

# A frequentist estimation of duplicate probability as a baseline for person identification from image and video material using anthropometric measurements

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**Abstract:** Video and image material is becoming increasingly ubiquitous thus its potential as evidence in forensic investigations is growing. Once faces are hidden however, the value of surveillance footage is restricted unless there is another biometric trait that can be observed by camera such as linear body measurements. There is much biological evidence for human body proportions exhibiting much individual variation. Nevertheless, the probability of there being two individuals that match in their respective proportions ultimately determines its usability for the assignment, exclusion and even identification of persons in the forensic domain. This work is concerned with approaches for duplicate probability estimations derived from anthropometric measures.

Here, we present a novel frequentist estimation using a dataset of 340 individuals and their respective anthropometric measurements. Drawing on density kernel estimations of measurement dissimilarity, we propose the duplicate probability to be in the order of  $10^{-15}$  to  $10^{-8}$ .

**Keywords:** Biometric features; anthropometric measurements; duplicate probability

## 1 Introduction and Motivation

Biometric research increasingly goes beyond established biometric traits such as fingerprints, DNA, iris, and facial characteristics [RSV19] investigating the body for other traits such as linear body measurements i.e. heights, lengths and widths [ONS10] that could be used for matching and identification in order to increase and diversify possible use cases [Da11]. The idea is not new as anthropometric measurements had been part of Bertillonage, a pioneer biometric system developed at the end of the 19th century [AI18]. A reason why this system did not last and was surpassed by fingerprinting some 30 years later, was that such measurements - in contrast to fingerprints - were not left as traces at a crime scene [Co07, DC08, Ka17]. With the ever-increasing amount of image and video material available that is no longer true since a person's body shape including their dimensions and proportions can now be caught on camera. Indeed, when the face is concealed as it often happens during a crime, they might be the only hint at a person's identity [AA14]. Body dimensions and proportions are universal with the only limitation being the number of features, for instance brought about by the loss of a limb. Even though temporary and long-term fluctuation, e.g. resulting in a slight decrease in body height over the course of the

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day and in old age respectively [LTZ87], must be accounted for, linear body dimensions that equal bone lengths can be considered quite permanent [SS13] as soon as an individual is fully grown between 18 and 21 years of age [SSS14, LTZ87]. The literature provides ample evidence that body measurements and their respective proportions show much individual variation [He60, JMW98, Gr12, SS13] ensuing in people of the same height having different proportions [Lu98, BHM16] or all kinds of proportions occurring across all heights [Ka69]. These differences become apparent even within a homogenous population [Bu15]. However, as this kind of evidence remains exemplary in nature, eventually it is up to the probability of there being two individuals that match in their respective proportions that determines whether linear body measurements may qualify as a biometric identifier. With only limited information insufficient for statistic model building available the challenge is to ensure a correct probability estimation which will be the focus of this paper.

## 2 Datasets and Methods

### 2.1 Considered Data

The data is a subset of the SizeGermany, a nationwide survey that was conducted between 2007 and 2009 and includes more than 13,000 3D bodyscans (average error less than 1 mm [circumference]) as well as anthropometric measurements that were derived from these scans [RT10, STW09]. Provided by Avalution GmbH, the subset consists of eleven height, length and width measurements compliant with the ISO 8559, ISO 7250 and RAMSIS (associated with the RAMSIS digital human model) standards [RT10] and of high-resolution 3D bodyscans taken from 170 female and 170 male individuals. The data was further selected with regard to age (18-55 years) and two body height classes for each of the sexes. Thus, it is comprised of four groups (labelled F1, F2, M1 and M2 in the following sections) here group F1 corresponds to 85 females with a measured body height of approx. 163 cm (sd = 0.13 cm, max. deviation: 0.2 cm). F2 consists of 85 females at body height 173 cm (sd = 0.14 cm, max. dev.: 0.2 cm). For male individuals, measurements of 85 men with an approx. body height of 175 cm (group M1, sd = 0.17 cm, max. dev.: 0.3 cm) respectively 185 cm (group M2, sd = 0.22 cm, max. dev.: 0.4 cm) were acquired. The grouping of four subsets was intended for exploratory analysis of intra- and inter-group correlations with respect to the eleven measurement features.

Table 1 gives an overview of the features considered in this study as well as the minimum measurement resolutions.

### 2.2 Probability estimations

One aim of this study is to give an estimate on the probability for obtaining *matching* measurement values for two unrelated individuals with respect to all considered features,

Tab. 1: Anthropometric measurement features, applied measurement standards and minimum resolution per feature.

Feature description	Measurement std.	Resolution (cm)
Stature (body height)	ISO 7250 Nr. 4.1.02	0.1000
Shoulder height (standing)	ISO 7250 Nr. 4.1.04	0.0500
Tibial height	ISO 7250 Nr. 4.1.08	0.1000
Shoulder-elbow length	ISO 7250 Nr. 4.2.06	0.0125
Elbow-wrist length	ISO 7250 Nr. 4.2.07	0.0500
Shoulder (biacromial) breadth	ISO 7250 Nr. 4.2.08	0.1000
Forearm-fingertip length	ISO 7250 Nr. 4.4.05	0.1000
Buttock-knee length	ISO 7250 Nr. 4.4.07	0.0500
Pelvis breadth	RAMSIS 1.1	0.1000
Waist Height	ISO 8559 Nr. 2.2.3	0.1000
Outside Leg Length	ISO 8559 Nr. 2.2.25	0.0500
Inside Leg Length	ISO 8559 Nr. 2.2.27	0.1000

based on the data at hand. First, one has to note the notion of what is actually meant by stating that two *exactly identical* measurements are obtained: Regarding to experimental data acquisition one has to account experimental errors and deviations as well as the measurement method's specific resolution itself, which leaves one with feature scale intervals and length thresholds within respectively below no meaningful statements about measurement deviations can be made. Secondly, deriving (and experimentally confirming) such a probability estimation based on first principles requires to understand all underlying stochastic and correlated processes, and to enclose that knowledge in a self-consistent statistical model, which in turn provides the means for making such estimations. These two aspects result to the basis at which the match estimations are made in this study: First, identity ought to be assumed if absolute measurement differences between two individuals are below the respective feature resolutions (and experimental measurements would trivially read the same values). On a more formal note, we here propose the euclidean distance  $d(\mathbf{x}_i, \mathbf{x}_j)$ , defined as

$$d(\mathbf{x}_i, \mathbf{x}_j) = \sqrt{\sum_{l=1}^{11} (x_{i,l} - x_{j,l})^2} \quad (1)$$

as a function for measurement dissimilarity, where  $\mathbf{x}_i$  and  $\mathbf{x}_j$  are the eleven measurements of two individuals. With this definition we can reflect the first notion in a more formal manner: With respect to the feature resolutions given in Table 1, there is a minimum, non-zero distance  $d_{min}$  which can be experimentally measured and below which identity for two given  $\mathbf{x}_i$  and  $\mathbf{x}_j$  can be assumed. Regarding the second notion, this study focusses on providing match probability estimations straightforwardly from distance distributions, thus without to

consider underlying feature correlations or to state any statistical model.

Exploratory data analysis indicated that the distributions of intra-group measurement distances, as defined in Equation 1, can be described by means of the gamma distribution. Subfigure 1a shows the four distributions of the  $N(N-1)/2$  pairwise measurement distances for each group F1, F2, M1 and M2, where  $N = 85$  in each group. A straightforward approach to give an estimate on the probability for obtaining two identical measurements (in the sense as noted above) at random—denoted as  $p_{\text{match}}$  in the following text—is to first obtain the cumulative gamma density function parameters  $\alpha$  and  $\beta$  which fit a given set of pairwise distances  $D$  best, and second to retrieve  $p_{\text{match}}$  from the fitted distribution by numerical integration. Thus,  $p_{\text{match}} = F(d < d_{\text{min}} | \alpha, \beta)$ , where  $F$  is the cumulative density function of the gamma distribution. However, the four initial distance distributions are noisy to some extent, as seen in Figure 1a. Hence following steps 1 and 2 on these four distributions would give four point estimates prone to error. A further source for error is that each of the four sets of pairwise distances  $D$  holds  $d_{\text{min}} \ll D$ , whereas the computed density estimation  $F(d < d_{\text{min}} | \alpha, \beta)$  is many orders smaller than  $2/N(N-1)$  and thus highly sensitive to the fitted distribution parameters. To cope with these problems, we conducted bootstrapping with  $n = 250$  runs on each distance set  $D$ . In each run, half of the pairwise distances were sampled randomly and steps 1 and 2 were conducted on this subset. This strategy resulted in 250 bootstrap distribution fits for each sampled pairwise distance set. The fitted distributions were used in turn for computing 250  $p_{\text{match}}$  estimations. Furthermore, note that neither in nor between all four groups a match of two individuals was observed. In Figure 1b and c, 250 goodness-of-fit statistics (expressed by harmonic relative mean errors) and the resulting distributions of  $p_{\text{match}}$  estimations are shown.

### 3 Results and Discussion

Based on bootstrapping approximation,  $p_{\text{match}}$  estimates range from the order of  $10^{-15}$  to  $10^{-8}$  over all four investigated intra-group distances (1st quartile:  $2.2 \times 10^{-12}$ , median:  $1.2 \times 10^{-11}$ , 3rd quartile:  $9.4 \times 10^{-11}$ ). The harmonic relative mean errors indicate that observed distribution frequencies are approximated well by all fitted density functions. In fact, all fitted functions give estimates deviating by less than 1% wrt to the harmonic relative mean error (see Figure 1b). As no matching pair of individuals within nor between the four groups was observed with respect to all eleven features, there are only limited ways to further test obtained probability estimations. A simple testing approach is to interpret the observation of obtaining  $k = 0$  matches over the total number of pairwise comparisons  $N_{\text{total}}$  as the result of some binomial process. Following this assumption one can estimate the probability of obtaining at least one match by chance using a binomial distribution  $P_{k \geq 1} \approx 1 - B(N_{\text{total}}, k = 0, p = p_{\text{match}})$ , where  $N_{\text{total}} = 340 \cdot (340 - 1)/2$ . Plugging in above estimates into the binomial gives approximate probabilities in the order of  $P_{k \geq 1} \approx 10^{-7}$  to  $10^{-6}$ . Conversely, a conservative assumption that  $P_{k \geq 1} = 0.5$  or  $0.05$  would correspond to baseline approximations of  $\tilde{p}_{\text{match}} \approx 1.2 \times 10^{-5}$  and  $5.2 \times 10^{-5}$ , respectively. As the  $P_{k \geq 1}$  estimations is consistent with observing  $k = 0$  on the one hand, and the conservative

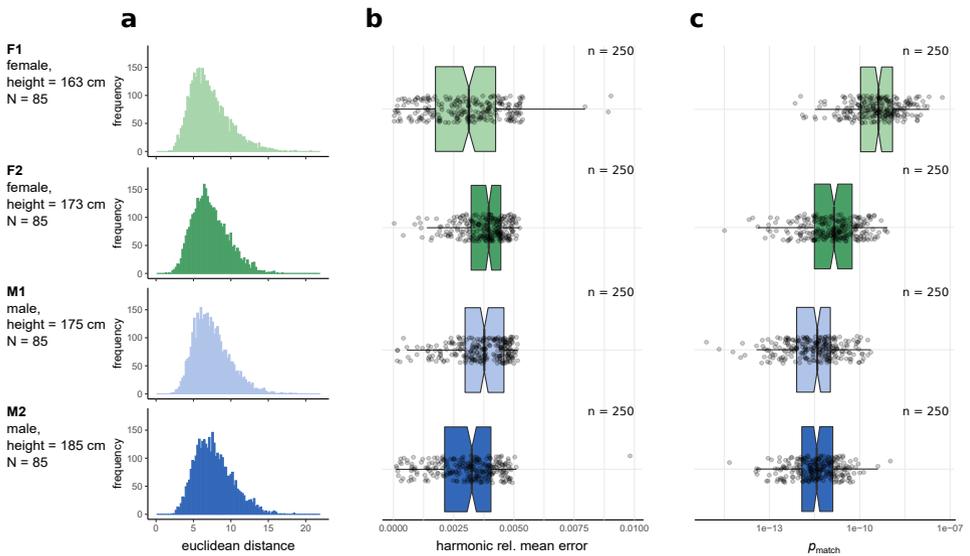


Fig. 1: Frequency distributions of intra-group feature dissimilarities (a), expressed by the euclidean distance, provide the basis for model-free duplicate probability estimation. b: Goodness-of-fit statistics (as harmonic relative mean error) of Gamma distributions fitted to 250 dissimilarity frequency distributions obtained from each group by bootstrapping. c: Duplicate probability estimations obtained from bootstrapping. Estimations range in the order of  $10^{-15}$  to  $10^{-8}$  over all four groups.

$\tilde{p}_{\text{match}}$  approximations being too large to be compatible with density estimations, one can cautiously regard the  $p_{\text{match}}$  estimate range as reasonable. Next, this consistency check was further applied to subsets of features for which identities can be observed, in order to verify if the proposed  $p_{\text{match}}$  estimation approach holds when  $k > 0$ . For example, such a set of features is {Tibial height, Elbow wrist length, Buttock knee length}. Considering only these three features, a single match can be observed between groups F2 and M1. Estimating  $p_{\text{match}}$  based on the inter-group distance distribution, one obtains  $P_{k \geq 1} \approx 0.32$  (std. dev: 0.04) under the binomial model, which in turn is compatible with the observation. This gives an indication not just that match probability estimations might be reasonable, but also that the model-free estimation strategy presented here is compatible with the goal of making estimations in the first place. Further research will involve investigating the reasoning behind dissimilarities following the gamma distribution—which is some aspect the general notion of the gamma distribution is hardly conform with.

Putting the presented results into perspective, one first has to reflect that the proposed estimation strategy is tied to the empirically determined measurement distance distribution and the underlying measurement features inspected. However, there is indication that, given the data and features investigated, match probabilities might be in the order of magnitude where forensic applicability can be reasonable.

## 4 Conclusion and Outlook

In this work, an estimation for feature match probabilities is given based on experimental anthropometric measurement features and intra-group measurement dissimilarity distributions. These probability estimates give some insights into whether anthropometric measurements can be valuable in forensic applications, e.g. person identification. The results presented in this study are an indication of that.

Going hand in hand with the advances in the field of 3D digitalisation and modelling that allows for these proportions to be extracted from digital material, this estimation may serve as a foundation for further application of anthropometric measurements in the forensic domain, especially when it comes to the detection and measurement of individuals depicted in images and videos for the purpose of some level of identification thus rendering novel biometric methodologies feasible.

A critical aspect to consider is that, the here presented estimations are 'statements on the statistical mean' and that proper systematic estimations would require knowledge about the fundamental correlations and dynamics that drive anthropometric measure variations in individuals and, most importantly, determine a person's specific measurements. Such first principle model-based estimations are of most value in the forensic context, since statistical statements are not just made upon mean estimates deduced from empirical data, but are rather embedded in a theoretical statistical framework capable to include other forensic evidence as well.

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