HUMAN BODY TRACKING BASED ON PROBABILITY EVOLUTIONARY ALGORITHM

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Abstract: A novel evolutionary algorithm called Probability Evolutionary Algorithm (PEA), and a method based on PEA for visual tracking of human body are presented. PEA is inspired by the Quantum computation and the Quantum-inspired Evolutionary Algorithm, and it has a good balance between exploration and exploitation with very fast computation speed. The individual in PEA is encoded by the probabilistic compound bit, defined as the smallest unit of information, for the probabilistic representation. The observation step is used in PEA to obtain the observed states of the individual, and the update operator is used to evolve the individual. In the PEA based human tracking framework, tracking is considered to be a function optimization problem, so the aim is to optimize the matching function between the model and the image observation. Then PEA is used to optimize the matching function. Experiments on synthetic and real image sequences of human motion demonstrate the effectiveness, significance and computation efficiency of the proposed human tracking method.

1 INTRODUCTION

With the fast developments of computer science and technology, visual analysis of human motion in image sequences interests more and more researchers from both laboratory and industry. Human motion analysis has many potential application areas such as intelligent visual surveillance, advanced human-computer interface, virtual reality, etc. Human tracking is a particularly important issue in human motion analysis. How to track human accurately and fast is a challenging task, and it has been a popular topic in the research of computer vision.

Tracking can be considered to be equivalent to establishing coherent relations of image features between frames with respect to position, velocity, shape, texture, color, etc (Hu et al., 2004). Tracking can be divided into region-based tracking (Haritaoglu et al., 2000; Collins et al., 2000), feature -based tracking (Breit et al., 2003), active-counter -based tracking (Zhong et al., 2000; Paragio et al., 2000), and model-based tracking. Model-based tracking can provide abundant information of human motion, but the increasing of subparts of the human model would potentially incur high dimensionality and make tracking a difficult task. To solve the problem, many approaches have been investigated. Gavrila *et al*. (Gavrila et al., 1996) split human model into torso-head and limb partitions, and then matching is implemented in the partitioned search space. The Pfinder developed by Wren *et al*. (Wren et al., 1997) employ a multi-class statistical model of color and shape to obtain a 2D representation of head and hands in a wide range of viewing conditions. Isard *et al*. (Isard et al., 1998) propose Condensation algorithm, which is a conditional density propagation method for visual tracking. Condensation is a useful approximate method for nonlinearity and non-gaussianity posterior probability within the Bayesian framework. Condensation has various versions, and these algorithms have been widely used now. Deutscher *et al*. (Deutscher et al., 2001) present an Annealed Particle Filtering (APF) method combined with hierarchical search strategy and crossover operator. Wu *et al*. (Wu et al., 2003) proposed a tracking approach using mean field Monte Carlo (MFMC) algorithm. In the approach, the subparts of human model are considered to be independent and a set of low dimensional particle filters interact with each other to solve the high dimensional problem collaboratively. Zhao *et al*. (Zhao et al., 2003)

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employ a 3D elliptical human model and segment human body in crowed situations using Data-Driven Markov Chain Monte Carlo (DDMCMC) algorithm. In their further work (Zhao et al., 2004), Markov chain Monte Carlo (MCMC) was used to tracking segmented human in sequences.

Different from using particle filters within the Bayesian framework, human tracking is considered to be a function optimization problem in this paper, so the aim is to optimize the matching function between the model and the observation. Function optimization is a typical application area of Genetic Algorithms (GAs), but canonical genetic algorithms is hard to be used here due to the high dimensionality of human model and the requirement of computation speed. In this paper, we present a novel evolutionary algorithm called Probability Evolutionary Algorithm (PEA) which is inspired by the Quantum computation (Nielsen et al., 2000; Hey, 1996) and Quantum-inspired Evolutionary Algorithm (QEA) (Han et al., 2002; Kim et al., 2003), and then the PEA based human body tracking is proposed in which PEA is used to optimize the matching function. PEA has a good balance between exploration and exploitation with very fast computation speed, and it is suitable for human tracking and other real-time optimization problems.

The rest of the paper is organized as follows. Section 2 contains the Probabilistic Evolutionary Algorithm (PEA). Section 3 describes the PEA based human body tracking. Section 4 shows the experimental results of our proposed tracking algorithm. Finally, the conclusion follows in section 5.

2 PROBABILISTIC EVOLUTIONARY ALGORITHM

Probabilistic Evolutionary Algorithm (PEA) is inspired by the Quantum computation and the Quantum-inspired Evolutionary Algorithm (QEA). QEA is characterized by the representation of quantum-bit, the observation step and the update step with quantum gate. QEA performs well in the function optimization and the knapsack problems. For the full details of QEA, one can peruse Ref. (Han et al., 2002; Kim et al., 2003). Considering that QEA has only two observed states (0,1), it is more suitable for the problem use binary coding than multi-nary coding. Although multi quantum-bit can be used to obtain multi observed states, this need to use multi quantum gate which is extraordinarily hard to design, and this shortcoming confines the application area of QEA (Nielsen et al., 2000; Hey, 1996). To overcome the disadvantage, we present the probability evolutionary algorithm (PEA).

2.1 The Individual's Representation in PEA

In PEA, the individual is encoded by the probabilistic superposed bit, which is defined as the smallest unit of information in PEA, as below.

Definition 1: A probabilistic superposed bit is a vector that consists of the observation probabilities, as:

$$\begin{bmatrix} p_0 \\ p_1 \\ \vdots \\ p_k \end{bmatrix}, p_0 + p_1 + \cdots + p_k = 1 \tag{1}$$

Where P_0, P_1, … P_k give the probability that a probabilistic superposed bit will be observed in the '0' state, the '1' state, …, and the 'k' state, respectively. So a probabilistic superposed bit is a linear superposition of the states 0 to k.

In PEA, an individual is defined as a string of the probabilistic superposed bits. The individual is no longer a deterministic state, but a linear superposition of all kinds of states.

Definition 2: An individual $\mathbf{p}$ is a string of m probabilistic superposed bits, as:

$$\mathbf{p} = \begin{bmatrix} p_0^1 p_0^2 \cdots p_0^m \\ p_1^1 p_1^2 \cdots p_1^m \\ \vdots \quad \vdots \quad\quad \vdots \\ p_k^1 p_k^2 \cdots p_k^m \end{bmatrix}, p_0^j + p_1^j + \cdots + p_k^j = 1, j = 1,2,\ldots,m \tag{2}$$

Where m is the length of the string. A PEA individual can represent a linear superposition of $(k+1)^m$ deterministic states probabilistically. For example: for an individual with m=3 and k=9, the probability to represent the state "123" is $p_1^1 \times p_2^2 \times p_3^3$, and the probability to represent the state "709" is $p_7^1 \times p_0^2 \times p_9^3$, etc. In the initialization of the individual, all p_i^j ,i=0,1,…,k, j=1,2,…,m, are set to 1/(k+1), so the initial individual represents the linear superposition of all possible states with the same probability.

2.2 The Observation in PEA

The individual $\mathbf{p}$ in PEA can't be used in the fitness function directly, and an observation step should be used to get the observed individual $\mathbf{s}$. For $\mathbf{p}$ with length m, it's observed individual $\mathbf{s}=[s_1,s_2,\ldots,s_m]$, where s_i (i=0,1,…,m) is a deterministic k-nary value and **s** is a deterministic k-nary string.

For the i-th probabilistic superposed bit $[p_0\ p_1 \ldots p_k]^T$ in **p**, its observed value s_i is obtained by the following step. First, a random number r is generated from the range [0,1]. Second, if $P_0 + \ldots + P_{v-1} < r < P_v + \ldots + P_k$, s_i is set to v.

Figure 1 shows an example of the observation step when k=4, r=0.6 and the i-th probabilistic superposed bit in **p** is $[0.25, 0.125, 0.375, 0.125, 0.125]^T$, here the observed value is $s_i = 2$.

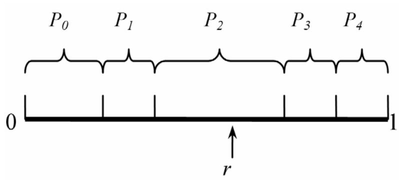

Figure 1: Observation.

2.3 The Update in PEA

The update operator is the only evolutionary operator in PEA which can increase the observation probabilities of some states, and decrease the observation probabilities of some other states, in order to make the high fitness state be observed more likely.

Let **s** be the observed individual of **p**, and **b** be the best solution of **p** at current generation. The update value Δp of the i-th probabilistic superposed bit $[p_0\ p_1 \ldots p_k]^T$ in **p** can be formed from **s** and **b**, and it can be found in Table 1.

Table 1: Lookup table of Δp, where $f(\cdot)$ is the fitness function, s_i and b_i are the i-th bits of **s** and **b**,

$s_i = b_i$	$f(\mathbf{s}) \geq f(\mathbf{b})$	Δp
false	*false*	δ
true	*true*	0
false	*true*	0
true	*false*	0

The update process is described in equation 3.

$$\begin{cases} p_{s_i} \leftarrow p_{s_i} - \Delta p \\ p_{b_i} \leftarrow p_{b_i} + \Delta p \end{cases} \quad (3)$$

Considering that the observation probability can not be negative, and to ensure the decreased probability will not attenuate too fast, we make the change value δ adaptively change according to the decreased observation probability, as:

$$\delta = d \times p_{s_i} \quad ,0 < d < 1 \quad (4)$$

Where d is the update rate that controls the convergence speed of PEA. A bigger d leads a rapid convergence speed but a rough search in the search space, a smaller d has the opposite effect.

Figure 2 shows an example of the update step when k=4, s_i=2, b_i=0 and Δp=0.05, here p_2 decrease, p_0 increase, p_1, p_3 and p_4 have no change.

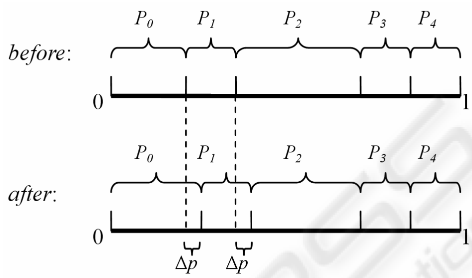

Figure 2: Update.

2.4 The Procedure of PEA

The procedure of PEA is described in the following.

Begin
$t \leftarrow 0$
Initialization: Initialize population $P(0)$
Observation: Obtain the observed population $S(0)$ by observing $P(0)$
Evaluation: Calculate the fitness of the observed individuals in $S(0)$
Store: Store $S(0)$ into $B(0)$
While Termination-condition = *false*
$t \leftarrow t+1$
Observation: Obtain the observed population $S(t)$ by observing $P(t\text{-}1)$
Evaluation: Calculate the fitness of the observed individuals in $S(t)$
Update: Obtain the population $P(t)$ by update $P(t\text{-}1)$
Store: Store the best solution among $B(t\ \text{-}1)$ and $S(t)$ into $B(t)$, Store the best solution in $B(t)$ into gb
If Migration-condition = *true*
Migrate individuals in $B(t)$ Locally or globally
End If
End While
End Begin

$P(t)$ is the population, $P(t)=\{\mathbf{p}_1^t, \mathbf{p}_2^t, \ldots, \mathbf{p}_n^t\}$. $\mathbf{p}_j^t$ is the j-th individual at the t-th generation, where n is the population size. In the initial population $P(0)$, all possible states in the search space should be observed with the same probability.

$S(t)$ is the observed population, $S(t)=\{\mathbf{s}_1^t,\mathbf{s}_2^t,\ldots,\mathbf{s}_n^t\}$. $\mathbf{s}_j^t$ is the observed individual of $\mathbf{p}_j^t$, and it is obtained by the observation step described in section 2.2.

$B(t)$ is the best solution population, $B(t)=\{\mathbf{b}_1^t,\mathbf{b}_2^t,\ldots,\mathbf{b}_n^t\}$. $\mathbf{b}_j^t$ is the best solution of $\mathbf{p}_j^t$ at the t-th generation. gb is the global best solution. When the local migration condition is satisfied, the best solution among some of the solutions in $B(t)$ is migrated to them. When the global migration condition is satisfied, the global best solution gb is migrated to $B(t)$.

Update operator generates the update position and update value according to $\mathbf{s}_j^t$ and $\mathbf{b}_j^t$, and evolves $\mathbf{p}_j^{t-1}$ to $\mathbf{p}_j^t$ by the update step described in section 2.3.

3 PEA BASED HUMAN BODY TRACKING

3.1 The Framework of PEA Based Tracking

Different from tracking human using particle filters within the Bayesian framework, tracking is considered to be a function optimization problem in this paper. We denote the human model by $\mathbf{X}$, and denote the observation associate with $\mathbf{X}$ by $\mathbf{Z}$. The function $f(\mathbf{X},\mathbf{Z})$ represents the matching degree between $\mathbf{X}$ and $\mathbf{Z}$. Assume that we have known that the model at time instance t-1 is X^{t-1}, so the model $\mathbf{X}^t$ at time instance t can be get by equation 5.

$$\mathbf{X}^t=\mathbf{X}^{t-1}+\Delta\mathbf{X} \quad (5)$$

Here, $\Delta\mathbf{X}$ is the change of the model $\mathbf{X}^{t-1}$. After we get $\mathbf{X}^t$, the matching function $f(\mathbf{X}^t,\mathbf{Z}^t)$ can be calculated. Since $\mathbf{X}^t$ is associated with $\Delta\mathbf{X}$, the matching function can be written as:

$$f(\mathbf{X}^t,\mathbf{Z}^t) = g\ (\Delta\mathbf{X}) \quad (6)$$

So tracking at time instance t is to optimize $g\ (\Delta\mathbf{X})$ in $\Delta\mathbf{X}$'s search space. Generally, $g\ (\Delta\mathbf{X})$ is a multi-modal function with many local best solutions, and conventional optimization methods are difficult to get the global best solution, so we use PEA to optimize $g\ (\Delta\mathrm{X})$.

3.2 Search Strategy

Human model always has high dimensionality, and search space partition is a useful strategy to change the high dimensional problem into some low dimensional problems and improve the matching results (Gavrila et al., 1996; Deutscher et al., 2001; Chen et al., 2005). Here we split the human model into five partitions including the trunk-head partition and four limb partitions. First, PEA is used to match the trunk-head partition. Then, keeping the best matched parameters of the trunk-head partition constant, and PEA is used to math the four limb partitions respectively.

In PEA based tracking, the model for the previous frame only gives the initial position for the current frame, so even if there are some matching errors at the previous frame, the matching is easy to be recovered in the following frames as long as the search space of $\Delta\mathbf{X}$ is enough.

3.3 Human Model

We employ a 10-part articulated human body model which consists of 10 parts and each pairs of neighbor parts are connected by the joint point, as shown in Figure3.

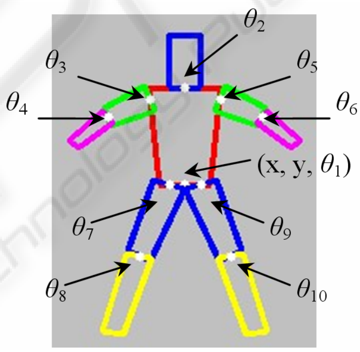

Figure 3: 2D human body model.

The model has 10 joints, and the root joint is at the middle bottom of the trunk. The root joint has 3 degrees, and each of the other 9 joints has 1 degree. The model $\mathbf{X}$ can be written as:

$$\mathbf{X} = \{x,\ y,\ \theta_1,\ \theta_2,\ \ldots\theta_{10}\} \quad (7)$$

Here, x and y represent the location of the root joint, and $\theta_1,\theta_2\ldots\theta_{10}$ represent the swiveling angles of the 10 joints. $\Delta\mathbf{X}$ can be written as:

$$\Delta\mathbf{X}=\{\Delta x,\ \Delta y,\ \Delta\theta_1,\ \ldots\Delta\theta_{10}\} \quad (8)$$

Human motion is a gradually changed movement, so ΔX can be limited in a logical small scope. This scope can be learned or man-made. For example, Δx and Δy are in the range [-19,19] (integral pixel), $\theta_1,\theta_2\ldots\theta_{10}$ are in the range [-29,29] (integral degree). Apparently, $\Delta\mathbf{X}$ is suitable for decimal encoding here, so the initial PEA individual of the trunk-head partition and that of the limb partitions are shown in Figure 4 and Figure 5 respectively.

In the observation step, the probabilistic superposed bits corresponding with Δx and Δy can be observed as {0,1,…39}, and subtracting 20 from these values give the true values of Δx and Δy. The probabilistic superposed bits corresponding with $\theta_1,\theta_2 ... \theta_{10}$ can be observed as {0,1,…59}, and subtracting 30 from these values give the true values of $\theta_1,\theta_2 ... \theta_{10}$.

$$\begin{array}{cc} & \begin{array}{cccccccc} \multicolumn{2}{c}{\Delta x} & \multicolumn{2}{c}{\Delta y} & \multicolumn{2}{c}{\Delta\theta_1} & \multicolumn{2}{c}{\Delta\theta_2} \end{array} \\ \begin{array}{c} 0\\1\\2\\3\\4\\5\\6\\7\\8\\9 \end{array} & \begin{bmatrix} 1/4 & 1/10 & 1/4 & 1/10 & 1/6 & 1/10 & 1/6 & 1/10 \\ 1/4 & 1/10 & 1/4 & 1/10 & 1/6 & 1/10 & 1/6 & 1/10 \\ 1/4 & 1/10 & 1/4 & 1/10 & 1/6 & 1/10 & 1/6 & 1/10 \\ 1/4 & 1/10 & 1/4 & 1/10 & 1/6 & 1/10 & 1/6 & 1/10 \\ 0 & 1/10 & 0 & 1/10 & 1/6 & 1/10 & 1/6 & 1/10 \\ 0 & 1/10 & 0 & 1/10 & 1/6 & 1/10 & 1/6 & 1/10 \\ 0 & 1/10 & 0 & 1/10 & 0 & 1/10 & 0 & 1/10 \\ 0 & 1/10 & 0 & 1/10 & 0 & 1/10 & 0 & 1/10 \\ 0 & 1/10 & 0 & 1/10 & 0 & 1/10 & 0 & 1/10 \\ 0 & 1/10 & 0 & 1/10 & 0 & 1/10 & 0 & 1/10 \end{bmatrix} \end{array}$$

Figure 4: Initial PEA individual of the trunk-head partition.

$$\begin{array}{cc} & \begin{array}{cccc} \multicolumn{2}{c}{\Delta\theta_{3/5/7/9}} & \multicolumn{2}{c}{\Delta\theta_{4/6/8/10}} \end{array} \\ \begin{array}{c} 0\\1\\2\\3\\4\\5\\6\\7\\8\\9 \end{array} & \begin{bmatrix} 1/6 & 1/10 & 1/6 & 1/10 \\ 1/6 & 1/10 & 1/6 & 1/10 \\ 1/6 & 1/10 & 1/6 & 1/10 \\ 1/6 & 1/10 & 1/6 & 1/10 \\ 1/6 & 1/10 & 1/6 & 1/10 \\ 1/6 & 1/10 & 1/6 & 1/10 \\ 0 & 1/10 & 0 & 1/10 \\ 0 & 1/10 & 0 & 1/10 \\ 0 & 1/10 & 0 & 1/10 \\ 0 & 1/10 & 0 & 1/10 \end{bmatrix} \end{array}$$

Figure 5: Initial PEA individual of the limb partition.

Here, we have a comparison of PEA with QEA. If we use QEA here, $\Delta\mathbf{X}$ should be encoded in binary. For the same range of $\Delta\mathbf{X}$ mentioned above, the lengths of QEA's individuals for trunk-head partition and limb partitions are 24 and 12 respectively, and those lengths of PEA's individual are 8 and 4 respectively. In PEA and QEA, the most intensive computation is the observation and the update for each bit in the individual, so the shorter length of individual make PEA run much faster than QEA.

4 EXPERIMENTAL RESULTS

Two image sequences are used here to demonstrate the effectiveness of PEA. Sequence 1 is a synthetic image sequence generated by Pose software which consists of 100 frames. Sequences 2 is a real image sequence which consists of 325 frames. The observation **Z** is also an important factor in tracking. Here we use two types of visual cues: edge and intensity. We compared the tracking results from PEA with Annealed Particle Filtering (APF). All the algorithms run on a 2.4GHz PC without code optimization.

4.1 Parameters Setting

In APF based tracking, 200 particles are used, and the particles are annealed for 8 times.

In PEA based tracking, we test two population sizes. The population sizes of PEA1 and PEA2 are set to 1 and 4, respectively. In PEA2, the local migration occurs every generation between each pair of neighboring individuals, and the global migration occurs every 100 generations. The maximum number of generations is 200.

4.2 Results

Some tracking results of PEA and APF for sequence 1 and sequence 2 are shown in Figure 6 and Figure 7 respectively. The average computation time for one frame of PEA and APF are shown in table 2.

Table 2: Average computation time for one frame.

Algorithm	Particles or Population size	second/frame
APF	200	3.77s
PEA2	4	1.62s
PEA1	1	0.41s

The results show that the PEA based tracking algorithm yields more stable results than APF, and run much faster than APF.

In some frames, PEA1 has some matching errors, this is because there is only one individual in the population and the premature convergence is happened sometimes. PEA2 generates very stable results in all the experiments.

In the experiments we also found that, when the population size is bigger than 10, the tracking result can not be improved further, so we suggest that the population size is set to 2 to 8 in applications in order to get a balance between the tracking accuracy and the computation time.

5 CONCLUSIONS AND FURTHER WORK

Model-based human tracking is a challenging problem, since the human model has high dimensionality. Different from tracking human using particle filters, we consider tracking to be a function optimization problem, and a novel evolutionary algorithm called Probabilistic Evolutionary Algorithm (PEA) is proposed to optimize the matching function between the model and the observation. PEA has a good balance between exploration and exploitation with very fast computation speed. Experiments on synthetic and real image sequences of human motion demonstrate the effectiveness, significance and computation efficiency of the PEA based human body tracking algorithm.

This paper mainly concerned to 2D tracking, but the PEA based tracking method is easy to be extended to 3D tracking, and our further work is to extend our algorithm to 3D and combine more observed cues such as motion and color. Our further work also includes the further improving of the searching ability and the computation speed of PEA.

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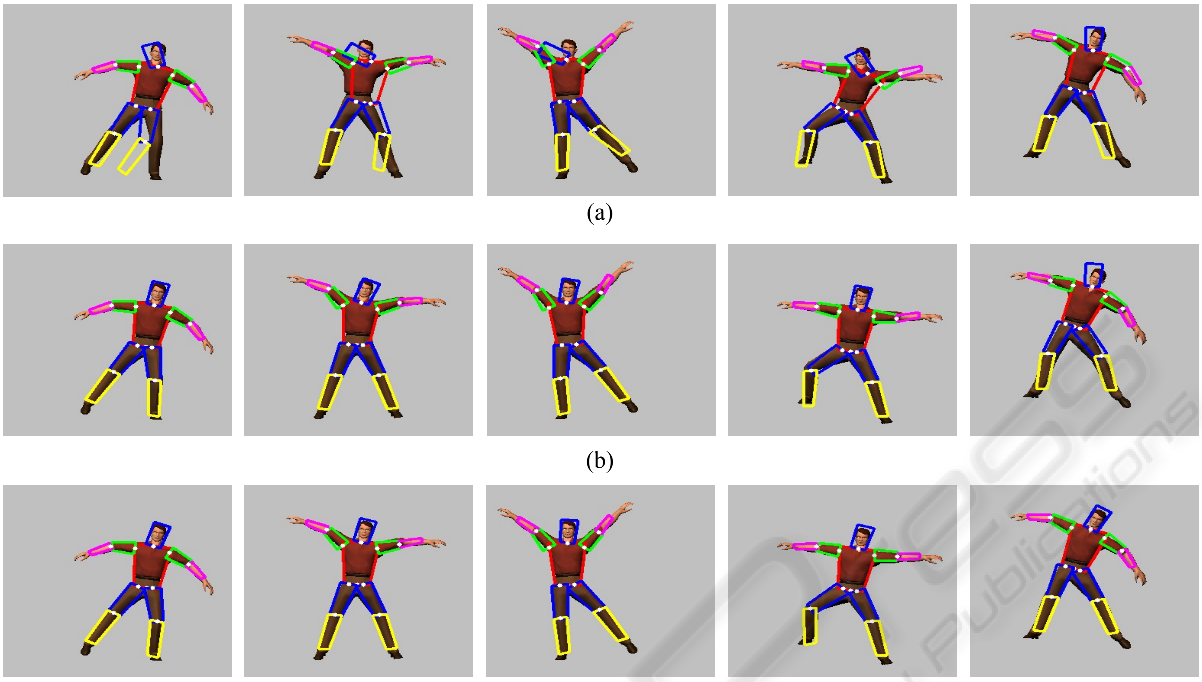
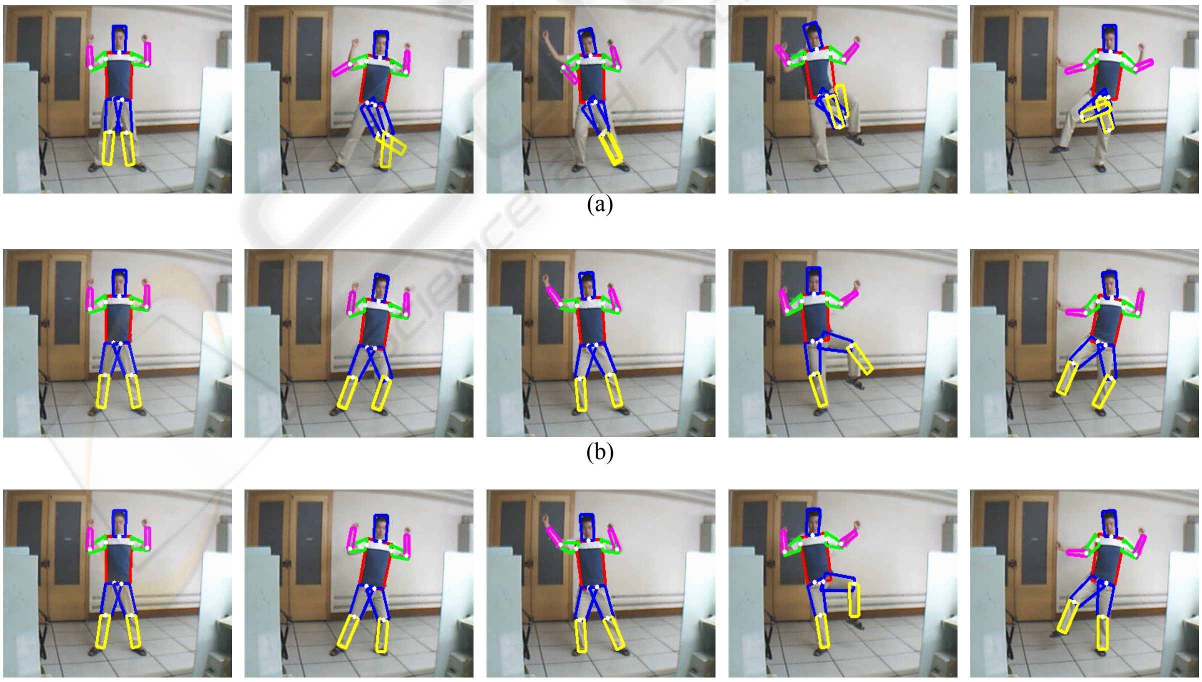


(a)

(b)

(c)

Figure 6: Some tracking results of sequence 1. (a) Tracking based on APF. (b) Tracking based on PEA with population size 1 (PEA1). (c) Tracking based on PEA with population size 4 (PEA2).



(a)

(b)

(c)

Figure 7: Some tracking results of sequence 2. (a) Tracking based on APF. (b) Tracking based on PEA with population size 1 (PEA1). (c) Tracking based on PEA with population size 4 (PEA2).