment approach was evaluated using the SW parameters from section 6.1 and ten accurately segmented training sequences with cross-validation. To show that the proposed 2D SW algorithm provides higher discrimination with spatial sequences than the original 1D SW algorithm, we compare the resulting recognition performance using the three class data set. 1D SW parameters were optimised using the same procedure as outlined in section 6.1. The results of the comparison are given in Fig. 1. The observed higher accuracy of the proposed 2D SW algorithm demonstrates that the addition of euclidean based trajectory matching, a matching threshold and a real mismatch penalty increases the algorithms discrimination performance with spatial activity sequences.

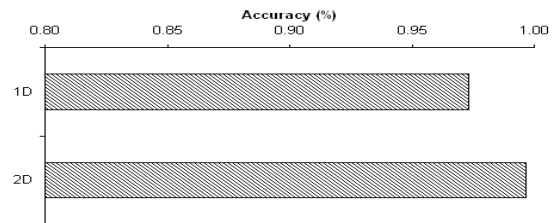


Figure 1. Recognition performance of the original 1D SW versus the proposed 2D SW.

To provide a benchmark of the performance of SW with accurately segmented spatial sequences for training and testing, we also compare the results to the discrete HMM. Results are shown in Fig. 2.

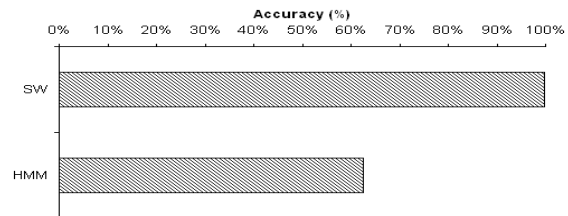


Figure 2. Recognition performance of SW versus the discrete HMM.

Evaluation of the proposed SW algorithm with the given data set demonstrates that the SW approach is capable of accurate discrimination, outperforming the discrete HMM by $> 30\%$. The poor performance of the HMM in this instance may be attributed to the significant noise apparent in the three class data set and/or the high degree of spatial

overlap in the sequences preventing generation of a good generalised model. The high recognition performance exhibited by SW with the accurately segmented activity sequences clearly shows that the approach can behave as per global alignment techniques, thus maximising similarity across the entirety of similar sequences.

6.3. Local alignment using SW

SW is able to locate and quantify optimal subsequences embedded within another sequence, referred to as local sequence alignment in bioinformatics. It is able to do this as the zero value terminates poor subsequence alignments, corresponding to negative similarity scores, and optimally finds and quantifies the maximum corresponding spatial subsequence(s) between two sequences. This characteristic allows the proposed SW approach to be directly applied to spatial sequences, without the need for accurate activity sequence segmentation. To demonstrate the local alignment characteristic of the proposed SW algorithm we evaluate SW with ten accurately segmented training sequences in comparison to the HMM. Testing sets of size ten that contain additional subsequences applied to the ends of the original sequences are used to mimic the inaccurately segmented sequences found in sliding window, online recognition systems. The results are presented in Table 1.

Table 1. Evaluation of SW and HMM with embedded spatial sequences.

Technique	Accuracy (%)
SW	98.3
HMM	0.0

The SW approach is capable of accurately recognising embedded sequences, producing a classification accuracy of 98.3% with the given data set. In contrast, the discrete HMM is unable to correctly classify any of the sequences. This occurs due to the derived HMMs encountering large numbers of symbols in the observed sequences, not present in the training sequences and therefore having a symbol probability $b_j(k)$ of zero or close to zero. When the scaled forward procedure is applied for inferencing, with the zero probability symbols, the derived probability of the overall sequence tends to zero, preventing accurate classification.

6.4. Training Set Size versus Recognition Performance

Ideally a classification technique should obtain high classification accuracy with a minimal training set. In order to ascertain how SW performs with fewer training sequences

for classification, we evaluate the technique using cross validation with 1 to 10 training sequences and contrast the results to the HMM. The intention of this experiment is to determine the viability of using limited training data in order to accurately recognise spatial activities. Models such as the HMM require larger training sets in order to produce good generalised models. The recognition performance with differing training set sizes can be found in Fig. 3.

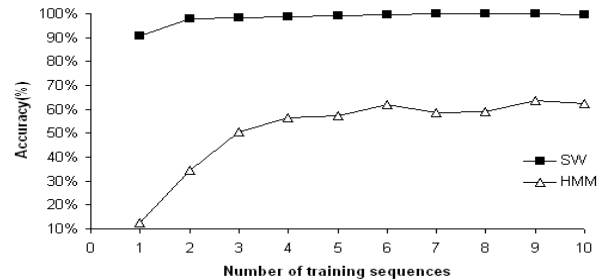


Figure 3. Recognition performance of SW versus the discrete HMM.

Analysis of Fig. 3 shows that the SW algorithm consistently achieves high accuracy across the different training set sizes and maintains that accuracy in comparison to the HMM. This contrasts the discrete HMM, which produced a classification accuracy of 62% with the maximum ten training sequences and only 12% with one training sequence. The low accuracy of the discrete HMM with small training sets is expected as the approach requires large numbers of training sequences in order to produce good approximations of the data. Unlike the HMM, the proposed SW approach is capable of high accuracy ($> 90\%$) using only one training sequence, indicating a strong discrimination capability. This attribute allows the technique to be used successfully with limited sequence data.

6.5. Effect of Noise on Recognition Performance

We evaluate the empirical robustness of SW in comparison to the HMM by cross validating ten accurately segmented training sequences with ten testing sequences containing varying magnitudes of artificially introduced random noise. The significance of such an experiment is to emphasise the robust characteristics of the proposed SW algorithm, in relation to the HMM, which is known for being robust to noise. The experimental results with noise magnitudes of between 0 to 2.5 metres are shown in Fig. 4.

These results demonstrate that the proposed SW algorithm is more resilient to noise than the HMM, as indicated by the lesser decrease in accuracy with the increased magnitudes of noise: $< 1\%$ decrease for SW versus 12% for the

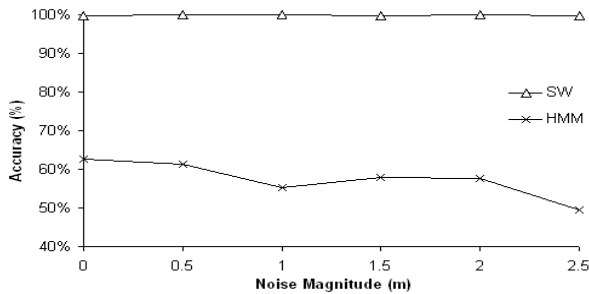


Figure 4. Noise magnitude versus classification accuracy.

HMM. Importantly, SW was able to maintain a classification accuracy of $> 99.0\%$ with the largest evaluated magnitude of noise, while the discrete HMM achieved only 49%. The maintenance of high accuracy across the different magnitudes of artificially introduced noise demonstrates that our proposed SW approach is robust to noise and moreso than the discrete HMM.

7. Conclusion

In this paper we have proposed an SW based algorithm for spatial activity recognition and demonstrated the technique's performance with classification of accurate and inaccurately segmented spatial sequences. With the accurately segmented sequences results were contrasted to the HMM, with SW producing 30% higher accuracy with the given data set. Evaluation of SW and the HMM with inaccurately segmented testing sequences, highlighted the local alignment property of SW. Here, SW had a similar performance to the accurately segmented testing sequences, with the HMM failing to recognise any of the inaccurately segmented sequences. Further experimentation also confirmed that SW is capable of accurately recognising activities with limited training data and is highly robust to the intrinsic noise of spatial sequences. In future work, we wish to extend the proposed SW technique to an online context and evaluate it with a larger data set, and in comparison to similar sequence alignment approaches such as DTW.

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