Person Re-identification based on Human query on Soft Biometrics using SVM regression

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Keywords: Soft biometrics, Shape Context, SVM regression, Re-identification, Silhouettes, Retrieval, Surveillance.

Abstract: We propose a novel methodology for person re-identification (Re-ID) based on the biometric description of the upper-torso region of the human body. The proposed methodology leverages soft biometrics via Support Vector Regression (SVR) and Shape Context (*SC*) features obtained from the upper-torso silhouette of the human body. First, mappings from the upper-torso Shape Context to soft biometrics are learned from virtual avatars rendered by computer graphics engines, to circumvent the need for time consuming manual labelling of human datasets. Second, it is possible to formulate a human query of a given suspect against a gallery of previously stored soft biometrics. At this point, the proposed system is able to provide a ranked list of the persons, based on the description given. Third, an extensive study on the different regression methodologies to achieve the above mentioned mappings is carried out. We also conduct real time Re-ID experiments in an existing Re-ID dataset, and promising results are reported.

1 INTRODUCTION

In order to re-identify a person in a video surveillance, we usually rely on previously stored image/videos of the person or a verbal description of its biometric features. In this paper, we focus on the latter case via soft-biometric descriptions. Soft biometrics are the human characteristics providing categorical information such as age, gender, height, weight, length of arms and legs, skin/ hair color, gait and gestures, accent, etc. (Jain et al., 2004). In contrast to "hard" biometrics, such as fingerprint, retina, that encode unique and permanent personal characteristics, soft biometrics provide vague physical or behavioral information which may not be permanent or distinctive. However, there are certain advantages that make soft biometrics well suited to surveillance applications: they are usually easier to capture from a distance or from low quality data, and do not require cooperation from the subjects. Since these features are human interpretable, people can use them to refer to other people in re-identification (Re-ID) scenarios e.g., eyewitness of the suspect in a criminal scene (long face, fat, bald person).

With the arrival of sophisticated measurement systems such as 3D sensors (Kinect) and high definition cameras, several applications of soft biometrics for video surveillance were reported in the last decade. (Barbosa et al., 2012) presented a set of 3D soft biometric cues related to anthropometric measurements, obtained from KINECT RGB-D sensors and employed in person Re-ID. Many studies on gait based person recognition and re-identification were reported in (Bedagkar-Gala and Shah, 2014), (Goffredo et al., 2009) and (Nambiar et al., 2012). In (Le-An. et al., 2013), new methods for improving the Re-ID performance by re-ranking based on Soft biometric attributes are discussed. Some works addressed the issue of person Re-ID based on human query as well. (Dantcheva et al., 2010) proposed a BoSB bag of soft biometric traits (e.g., facial and body soft biometrics) for person Re-ID. In (Reid and Nixon, 2011) a large number of manual annotations of comparative biometric measurements was collected from numerous human annotators. In (Denman et al., 2012), person matching using semantic description is achieved using size and colour cues.

Person retrieval based solely on biometrics presents several challenges: *(i)* many people may share similar biometrics; *(ii)* verbal descriptions are qualitative and relative among individuals; *(iii)* it is difficult to bridge the semantic gap between human descriptions and real measurements. In this work, we explore new strategies to tackle these issues by linking these human interpretations to those of machine representations. With the aid of a machine learning

technique (Regression), we find the relationship between biometric features of a person and its computer vision features – histograms of Shape Context *(SC)* descriptors (Belongie et al., 2002) to encode the upper-torso silhouette of the humans.

One of the main challenges to train regression models is the availability of the ground truth biometric features. Due to the urge for a large datasets, human annotation of video sequences does not seem a feasible approach. Instead, we propose the generation of a database of synthetic avatars, whose bodily proportions can be manipulated easily. Regression analysis is then achieved via SVM Regression.

With respect to works in the state-of-the-art, our retrieval system using soft biometrics neither requires very high image resolution, as for facial features in (Dantcheva et al., 2010), nor laborious and plentiful manual annotations over real world dataset as in (Reid and Nixon, 2011). Also, in contrast to (Denman et al., 2012) and (Dantcheva et al., 2010), our system doesn't consider the appearance cues such as clothing colour, thus enabling towards long-term person Re-ID. Hence, we propose a novel automatic person Re-ID system solely based on biometric features, exploiting regression models and modern computer graphics technology.

The rest of the paper is organized as follows: The system architecture is explained in Section 2. In Section 3, the image features descriptors are explained. Then, Section 4 explains the regression process we carried out, including the generation of the dataset of avatars and the basics of SVM regression. In Section 5, the various experiments conducted and their results are detailed along with a real world case study of Person Re-ID. We summarize our work and enumerate some future work plans in Section 6.

2 SYSTEM ARCHITECTURE

The objective of our proposed system is to re-identify the person purely based on semantic human descriptions on his/her soft biometric features *(BF)* of the upper torso, such as chest width, shape of the face, neck size etc. We design our system in order to link these human compliant soft biometric cues with those of the machine interpretable computer vision features extracted from people. So, whenever the human query is provided, our system will provide the list of people observed in the system with biometric features similar to that query. Basically, there are two training phases involved in our procedure. The first one is for obtaining the regression model and the second one is the training for holistic Re-ID system.

Training regression model: To gather a large enough set of data for regression, we generate avatars in virtual reality based on groundtruth soft biometric values, and extract the corresponding *SC* feature descriptors. Then, regression analysis is carried out to obtain the regression parameters. A pictorial representation of the regression block is given in Fig. 2.

Training the Re-ID system: The general framework of the proposed system is presented in Fig. 1. During the training stage for the re-identification, we acquire the image data for all people appearing in the surveillance scenario via a number of cameras situated at various positions in the network. This set is denoted as "Gallery". Afterwards, we carry out the feature extraction from the collected data. We leverage Shape context (*SC*) descriptors for the extraction of features of the upper torso of each person. These extracted *SC* features are stored in a Gallery Database of *SC* features. A regression block will process the data on this set. As mentioned earlier, this block divulges the relation of *SC* descriptors with soft biometrics, and it estimates biometric feature (*BF*) values corresponding to each sample. Hence, for each Gallery image, the corresponding biometric value is estimated and stored in the Gallery Database of Soft Biometrics. This data is further processed and a statistical analysis is generated among the whole population and stored for later use.

Using the Re-ID system: Whenever a human probe query (in terms of the biometric description of the suspect) is entered in the system by an operator, the Biometric gallery is revisited by the system. Based on the statistical profile of the whole biometric info as well as the current query, the decision module will determine the most appropriate category of the suspect. Each category is identified via range of quartiles in this statistical chart. More details are explained later in Section 5.2. Since many people might have similar semantic labels resulting in subject interference, we propose that grouping them into classes with similar traits could be the best technique to tackle this scenario. Hence, the output of the system will be a ranked list of persons that share the similar human compliant traits. By considering many biometric cues, we can fine tune the person to be re-identified. This is a kind of pruning method, which normally the security people do manually on receiving the human queries; we do it here automatically.

3 IMAGE DESCRIPTORS

Silhouettes: Of the many different image descriptors that could be used for feature extraction of the person,
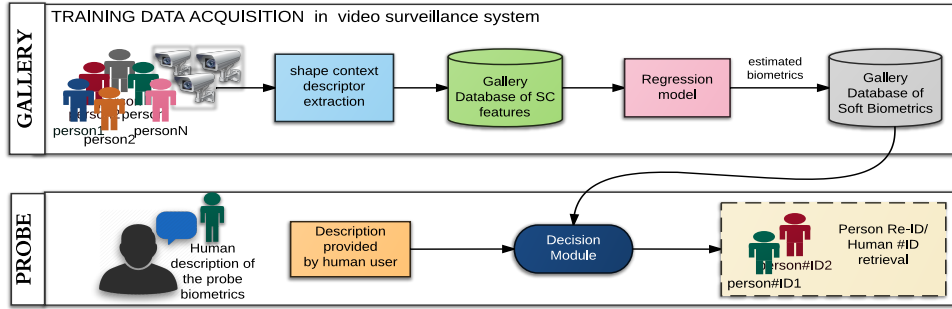
Figure 1: The scheme presents the holistic framework of our human re-identification (Re-ID) system. Gallery is the storage of data collected in the training phase, and probe is a human description of the subject provided by a human operator such as eyewitness statement in a criminal scene.
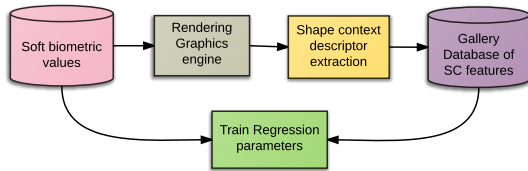

Figure 2: Framework for training the Regression model.

we have chosen image silhouettes. Silhouettes have a number of interesting properties: (*i*) they yield the shape of the person which encodes soft biometric traits such as lengths, curvatures and size ratios in the human body; (*ii*) they are insensitive to the surface attributes such as clothing colour and texture, thus better for long term based person re-identification; (*iii*) they are basic image edge information and could be extracted reliably using many techniques such as background subtraction, gradient analysis, depth map in 3D sensors, etc.

Shape Context: In this work, we use shape context descriptors to encode the shape over a range of scales. The original idea of Shape Context was described in (Belongie et al., 2002). In order to compute shape similarity, they introduced a new descriptor called Shape Context which measures the distribution of points in a shape relative to each point in that shape. The silhouette shape is thus encoded as a distribution in the 60-D shape context space, by encoding the local edge pixels into log-polar bins of *12* angular ×*5* radial bins. Then, matching silhouettes is reduced to matching Shape context descriptors. This is accomplished by bipartite graph matching technique as explained in the original paper. In our previous study (Nambiar et al., 2015), the feasibility of using Shape context features for person re-identification using *SC* matching is validated by employing Hungarian algorithm as an instance of Bipartite graph match-

ing, and verified by achieving a higher performance accuracy of 95% in virtual avatars and 92.5% in real imagery.

4 REGRESSION ANALYSIS

We leverage recent work on Support Vector Regression (SVR) to test linear as well as nonlinear models on the ability to predict biometric features from image data. A detailed explanation of our experimental dataset, SVM regression, the choice of basis, meta parameters and the cross validation strategies are provided in this section.

4.1 Database of Generic Avatars

For the learning phase of the regression, we need to have a benchmark dataset with the image descriptors and the corresponding soft biometric information. To collect these information by manually annotating on a large real world human population is not only a very strenuous task, but also prone to segmentation errors. Thus, we simulated a large number of virtual silhouettes using the graphics engine *Unity3D®*, with the standard avatars viz. Male character pack and female character pack (shown in Fig. 3) from Mixamo 3D character animation service, as the baseline avatars. Then the rest of the avatars were created by imposing variations to the biometric features with respect to these standard models, as explained in (Nambiar et al., 2015).

For the standard avatars models, we assumed a unitary scale factor of each biometric measurement (see Fig. 4(a)). The soft biometric parametrization imposed for simulating the generic avatar population is shown in Table 1, where each value corresponds to the scale applied to the standard model counterpart

Figure 3: Six standard avatars used in the synthetic platform for the generation of large dataset by changing the biometric features. We make use of only the upper-torso region including head, shoulder and chest.

of that anthropometric measurement. These scale parameters were defined by analysing the variability in real world human population. Fig. 4 shows an example of the different virtual avatar samples generated out of a single basic standard avatar, by changing each biometric feature individually. So, altogether 9 variations were generated out of each of the 6 standard avatars. Then, we executed walking animations and captured random 4 frames for each person which resembled the video surveillance image acquisition. Thus we created our *Generic* avatar dataset consisted of 216 images.

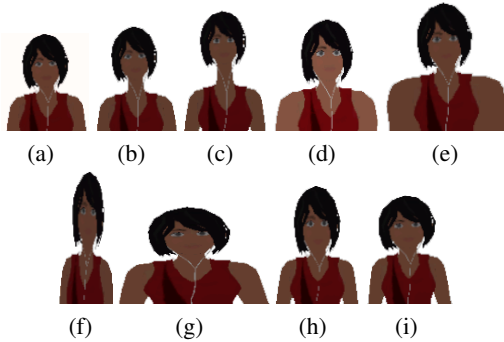| (a) | (b) | (c) | (d) | (e) |

| (f) | (g) | (h) | (i) |

Figure 4: The nine variations of biometrics simulated in the generic avatars. Only the upper torso region is shown since it is the region of our interest. Please refer to Table 1 for measurement details.

Table 1: Chart showing the soft biometric scale factors for the simulated avatar versions in Fig. 4. Values highlighted in **bold** characters in each row represents the modification imposed for that particular avatar.

Avatar Index	Neckness (N)	Chestsize (C)	Bodysize (B)	Head-length (HL)	Head-width (HW)	Human description label
(a)	100%	100%	100%	100%	100%	Standard
(b)	**200%**	100%	100%	100%	100%	Large neck
(c)	**300%**	100%	100%	100%	100%	Very large neck
(d)	100%	**200%**	100%	100%	100%	Large chest
(e)	100%	**300%**	100%	100%	100%	Very large chest
(f)	100%	100%	**50%**	100%	100%	Thin body
(g)	100%	100%	**200%**	100%	100%	Fat body
(h)	100%	100%	100%	**125%**	100%	Long head
(i)	100%	100%	100%	100%	**125%**	Wide head

4.2 Dataset for regression

Let the regression be carried out from an input space of dimension $\mathbb{R}^p$ to an output space of dimension $\mathbb{R}$. Each element in the input space is a feature vector of size $p \times 1$. i.e. $\mathbf{x} = \left[x^1, \cdots, x^p\right]^T$. We collect n such samples and represent them as a matrix $\mathbf{X} \in \mathbb{R}^{n \times p}$:

$$\mathbf{X} = [\mathbf{x}_1 \mid \cdots \mid \mathbf{x}_n]^T \qquad (1)$$

Each row in the $\mathbf{X}$ matrix represents a feature vector corresponding to the n'th sample in the dataset. We collect the response variables y_i corresponding to each input sample $\mathbf{x}_i$ and represent them as a vector $\mathbf{y} \in \mathbb{R}^{n \times 1}$, as follows:

$$\mathbf{y} = \left[y_1, y_2, y_3 \ldots, y_n\right]^T \qquad (2)$$

In our case, $\mathbf{X}$ contains the input *SC* descriptors and $\mathbf{y}$ holds the Biometrics values of the simulated avatars. We have 216 avatar samples corresponding to 4 different views of each of the 54 different avatars. The Shape Descriptors are composed of 40 points across the edge of the upper torso silhouette, each with 60D shape context descriptor and thus producing a 2400 dimensional feature vector corresponding to a person, i.e., input matrix $\mathbf{X}$ is of dimension $\mathbb{R}^{216 \times 2400}$. The output biometric consists of 5 biometrics say, *BF= (N, C, B, HL, HW)*. In our experiment, we conduct regression analysis individually for each of the biometrics in the set *BF*. More specifically, $\mathbf{y}$ in equation (2) will be a vector of dimension 216 containing a given biometric feature for all the avatars. Thus, each regression analysis will be from $\mathbb{R}^{216 \times 2400}$ matrix to $\mathbb{R}^{216}$ vector.

4.3 Support Vector Regression

Support Vector Machines (Cortes and Vapnik, 1995) can be applied not only to classification problems but also to the case of regression (Smola and Schlkopf, 1998), (Chapelle and V., 1999).

Training the original SVR as per (Smola. and Schlkopf., 2004) is mentioned below. Suppose the training data $\{(x_1, y_1), \ldots (x_n, y_n)\} \subset \mathcal{X} \times \mathbb{R}$ where, $\mathcal{X}$ denotes the space of the input patterns. (e.g. $\mathcal{X} = \mathbb{R}^d$) Consider linear functions f, taking the form

$$f(x) = <w, x> + b, \ w \in \mathcal{X}, b \in \mathbb{R} \qquad (3)$$

where $< .,. >$ denotes the dot product in $\mathcal{X}$. Solving this convex optimization problem yields the formulation below. In order to cope with the infeasibile constraints of the optimization problem, slack variables ξ_i, ξ_i^* are introduced to perform the minimization of the following cost function:

$$minimize \frac{1}{2}||w||^2 + C\sum_{i=1}^{n}(\xi_i + \xi_i^*),$$

$$s.t. \begin{cases} y_i - <w,x_i> -b \leq \varepsilon + \xi_i \\ <w,x_i> +b - y_i \leq \varepsilon + \xi_i^* \\ \xi_i, \xi_i^* \geq 0 \end{cases} \quad (4)$$

The constant $C > 0$ determines the trade-off between the flatness of such a function f and the amount up to which deviations larger than ε are tolerated. To extend this towards nonlinear functions, the main strategy is dual formulation. Hence, the optimization problem could be transformed into a dual problem and its solution is given by:

$$f(x) = \sum_{i=1}^{n}(\alpha_i - \alpha_i^*)K(x_i,x_j) + b, \quad s.t., \begin{cases} 0 \leq \alpha_i^* \leq C, \\ 0 \leq \alpha_i \leq C \end{cases} \quad (5)$$

where, α_i, α_i^* are the dual variables and $K(x_i,x_j)$ is the Kernel function.

4.4 Meta parameters

The performance of Support Vector Regression (SVR) depends on a good setting of meta parameters. We tested two kinds of regression kernels: *(i)* Linear Kernels

$$K(x_i,x_j) \equiv <x_i,x_j> \quad (6)$$

which implies that the regressor is linear with respect to the input vector ; *(ii)* Radial basis kernel, where

$$K(x_i,x_j) \equiv exp(-\gamma||x_i - x_j||^2), \gamma = \frac{1}{2\sigma^2} \quad (7)$$

To determine which values of C and γ are best for our problem we use grid search with cross-validation. We used logarithmic grids both for C ($C = 2^{-15}, 2^{-13}....., 2^{15}$) and γ ($\gamma = 2^{-15}, 2^{-13}....., 2^{15}$). For each pair, we measure the prediction error (Mean Square Error- *MSE*) and the lowest *MSE* corresponds to the best parameters. We conducted two different cross validation techniques:

(a) K-fold cross validation: We first divide the training set into k subsets of equal size. Sequentially, one subset is tested using the regressor trained on the remaining k-1 subsets. This rotation estimation will go on k times, and finally, the prediction errors over k folds will be averaged to produce a single estimation.

(b) Stratified K-fold cross validation: In stratified k-fold cross validation, the folds are selected such that each set contains approximately the same percentage of samples of each target class as the complete set. "Stratified" cross-validation is a simple variant of classical k fold cross-validation. It basically makes sure that we choose a division that has approximately the right representation of class values in each

of the folds. It helps reduce the variance in the estimate a little bit more.

After the cross validation is done, we will get a single estimation of the measure of fit viz., the average *MSE_Train* and the corresponding meta parameters. Based on this model, we train the whole system so that whenever the test data enters, it will estimate the output variables.

5 EXPERIMENTAL RESULTS

We conducted experiments using the database of 54 avatars, with 4 samples each. The regression analysis is conducted from the input space of $\mathbb{R}^{2400}$ to output space of $\mathbb{R}$. Among the output biometrics to be estimated say, *BF= (N, C, B, HL, HW)*, we perform regression analysis individually for each of them i.e., we regress the scalar estimate of each biometric from a 2400-D shape context vector. In our experiments, we selected 2 random avatars, each with 4 samples (total 8 samples), as the test set and the remaining 52 people, each with 4 samples as the training set (total 208 samples).

5.1 Regressor performance

We conducted 6 different experiments on our data, over different kernels as well as different cross validation schemes. Out of these experiments, we report the Mean Squared error viz., *MSE_Train* and *MSE_Test* in both the training and test sets, as well as the best meta parameters (the ones leading to the least *MSE_Train*).

Table 2 summarizes the test and train set performances of the various regression methods studied on a single biometric feature (Neckness). Linear and kernelized basis versions were tested with different cross validation schemes, at manual and optimal regularizer settings. *MSE_Train* corresponds to the Mean Square Error obtained for the training set obtained via Cross validation, and the *MSE_Test* is the the Mean Square Error obtained for the test set. In the default parameter setting, the default meta parameters are activated (C=1, γ=1/num_features, ε=0.1), whereas in exhaustive grid search, the optimal values of meta parameters are selected as the pair of (C,γ) producing the least *MSE_Train* in the training set. A sample grid search selection of optimal meta parameters for *Exp.5* (in Table 2) is depicted in Fig. 5(a).

In order to verify the repeatability/consistency of the measure of fit, we executed 10 runs of random trials (with Cross validation of 2 fold) for the same biometric. The boxplot representation of the variability of regression performance in terms of Mean Squared

Table 2: Performance of Linear and Nonlinear regression models studied in this work on biometric1 (Neckness), for different parameter settings as well as cross validation schemes. The experimental results over 2-fold as well as 4-fold cross validation settings are shown below. Least values of *MSE_Train* and *MSE_Test* are shown in **bold** characters and the second least in *italics*.

Exp	Kernel	Parameter Setting	Cross validation (CV)	No. of CV fold	MSE_Train	MSE_Test	Meta parameter
(1)	Linear	Default	-	-	*0.0100*	1207.5	default
(2)	Linear	Gridsearch	Stratified	2	17.2178	*991.1524*	*C= 0.5; γ= 9.5367e-07*
				4	94.1696	1319.5	
(3)	Linear	Gridsearch	K-fold	2	95.24996	1347.6	*C= 0.25; γ=3.0518e-05*
				4	468.1726	2986.8	
(4)	RBF	Default	-	-	4726.4	19211	*default*
(5)	RBF	Gridsearch	Stratified	2	0.3974	**985.2449**	*C=1024; γ=0.00024414*
				4	**0.00010061**	1240.0	
(6)	RBF	Gridsearch	K-fold	2	41.5721	1033.1433	*C=1024; γ= 4.8828e-4*
				4	0.5671	1924.0950	

Error for both train and test sets are shown in Fig. 5(b) and Fig. 5(c) respectively.

Next, we try to extend the case studies conducted on a single biometric feature (Neckness), over all the 5 biometrics say (Neckness, Chest width, Body size, Head length and Head width). Since the ranges of the various biometrics features are different, we use the normalized root mean square error *NRMSE* for the evaluation of our regressor.

$$NRMSE = \sqrt{\frac{1}{n}\sum_{i=1}^{n}(\hat{y}_i - y_i)^2} / (y_{\max} - y_{\min}) \qquad (8)$$

The visualization of the *NRMSE* values for all the regression methods over all biometrics under consideration, is given in Fig. 6. Following are the main findings from our experiments conducted above:

1) *Grid-search on meta parameters can fine tune the measure of fit, and thus the optimal nonlinear experiments outperforms the others in all the cases:* Our experiments with linear function and RBF kernel show that kernelization gives a slight improvement in performance. For e.g., referring to Table 2 as well as Fig. 6 we can observe that the default values of parameters produce very bad results for RBF kernel (worst results among all) whereas the grid search of the meta parameters could fine tune the performance. Similarly, applying grid search in linear regression also can reduce the estimation error to some extent.

2) *We observed a nearly linear relationship between SC descriptors and the corresponding Biometrics; In other words, Linear Regression lies very close to cross validated nonlinear regression modalities:* In the boxplots of Fig. 5 as well as the barplot in Fig. 6, we could observe that linear kernels as well as the cross-validated RBF kernel produced more or less the same range of estimation errors. Also in terms of consistency of estimation errors also similar results are observed. So we conclude that, the nonlinear kernelization could bring only a small advantage over purely linear regression against our descriptor set. This intuitively indicates that there exists a nearly linear relationship between the Shape Context descriptor and the corresponding Biometrics.

3) *Cross validation influences in the system performance:* Among two types of cross validation schemes we applied on our data, we could observe that Stratified k-fold CV outperforms the k-fold CV, in terms of accuracy and consistency. After learning the relationship among the Shape Context descriptors and the Soft Biometrics, we built the best regression model for our Re-ID system using *Nonlinear regression with RBF stratified CV*.

Table 3: Chart showing the meta parameters settings of RBF for the best regression performance.

Index	Biometric	Kernel type(t)	Cost (C)	Gamma (γ)	Epsilon (ε)
1	Neckness(N)	RBF	1024	0.00024414	0.01
2	Chestsize(C)	RBF	1024	0.00048828	0.01
3	Bodysize(B)	RBF	128	0.00024414	0.01
4	Headlength(HL)	RBF	64	0.00048828	0.01
5	Headwidth(HW)	RBF	64	0.00048828	0.01

5.2 Person Re-ID in real world

After pondering various regressor models on our Virtual Generic avatar dataset, we employ it in a real world dataset for person re-identification. In this work we conducted a pilot study using 20 people from RGB-D Person re-identification Dataset[1]. A subset of our real world dataset is given in Fig. 7.

Characterising the Gallery Soft-Biometrics: Referring to our proposed system in Fig. 1, the image descriptors for each person in the dataset are used in the training phase of Re-ID system in terms of *SC* descriptors of upper torso, and stored in the system
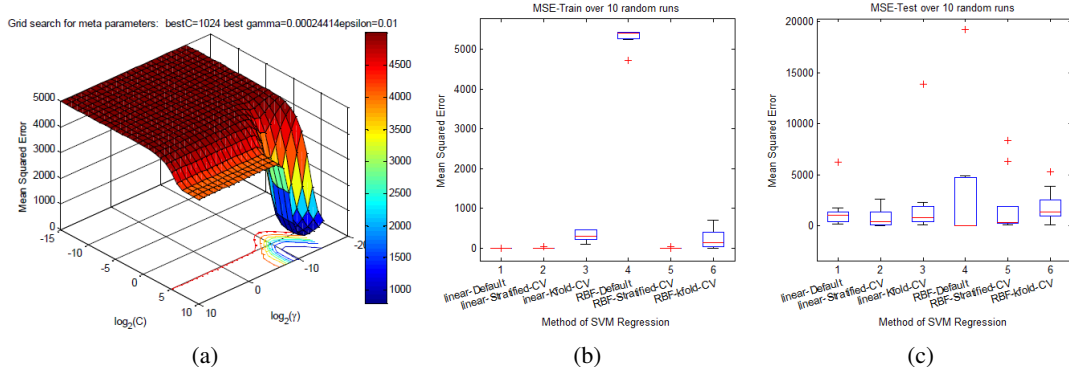
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[1] http://www.iit.it/en/datasets-and-code/datasets/rgbdid.html

Figure 5: (a) Contour and Surface plots of the *MSE_Train* distribution for various *C* and γ meta parameters. Blue corresponds to lowest *MSE_Train*. $log_2(C)$= 10 and $log_2(γ)$= -12 produces the least prediction error (lowest *MSE_Train*) (b) MSE for the trainset (*MSE_Train*) over 10 random runs (c) MSE for the testset (*MSE_Test*) over 10 random runs.
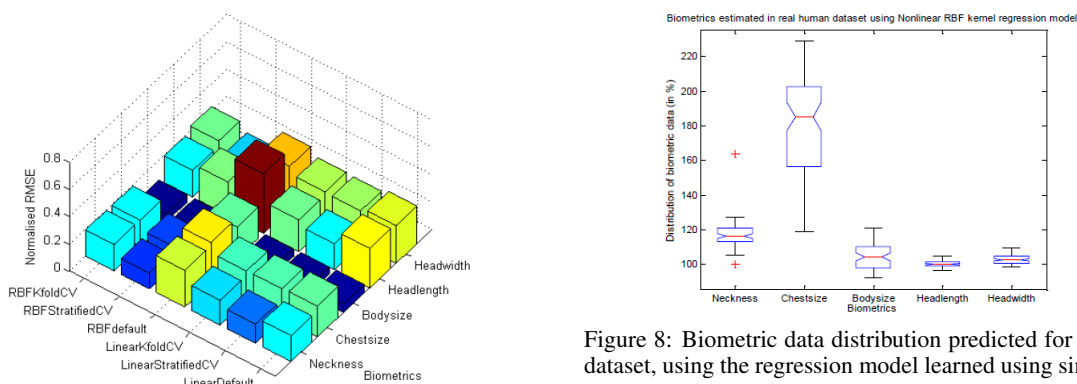

Figure 6: A summary of our various regressors' performance on different biometrics estimation.

Figure 8: Biometric data distribution predicted for the real dataset, using the regression model learned using simulated avatars.

(a) (b) (c) (d) (e) (f) (g) (h)
#P1 #P2 #P3 #P4 #P5 #P6 #P7 #P8

Figure 7: A sample real world dataset for the retrieval test based on human queries on biometric info.

gallery. Afterwards, these *SC* descriptors are processed using the Regression block designed as per Table 3, and the corresponding biometric estimation for each individual is made. Finally, a statistical distribution analysis of the stored biometrics is carried out in the same module and stored along with the biometric values, for later use. This statistical profile is the distribution chart of each biometric values observed among the whole population. The statistical analysis of estimated biometric values among our real human dataset is presented in Fig. 8.

We can observe a range of variances along the

biometrics estimated among the dataset. The distribution of Neckness ranges between 100% to 130% of the trained simulator models. The parameter distribution of chestsize ranges between 120% and 230%, with median close to 190%. Bodysize, Headwidth and Headlength are centered near the 100%, and have lower variances. Largest variance is observed for Chest size and least variances are observed for head length and head width. It is important to have certain biometrics with large variance in the population in order to avoid the problem of subject interference and to improve the distinctiveness among people. They act as the most discriminative features. In our case, Chest size is the most discriminative biometric feature.

Re-identification from verbal queries: When the query probe in terms of description of the human biometric is entered into the system (for instance, person with large chest and short neck), our system will analyse the biometric distribution of the training samples as in Fig. 8. The most acclaimed semantic categories are interpreted in terms of data ranges in this distribu-

tion profile as follows: Short (S-less than lower quartile), Medium (M-lower quartile to upper quartile) and Large (L-above upper quartile). Then, the biometric description in the query is compared against the aforementioned semantic categories, and the valid category of interest is retrieved. As an example, we will select the list of people with the biometric traits of chestsize$\geq$200% (more than the upper quartile of biometric *C*) and neckness$\leq$110% (less than the lower quartile of biometric *N*). In our case study of real dataset in Fig.7, person *ID*'s (f) **#P6** and (h) **#P8** were correctly re-identified under the query made, and their corresponding frames in the camera network were retrieved.

6 CONCLUSIONS

In this work, we presented a novel method for re-identifying people in a video surveillance system by means of verbal queries describing human compliant soft biometric labels. This was done by exploiting regression techniques associating Shape context features to Soft biometric values. In order to provide the best model for the Regression analysis, we conducted an extensive study on the impact of various regression schemes as well as cross validation schemes on Shape Context- biometrics pairs of our simulated dataset of Virtual reality avatars. We observed that the grid search for the best meta parameterized model can fine tune the system for the best performance. In our experiments nonlinear kernel (RBF) basis with stratified Cross validation excels in performance compared to all the other schemes. Interestingly, linear regression models are also found to provide good and fast results. This gives us the intuition that the correlation between the SC and biometrics are nearly linear. We trained our system with the best regression model *RBF kernel with Stratified cross validation*. Using the meta parameters obtained, we experimented for the biometric estimation not only in the simulated platform, but also in real imagery. We showed that, based on the statistical distribution of these biometrics, our system could retrieve promising results for person re-identification based on human query. In the future work, we plan to extrapolate our proposed methodology from upper torso towards full human body i.e. to extract the features over full body and to exploit a large set of soft biometrics defining the full body specifications such as height, weight, lengths of hands and legs, waist width etc. In addition to that, we also intend to combine other biometric cues such as gait, face etc. along with the current shape features using multi-modal fusion techniques.

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