Abstract—Template-based model-free approach provides by far the most successful solution to the gait recognition problem in literature. Recent work discusses how isolating the head and leg portion of the template increase the performance of a gait recognition system making it robust against covariates like clothing and carrying conditions. However, most involve a manual definition of the boundaries. The method we propose, the genetic template segmentation (GTS), employs the genetic algorithm to automate the boundary selection process. This method was tested on the GEI, GEnI and AEI templates. GEI seems to exhibit the best result when segmented with our approach. Experimental results depict that our approach significantly outperforms the existing implementations of view-invariant gait recognition.

Index Terms—Biometrics, gait recognition, genetic algorithms, Linear Discriminant Analysis.

I. INTRODUCTION

Gait recognition analyses the manner of walking for human identification. As it requires minimal cooperation from the subject compared to other modalities, it is considered to be an unobtrusive biometric. Gait recognition methods can be grouped into either model-based or model-free approaches. Model-based methods [1]–[4] attempt to track the dynamic changes in the articulation points during gait and hence require intense computational effort. Recent trends prefer the model-free approach as it captures the gait patterns without this requirement.

The notion of templates was introduced in [5] where the silhouettes of key frames are matched with that of the gallery for recognition. Han and Bhanu [6] projected a simple method that averages all silhouettes of a single gait cycle to produce a single image template called the gait energy image (GEI) to encompass the spatiotemporal characteristics. Its advent brought forth a new category of model-free gait recognition called template-based methods. The GEI quickly became the most successful method for multi-view gait recognition. Its major drawback was its weakness to covariates like clothing and load carrying which could adversely affect its performance. Many similar methods followed aiming to mitigate this weakness with their implementation of gait templates. Two of such notable templates were the active energy image (AEI) [7] and the gait entropy image (GEnI) [8]. With a slight trade-off in normal walk gait recognition, these new templates were able to produce a better recognition accuracy over the clothing and carrying covariates in gait. Bashir et al. [8] eliminated this trade-off by masking the GEI with the image of the respective GEnI.

In addition to clothing and carrying conditions, the view angle is found to be the most important covariate factor that affects gait recognition performance [9]–[12]. There are essentially two types of view-invariant gait recognition models: view transformation model (VTM) and view-preserving model (VPM).

VTMs [13]–[15] transform the probe sequence’s angle to match with that of the gallery sequence. The VTM methods may differ in the measures used to gauge the transformation accuracy [16]. However, a significant level of error is inevitable in VTM-based gait recognition [17], [18].

VPMs consider multiple views as part of the gallery itself. This process incorporates the view information within the feature set for the extraction of relevant view-invariant gait features. Various methods can be employed to facilitate this. Examples include varying width vectors [9], Grassmann manifold [19], geometric view estimation [20], and spatiotemporal foot positioning [21]. A variant of VPM involves extraction of view-independent features through multi-view training and then use a single gallery view for testing [17], [22].

Dupuis et al. [18] formulated a single mask through the ranking of pixel features using the Random Forests classifier. Their panoramic gait recognition (PGR) algorithm uses pose estimation for view prediction. Choudhury et al. [23] designed a VPM named view-invariant multiscale gait recognition (VIMGR) which applied Shannon’s entropy function to the lower limb region of the GEI. The sub-region selection was later modified by Rida et al. [24] automating this segmentation procedure with a process known as group lasso of motion (GLM). Their approach to the problem has shown significant improvement in the covariate recognition accuracy.

Though the following implementations do not concern view-invariance or covariate factors, their aspects add to the motivation of our approach. Jia et al. [20] have shown how incorporating the head and shoulder mean shape (HSMS) along with the Lucas-Kanade variant of the gait flow image (GFI) [25] greatly improves recognition accuracy. The genetic algorithm [26] was previously used in [27] to optimize the selection of model-based gait parameters and also in [28] for the selection of superimposed contour features.

In this article, we devise a VPM that can be applied to any gait template for gait identification. To refine the
templates themselves, a method is proposed to automate its
segmentation process with the use of the genetic algorithm
(GA). These segments depict the optimal regions of the gait
template that can be used to obtain the best recognition result
at any covariate factor. The contributions of this paper are
summarized as follows:

- A sub-region selection process through GA that greatly
  enhances the robustness of gait recognition against co-
variate factors.
- A separate mask is produced for multiple view angles to
  obtain the best possible feature set for any given view.
- A computationally efficient view-estimator design to de-
  tect the angle of view based on the slopes of the gait
  trajectory.

II. METHOD

An overview of the method is illustrated in Fig. 1. The first
step is to extract the gait template (such as the GEI) from
the video that contains the gait sequence. After which the database
is split into two disjoint sets – tuning set and evaluation set.
The tuning set is fed to the GA to formulate the segments for
optimal performance. Only those segments are extracted from
the evaluation set to test the final accuracy of the system. The
features are preprocessed by Principal Component Analysis
(PCA) followed by a multi-class Linear Discriminant Analysis
(LDA) and then classified using Bayes’ rule. The Multi-
class LDA, also referred to as Multiple Discriminant Analysis
(MDA) [29], is a supervised dimensionality reduction method
that would maximize inter-class distance while minimizing
intra-class distance. PCA [30] is an unsupervised dimen-
sionality reduction algorithm that projects the given features to
feature space that corresponds to the highest variance. The
use of PCA yields a net positive effect on the performance
of the classifier in terms of both processing time and accuracy. As
a design choice, we use Bayes’ rule over the widely adopted
kNN.

A. Gait Template Extraction

All gait templates are produced in a similar procedure to
the one given below. Silhouettes in here are obtained through
background subtraction and encoded in grayscale.
1) Extract only the silhouettes of the subject during a single
gait cycle.
2) The silhouettes are center-aligned and scaled to a stan-
dard size; 240 x 240 in this case.
3) The standardized silhouettes for a given gait sequence
are merged through a collation process to generate the
gait template.

Let \( N \) be the number of silhouettes for a gait cycle for
a given subject. Each \( i^{th} \) silhouette is denoted as \( B(t) \). The
novelty in a gait template is defined by its collation process.
For example, in GEI [6], the collation process is given by

\[
G_{GEI} = \frac{1}{N} \sum_{t=1}^{N} B(t)
\]

Similarly, the templates AEI [7] and GEnI [8] used in this
study also differ by their collation process.

B. Genetic Template Segmentation

The boundary selection process is automated through GA
to find the optimum boundary to segment the gait template
before the actual training process. The gait template is to be
split into four segments, viz., head portion \( H \), leg portion \( F \),
mid-left section \( L \), and mid-right section \( R \). The parameters
to be optimized are the split points to divide these sections and
a binary weight bit per region to decide whether the respective
region should be included in the training as shown in Fig. 2.
This process is used to produce a masking template for each
view angle.

The chromosome structure for the genetic optimization is
given as

\[
[S_H, S_M, S_F, W_H, W_L, W_R, W_F]
\]

The variables denoted \( S_i \) are split variables that determine
the boundary for the region to segment and is represented by 8
bits each. \( S_H \) defines the line between the head portion and the
midsections; \( S_F \) determines the split between the midsections
and leg region; \( S_M \) divides the two midsections. If \( d \) is the
decimal equivalent of the 8 bits used to represent the split
variables, then its value can be decoded as

\[
S_i = \min_i + (\max_i - \min_i) \times \frac{d_i}{255}
\]

where \( \min_i \) and \( \max_i \) are the minimum and maximum
possible values for the variable \( S_i \). The variables \( W_i \) are binary
variables that determine whether the segment is included for
training. \( 1 \) indicates inclusion while \( 0 \) represents masking. The
total size of chromosome hence becomes 28 bits.

A set of subjects with all covariates included is used as a
tuning set to determine boundary locations for segmentation.
The fitness function evaluates the hypothesis generated by
the chromosome against the tuning set to produce a fitness
measure. The three covariates considered here is \( A \): normal
walk, \( B \): carrying a bag and \( C \): clothing condition. If the fitness
measure is simply set to the average of the accuracy of the
three covariate sets, then the GA would make a significant
trade-off on the normal walk sequence to maximize the overall accuracy. This was experimentally observed to at 90% while the state-of-the-art approaches produce accuracies of above 95% [24]. The fitness measure, $F$ for a given chromosome, $h$, is calculated as

$$F(h) = \left(\frac{1}{2}\text{CCR}_A(h) + \frac{1}{6}\text{CCR}_B(h) + \frac{1}{3}\text{CCR}_C(h)\right)^2$$

where $\text{CCR}_K$ represents the correct classification rates for the corresponding covariate $K$. Giving equal weights to each of the $\text{CCR}_k$ causes a trade-off in normal condition performance leading to an accuracy of 95.6% which is among the lowest of the normal CCR (refer Table I). Thus, the highest priority was given to CCR of the normal setting, $\text{CCR}_A$, to compete with the state of the art. In most approaches, clothing conditions pose the greatest challenge to template-based recognition systems. Hence the accuracy pertaining to the clothing condition, $\text{CCR}_C$, was given the next highest weight after normal setting to boost its accuracy on par with the carrying condition, $\text{CCR}_B$. These priority weights were assigned empirically.

The elitist selection variant of the generation propagation is used for this implementation of the GA [31]. That is, the chromosome corresponding to the highest fitness of a generation $T_n$ is made sure to be propagated the next generation $T_{n+1}$. The GA is set to follow a uniform crossover with probability 0.6, a single bit mutation probability of 0.03 and populates 20 chromosomes per generation. The optimization runs for 15 generations although convergence was mostly attained before the 8th generation during experimental observation.

C. View Estimation

Under the assumption that the subjects walk in a straight line for verification, the first and last visible silhouettes, $S_1$ and $S_n$, are taken into consideration. Let $P_1$ and $Q_1$ be the topmost and bottom-most point of $S_1$ as illustrated in Fig. 3. Similarly, $P_n$ and $Q_n$ denote the topmost and bottom-most point of $S_n$.

Let $m_P$ and $m_Q$ be the slopes of the lines $P_1P_n$ and $Q_1Q_n$ respectively. These two slopes alone form the features required to train the view-estimation classifier with the view as output labels. To reduce the number of cases, the sequence is passed through a simple check to verify whether the angle lies in the coronal plane ($0^\circ$ or $180^\circ$). If the last silhouette overlaps the first, then the viewpoint is determined to be at $0^\circ$ and the direct opposite for $180^\circ$. If both of these cases fail, then the angle should be one among those other than the two in the coronal plane.

### III. Experimental Results and Discussion

The CASIA dataset B is the benchmark gait database used for the experimental validation. The dataset includes six instances of normal walk (Set-A), two instances of walking while carrying a bag (Set-B) and two instances of walking while wearing an overcoat (Set-C) of 124 individuals. Each instance is captured over 11 angles of view, from $0^\circ$ to $180^\circ$, adding up to a total of 13640 instances. Further detail can be obtained in [33]. Set-A is split to Set-A1 containing four instances and Set-A2 for the remaining. Only Set-A1 is used for training. 24 subjects were randomly selected from the CASIA-B dataset to participate in the tuning set. These subjects were removed from the gallery for the evaluation phase just as in [20].

The experiments were first executed under the sagittal angle, $90^\circ$ view, to focus on the effect of carrying and clothing covariates. The GEI, GENI, and AEI were used as the base templates. The templates before and after GTS appear as shown in Fig. 4. The performance of the proposed GTS is compared against that claimed by other approaches in Table I.

![Fig. 3. Estimating viewpoints from different views. The line joining the extremities depicts the path of gait.](image)

![Fig. 4. Template transformation using the GTS hypothesis. Original templates of the GEI and GENI, and their respective masked templates for each covariate.](image)

### Table I

| Year     | Method                   | Normal Bag Coat Mean | Std |
|----------|--------------------------|----------------------|-----|
| 2006 Han and Bhanu [24] | 98.60 75.80 91.86 88.70 11.64 | 96.60 73.80 90.86 87.70 11.64 |
| 2013 Dupuis et al. [18]  | 98.43 75.80 91.86 88.70 11.64 | 98.30 75.60 91.76 88.60 11.56 |
| 2014 Kasakumaran et al. [33] | 98.50 76.80 91.85 88.60 11.65 | 98.40 75.70 91.75 88.50 11.55 |
| 2015 Arora et al. [34] | 98.00 75.40 91.40 88.40 11.45 | 98.40 75.80 91.80 88.80 11.80 |
| 2016 Rida et al. [35] | 98.39 75.89 91.96 88.75 11.59 | 98.50 75.90 91.90 88.80 11.60 |
| 2017 Kusakunniran et al. [32] | 94.50 60.90 58.50 71.30 20.13 | 98.40 75.80 91.80 88.80 11.80 |

Under the assumption that the subjects walk in a straight line for verification, the first and last visible silhouettes, $S_1$ and $S_n$, are taken into consideration. Let $P_1$ and $Q_1$ be the topmost and bottom-most point of $S_1$ as illustrated in Fig. 3. Similarly, $P_n$ and $Q_n$ denote the topmost and bottom-most point of $S_n$.
TABLE II

| Angle | 0° | 18° | 36° | 54° | 72° | 90° | 108° | 126° | 144° | 162° | 180° |
|-------|----|-----|-----|-----|-----|-----|------|------|------|------|------|
|        | (a) Dupuis et al. [18] | Panoramic Gait Recognition on GEI | | | | | | | | | |
| Normal | 97.17 | 99.60 | 97.17 | 96.33 | 98.76 | 98.43 | 97.14 | 97.57 | 97.14 | 92.97 | 96.00 |
| Bag   | 73.15 | 74.07 | 74.70 | 76.33 | 78.49 | 75.81 | 76.79 | 76.71 | 73.41 | 73.19 | 74.56 |
| Coat  | 81.64 | 87.39 | 86.29 | 84.34 | 89.96 | 91.86 | 89.50 | 85.04 | 72.24 | 78.40 | 82.70 |
| Mean  | 83.99 | 87.02 | 86.05 | 85.67 | 89.07 | 87.80 | 87.64 | 86.44 | 80.93 | 81.52 | 84.42 |
|        | (b) Choudhury et al. [23] | View-Invariant Multiscale Gait Recognition on GEI | | | | | | | | | |
| Normal | 100.00 | 99.00 | 100.00 | 97.00 | 99.00 | 99.00 | 99.00 | 100.00 | 100.00 | 100.00 | 99.00 |
| Bag   | 93.00 | 89.00 | 89.00 | 90.00 | 77.00 | 80.00 | 82.00 | 84.00 | 92.00 | 93.00 | 89.00 |
| Coat  | 67.00 | 56.00 | 50.00 | 71.00 | 75.00 | 77.00 | 75.00 | 65.00 | 64.00 | 64.00 | 66.00 |
| Mean  | 86.67 | 81.33 | 89.67 | 86.67 | 84.00 | 85.67 | 85.33 | 82.67 | 85.67 | 84.67 | 84.67 |
|        | (c) Rida et al. [24] | Group Lasso of Motion on GEI | | | | | | | | | |
| Normal | 97.97 | 98.79 | 96.37 | 96.77 | 98.39 | 97.98 | 97.18 | 95.56 | 96.77 | 97.98 | 97.58 |
| Bag   | 72.76 | 72.58 | 75.81 | 76.42 | 75.81 | 73.66 | 74.60 | 76.92 | 76.11 | 75.10 | 76.11 |
| Coat  | 80.49 | 83.47 | 85.08 | 87.85 | 91.53 | 91.07 | 87.90 | 86.23 | 87.45 | 84.90 | 83.06 |
| Mean  | 83.74 | 84.95 | 85.75 | 87.01 | 88.58 | 87.57 | 86.56 | 86.24 | 86.78 | 85.99 | 85.58 |
|        | (d) Proposed Genetic Template Segmentation on GEI | | | | | | | | | |
| Normal | 98.50 | 98.98 | 99.00 | 97.00 | 97.50 | 96.00 | 95.00 | 97.50 | 94.00 | 93.85 | 98.99 |
| Bag   | 95.00 | 98.47 | 96.50 | 96.00 | 95.70 | 93.50 | 93.50 | 94.00 | 92.90 | 93.31 | 94.44 |
| Coat  | 97.00 | 99.49 | 97.50 | 94.00 | 88.00 | 90.50 | 94.50 | 94.50 | 92.00 | 92.18 | 93.94 |
| Mean  | 96.83 | 98.98 | 97.67 | 95.67 | 94.33 | 93.33 | 92.67 | 95.33 | 92.83 | 92.15 | 95.79 |

Table II is the baseline for Table III and Fig. 5. The former reports the CCR of the state-of-the-art view-invariant gait recognition methods along with the best-performing template with the GTS, the GEI. The latter shows the CCR of the state-of-the-art view-invariant gait recognition methods along with the best-performing template with the GTS, the GEI. All of the scores in this table have been claimed to be obtained without the prior knowledge of the actual view angle. The overall performance of the methods including the base templates taking into account all angles is provided in Table III. Fig. 5 compares the error associated for each covariate for different methods. It is evident that the GTS has improved the covariate performance of all of the base gait templates.

The VI-MGR shows the highest normal condition CCR, but with a substantially lower CCR for the clothing condition. The PGR and GLM perform equally well with a slightly trade-off in carrying condition. The GTS with the GEI shows the best CCR in both carrying and clothing condition with minimal trade-off in normal condition resulting in a far superior overall performance. The entire operation was also implemented with kNN in place of Bayes’ rule for comparison. On an average of all 11 views and 3 covariates, GTS-GEI with kNN (k=1) yielded an accuracy of 94.54% which is marginally lesser than Bayes’ rule with 95.05%.

IV. CONCLUSION AND FUTURE WORK

In this paper, a novel segmentation technique was proposed to find the optimal regions of a gait template for view-invariant gait recognition robust to covariate factors. The genetic algorithm automates the boundary selection for each angle while a view-estimator determines the probe angle and selects the suitable view-specific classifier for recognition. The overall results clearly depict that the proposed GTS method outperforms the existing methods in literature. The next step would be to extend this framework to gait authentication.
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