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AGE, SEX AND POSITIONAL VARIATIONS IN THE HUMAN EPIDERMAL RIDGE BREADTH BY MULTIPLE MEASUREMENTS ON A CROSS-SECTIONAL SAMPLE OF SCHOOL-AGE CHILDREN

ABSTRACT: A number of studies have used the measurement of density of epidermal ridges on human fingerprints (or average epidermal ridge breadth if the value is expressed in reverse) as a metric to estimate the age of the originator of the imprint at the time of growth and sex at maturity. A methodologically unsolved question is how the number of ridges measured together within one segment (or the length of the line segment across which the ridges are counted) affects the results. In this study, we therefore investigated how the count of ridges measured together within one segment, as well as the count of averaged segments per subject, when averaged, affect the resulting values of mean epidermal ridge breadth. Moreover, we investigated how different regions on the human fingers and palms differ in this respect. Using a cross-sectional sample of 90 school children (45 girls and 45 boys, age range from 6 to 16 years) from South Moravia, we compared the differences in epidermal ridge breadth in 29 different hand regions, particularly in terms of the degree of age differences. The results show that different regions on the hand vary significantly in the effect of age which might have consequences for estimating age and sex based on these epidermal ridge breadth measurements. However, the ability to statistically distinguish age or sex groups is affected by the number of measurement units (ridges, fingerprints) used to calculate mean epidermal ridge breadth (MRB). Therefore, in future research, it would be advisable to introduce computation with interval estimates of MRB or a hierarchical approach directly accounting for individual epidermal ridges.

KEY WORDS: Epidermal ridge breadth – Age estimation – Sex estimation – Dermatoglyphics

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1 INTRODUCTION

Epidermal ridge breadth (RB) is defined (Cummins, Midlo 1961, Penrose 1968) as a distance between the bottom of one epidermal furrow to the same point of an immediately neighbor furrow (*Figure 1*), measured across the given epidermal ridge in a direction perpendicular to its longitudinal axis. The variable is usually measured by dividing the length of segments (e.g., 1 cm) by the number of ridges it crossed and expressed as mean ridge breadth *or* frequency per a length unit.

Average values of RB differ significantly within the volar surface (Cummins *et al.* 1941, Ohler, Cummins 1942, Schlaginhaufen 1905a). Apart from the intra-individual regional differences on the volar surface, ridge breadth varies between individuals, sexes, and populations. However, for most of the 20th century, the scale of human populations measured for epidermal ridges (ER) was narrow, limited almost exclusively to people of European origins, with the exception of the *Yoruba* people (Jantz, Parham 1978) and the *Iranian* population in *a-b* ridge breadth (Kamali *et al.* 1994). Other exceptions include measurements taken from archaeologically excavated ceramics (Cseplák 1982, Kamp *et al.* 1999, Králík, Novotný, 2003, 2005, Primas 1975), but these cannot be regarded as standardized population samples.

In recent years the knowledge on the population diversity increased substantially thanks to the adoption of standardized methodology of three measuring squares by many researchers (Adamu *et al.* 2018, Ahmed, Osman 2016, Gutiérrez-Redomero *et al.* 2008, 2011, 2013, Mundorff *et al.* 2014, Oktem *et al.* 2015, Rivaldería *et al.* 2016, Soanboon *et al.* 2016). These researchers made great contributions to the topic both from the viewpoint of biological relationships on epidermal ridges as a basic structure of the friction skin, and in the field of population diversity. This methodology represents simple and unified tools to standardized measurements on complete and high-quality fingerprints which are necessary for a wide comparison between populations and different authors.

Despite all the advantages and advances, the standardized methods of RB measurement mentioned above, regardless of the expression of the results (mean ridge breadth or density), suffer from more or less evident technical shortcomings.

First, the perpendicular direction of the measurement line relative to the course of epidermal ridges cannot be granted since the position of the crossing segment is defined by criteria other than the course of the ridges itself. Despite Schlaginhaufen's method's seeming advantages in this respect (manual positioning of the measuring segment and its direction), the extensive length (1 cm) of the measuring segment and the heterogeneously curving and diverging stream of ridges often do not allow the measuring segment to be perpendicular to all of the ridges it crossed (cf. *Figure 1 D-G*). Therefore, the density might not (and frequently does not) precisely reflect the sum of breadths of the ridges included in the measured area. If populations and people within a population differ in, e.g., the shape of a patterns (e.g., high vs. wide loops), the changes in ridge densities might partially express differences in the pattern shape as it can change orientation/course of the ridges towards the course of the measuring segment (see also Appendix A1 for another technical issue).

Second, the above-mentioned approaches considered the measuring area (line segment, square) as a *statistical unit*. This has three not yet studied consequences: (A) It completely omits the internal variation of ridges *within* the studied area of the papillary terrain that might otherwise be of some analytical use. (B) This almost certainly *decreases variance* in the data as all kinds of raw data averaging do (standard error of mean is necessarily lower than standard deviation of the original raw measurements, i.e., individual ridges) which corresponds to the so-called Central Limit Theorem. Finally, (C) most of the mentioned kinds of measurement standardizations defined a measurement unit (segment or square) in a unified absolute size (1 cm or square root of 50 mm), which means that if subjects differ in size of ridges – which is the purpose of the study itself (!), each subject is represented by different numbers of recorded epidermal ridges. As a consequence of the objection (C), measurements in subjects with extremely fine ridges are more representative (e.g., measurement of 25 ridges) than in subjects with coarse ridges (e.g., 15 ridges). Therefore, measurements are not standardized when it comes to their representativeness between subjects. This situation also influences the objection (B) mentioned above: if each unit (segment or square) covers a different number of ridges, the averages are computed from different numbers of ridges (different sample size of ridges). Hence, the resulting averages correspond to different reduction in variance compared to the variance of the underlying units, the epidermal ridges. As a consequence, measurements of different subjects (including different fingers of one subject or different regions of one finger) may not be easily

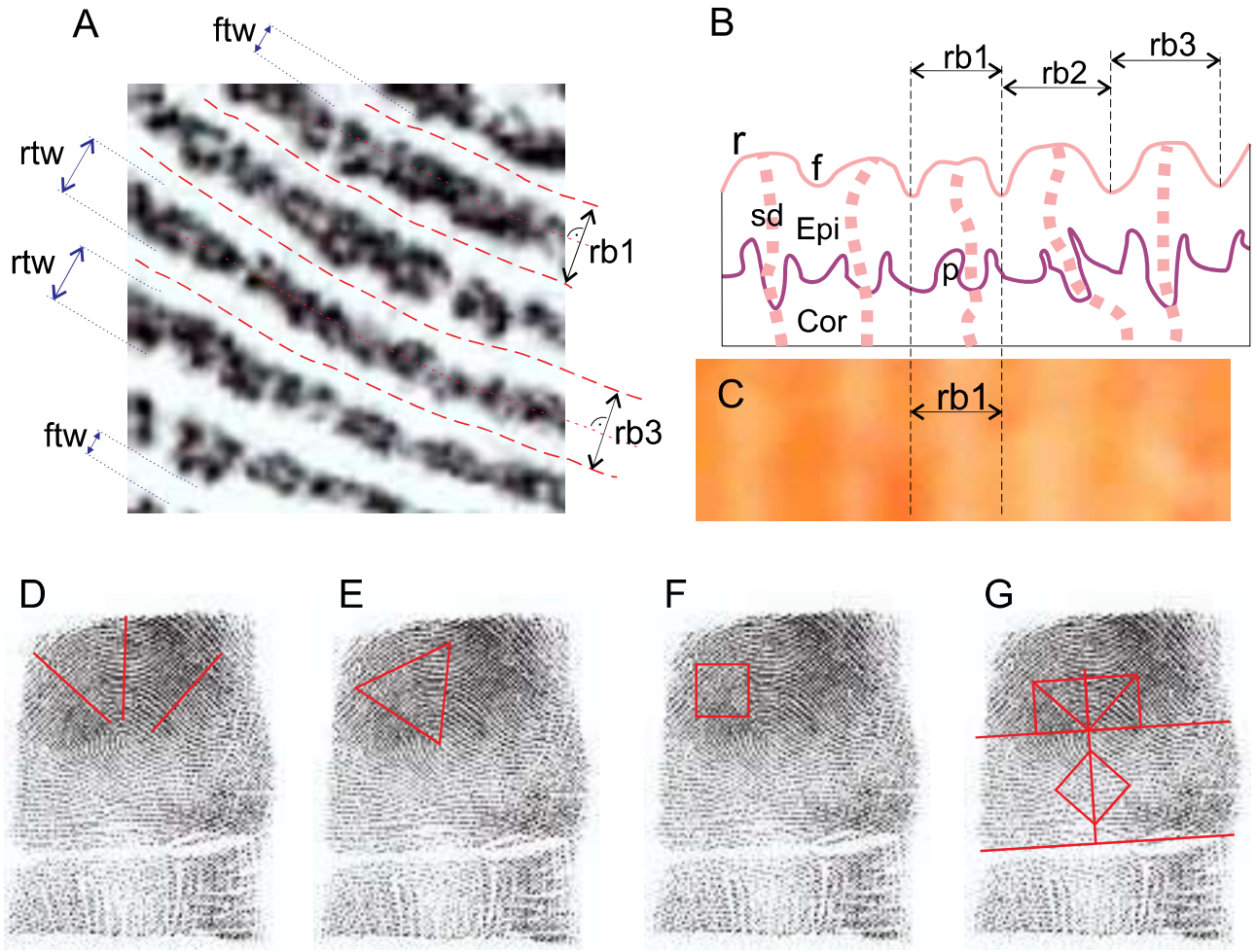

FIGURE 1: A – Scheme of distances defined on traditional black and white imprint of epidermal ridges on paper: rb1 – ridge breadth of the first ridge, rb3 – ridge breadth of the third ridge (as counted from the first one), rtw – width of the black ridge trace, ftw – width of the white (non-imprinted space) trace of epidermal furrow; B – Schematic histological cross-section through the friction (thick) skin with epidermal ridges in direction upright to the surface and course of epidermal ridges: r – epidermal ridge (*crista superficialis cutis*), f – epidermal furrow (*sulcus cutis*), Epi – *epidermis*, Cor – *corium*, sd – sweat duct (*ductus sudorifer*), p – *papilla corii*, rb1 – distance representing breadth of the first measured ridge, analogically rb2 and rb3; C – surface view on corresponding image of epidermal ridges from scanner with annotated width of the rb1, dark places – furrows, light places – tops of epidermal ridges; D–G – schemes of ridge breadth measurements methods by different authors: D – using 1 cm segments by (Schlaginhaufen 1905b) and Cummins *et al.* (Cummins *et al.* 1941, Ohler, Cummins 1942), using equilateral triangle by Loesch and Martin (Loesch, Martin 1984), using square of 5×5 mm side length (measurement on a diagonal) by Acree (Acree 1999) and Nayak (Nayak *et al.* 2010), and using system of three squares of the side length of 5 mm by Gutiérrez-Redomero *et al.* (Gutiérrez-Redomero *et al.* 2008).

comparable at a population level or the interpretation of the results might not be straightforward.

Perhaps an even more significant problem hindering the full use of epidermal ridges for practical estimations is the extent of our knowledge of their variability across the hand. Most recent studies of the density of the ridges have focused only on the dermatoglyphic patterns of the distal phalanges, while other regions remain unstudied, although they are also captured to varying degrees in the prints. Yet, based on the now classic studies by Cummins and colleagues (Cummins *et al.* 1941, Ohler, Cummins 1942), we

know that the density of the epidermal ridges at different regions of the adult hand varies considerably. Congruent results are also provided by one new study (Gutiérrez-Redomero, Alonso-Rodríguez 2013).

It is difficult to specify/foresee how significant of an impact could these controversial points have in forensic and archeological estimations of age (in growth) and sex estimation or comparisons between human populations. In any case, however, the above-mentioned shortcomings might limit the power of the methods in the sense of finding a difference.

2 GOALS OF THE STUDY

In this study, one aim of the study was to propose and test a new method for measuring of epidermal ridge breadth with one epidermal ridge as a statistical unit and to use it to study a cross-sectional sample of school-age children and describe their sex and age differences in epidermal ridge breadth. The second aim of the study was to test an effect of artificial manipulation with number of measured units (ridges and segments) on statistical differences between age and sex groups.

3 MATERIALS AND METHODS

3.1 Sample of fingerprints

The source sample represents archived 2D hand images in TIFF format collected during an anthropometric study conducted between 2005 and 2007. The sample was previously published in a study dealing with the effects of family setting on the digit length ratios of siblings (Králík *et al.* 2019), although not the fingerprint data. The children came from two primary schools in Moravia (Czech Republic), from Hovorany (Kyjov district) and Tišnov (Brno-venkov district). In the recent study, we utilized the scans for measurements of epidermal ridges. For this study, we divided the whole source sample (N=329) into 10 school classes (6 to 15 years) and randomly selected 5 boys and 5 girls from each of the nine primary school classes. The selected study sample consists of both hands of 90 individuals (45 boys and 45 girls).

First, we increased the resolution of the images from 150 ppi to 450 ppi, and the sharpness was increased to maximum (99) using IrfanView (Skiljan 2019). Then, we adjusted the contrast (+50) and saturation (-50) and increased the file size to 300%. The measurements were then taken in the computer software *Dermatoglyphix* (Králík *et al.* 2017) designed for the enhancement of dermatoglyphic analysis. Before measurement, left hands were flipped horizontally to pseudo-right views to avoid cognitive/visual side biases of the human cognitive system.

On the images of living humans' skin, epidermal ridges were colored in light orange/pink and furrows in dark red (*Figure 2*); compare with the C in *Figure 1*. Breadth of an individual ridge was represented by the distance from the middle of one furrow to the middle of the next furrow measured perpendicular to the course of the ridge. The measuring segment was defined as the line running across 10 epidermal ridges at manually/visually set perpendicular direction towards the majority of the measured ridges. Because the ridge breadth varies more significantly in close proximity to the minutiae (e.g., the elongated narrow end of some minutiae of the end of ridge type), we tried to avoid crossing the papillary terrain at the minutiae site when placing the measurement segment. Since the length of a segment crossing perpendicularly 10 ridges was usually ca. 0.5 cm or less, it was generally possible to set the position of the segment well perpendicular to the course of all involved epidermal ridges. Sometimes, however, the epidermal ridges run curved or diverge in a fan pattern. Then it is not possible to lay a segment so that it is exactly perpendicular to all the ridges. If it was not possible to place the line perpendicular across *all* the ridges, it was placed to be the most perpendicular to the majority of the ridges in the middle of the segment's length. Each segment was divided into 10 measured sections by points placed always in the middle of the furrows between the adjacent ridges.

On each hand (fingers and palms), measuring segments were placed on 29 defined *segment positions*, counted segments 1 to 29 on the right hand and equivalent segments counted from 30 to 58 on the left hand (*Figure 2*). Specifically, there were five positions for the proximal phalanges, four positions for the middle phalanges and 14 positions for the distal phalanges. Except for the position of the measuring segment, orientation of each segment and the position of each measured ridge on it was recorded, so the identity of each individually measured ridge was stated in the recorded raw data. Except for the thumb, there were three positions at the distal phalanges—proximal position placed just above the flexion crease in the middle of its length, and radial and ulnar areas located next to the core, each on the corresponding side. If there was a two-cores-pattern present, radial and ulnar areas were each located next to

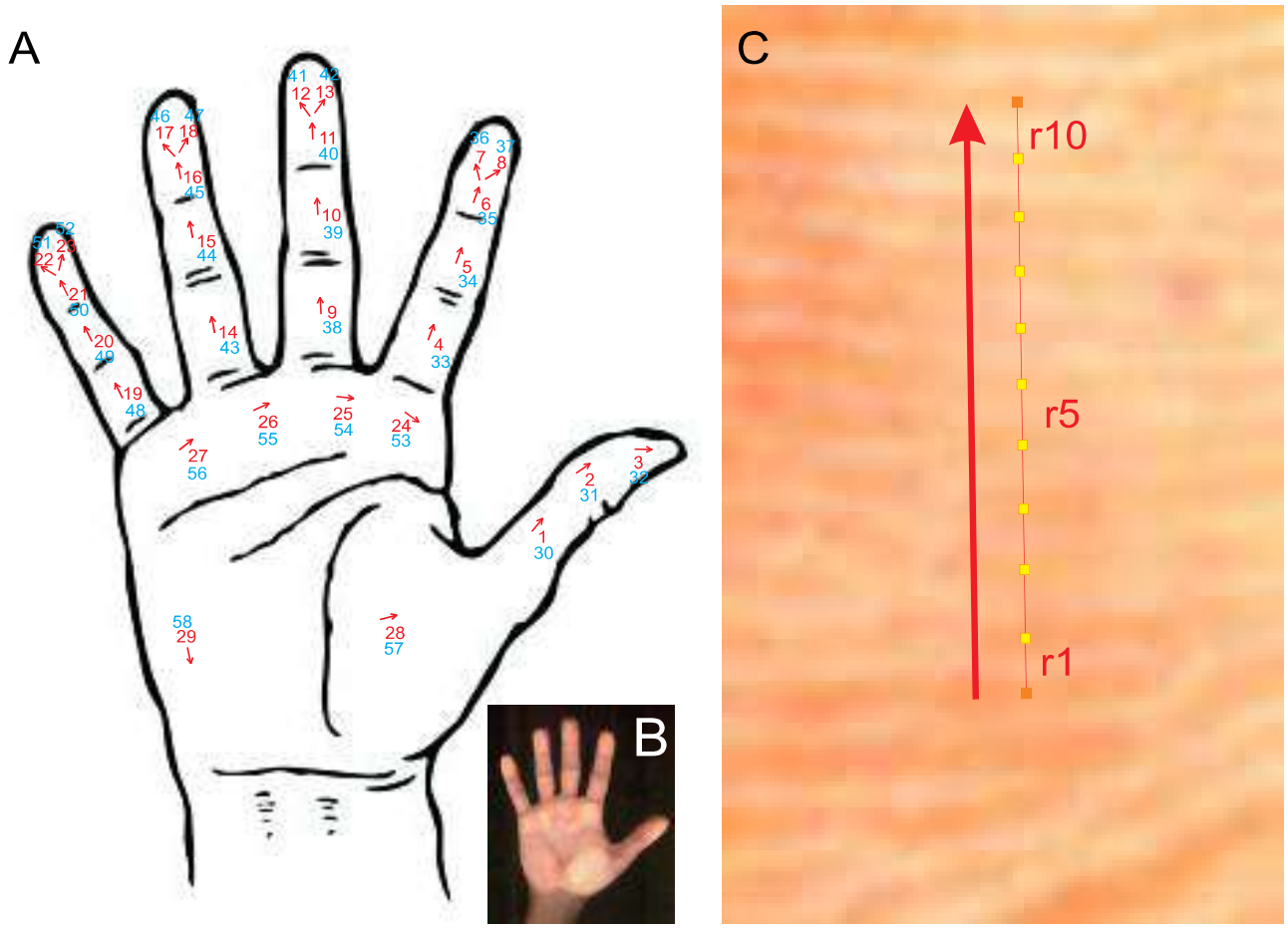

FIGURE 2: A – Scheme of placement of 29 measuring segments (i.e., 290 epidermal ridges) on each hand, (red) numbers 1–29 were defined on the right and corresponding (blue) numbers 30–58 were defined on the same (mirrored) positions of the left hand; B – An example of one image of a scanned hand used for measurements; C – Image of scanned surface of a hand with one measuring segment with 10 delimited ridges (r1 to r10), distances between points on the segment represent respective breadths of epidermal ridges, this segment (illustrated by red arrow) represents one of the 29 segments specified in the part A).

the corresponding core. If there was not a core (in archtype patterns), areas were located approximately in the center of the pattern (the peak of the arch). The ulnar area is not visible on the thumb so it could not be measured. The centers of phalanges were also used as measurement positions on the proximal and middle phalanges of fingers. On the palm, six measured areas were located on the standard dermatoglyphic positions related to embryonic hand pads. There were four interdigital areas on the interdigital pads between the finger bases. Measuring started radially from the digital triradii located on the interdigital regions. The fifth area of the palm was defined as the middle of the thenar, the proximo-radial area which contains short muscles controlling the thumb. And finally, the sixth area was in the middle of the hypothenar, area positioned along the ulnar side of the palm.

To sum up, 580 values of the epidermal ridge breadth were assembled for every individual supplemented by their age and body measurements data. All hands were scanned by the first author (M. K.) and measurements were carried out as part of the thesis of the second author (L. K.) (Koníková 2019).

3.2 Data analyses

3.2.1 Descriptive statistics

As a final data we worked with measurements of breadth (RB) of *individual epidermal ridges* in a count of

580 ridges per one subject hierarchically organized in 58 measurement segments. This scheme was true for all 90 studied subjects with several rare exceptions where ridges in a region were not visible locally and, therefore, a line was not possible to be measured. From the raw measurements (typically 580 values per subjects) overall descriptive statistical parameters (both location and dispersion, both absolute and relative) were computed for the whole sample and groups by sex and school class.

3.2.2 Inter-individual variation: sex and age differences

The practical aim of this study was to express the differences between individuals/subjects based on age and sex. However, since intra-individual differences between segments vary, we observed the influence of these factors in each of the 58 segments separately and expressed the differences between segments in these dependencies.

This time, we used the mean values calculated from all 10 epidermal ridges of each segment (MRB10). We then calculated the following statistical parameters and effects for the entire sample of children (N=90):

nM – sample size for males (number of available MRB10 values).
nF – sample size for females (number of available MRB10 values).
mM – mean value for males (boys) of all classes (n=45), in millimeters.
mF – mean value for females (girls) of all classes (n=45), in millimeters.
sdM – standard deviation for males (boys) of all classes (n=45), in millimeters.
sdF – standard deviation for females (girls) of all classes (n=45), in millimeters.
DiffMF – differences between mean values for males and females (males minus females), in millimeters.
PercDiffMF – percent differences between mean values for males and females (relative to mean value for males: (DiffMF/mM)×100.
CohenD – Cohen's D as a ratio between DiffMF to pooled standard deviation for males and females (since samples for males and females were identical, we simply averaged sdM and sdF).
P.p-val – p-value of permutation test of mean differences between males and females (H_0 – no difference). Computed by means of function *perm.test* in the R-package *exactRankTests* (Horthorn, Hornik 2021).
interceptM – intercept of regression line of MRB10 against age for males, in millimeters; computed using R-function *lm*.
interceptF – intercept of regression line of MRB10 against age for females, in millimeters; computed using R-function *lm*.
slopeM – slope of regression line of MRB10 against age for males, in millimeters per year; computed using R-function *lm*.
slopeF – slope of regression line of MRB10 against age for males, in millimeters per year; computed using R-function *lm*.
slopeDiffMF – difference between regression slopes for males and females, in millimeters per year.
PredDiffMF.y6 – difference in prediction of MRB10 in 6 years for males and females (males minus females), in millimeters.
PredDiffMF.o15 – difference in prediction of MRB10 in 15 years for males and females (males minus females), in millimeters.
PredictChange.y6o15 – change in difference in prediction (between sexes) between 6 and 15 years, in millimeters.
Equal.p-val – nonparametric test of equality between nonlinear models (smoothing splines) for males and females of relationship of MRB10 on age; computed using function *sm.ancova* available in the R-package *sm* (Bowman, Azzalini 2021). This tests whether the positions of 2D clouds are identical (H_0) or not.
Parallel.p-val – nonparametric test of parallelism between nonlinear models (smoothing splines) for males and females of relationship of MRB10 on age; computed using function *sm.ancova* available in the R-package *sm* (Bowman, Azzalini 2021). This tests whether the directions of the two nonlinear relationships are identical (H_0) or not.

Using the above noted statistical parameters, we tried to express the rate of change with age and the degree of sex differences (DiffMF, PercDiffMF, CohenD, P.p-val). The specific mean values of the whole population are not very important, because the epidermal ridge breadth changes with age in the age range studied. Nevertheless, it is possible to compare the sexes regardless of age, because men and women and the different age categories are quite evenly represented in the sample. It is therefore possible to test for overall inter-sex differences in the whole sample (in the sense of: do the sexes differ in epidermal ridge breadth at school age?). Significant differences cannot be expected because a substantial proportion of the children are prepubertal.

The highest value of the slope of the MRB regression line against age (slopeM, slopeF) was regarded

as the largest age change. Since the intersex differences are small initially and increase during growth (most so at puberty), we therefore considered the positions (segments) with the highest dimorphism to be those segments where the age trends diverge the most between girls and boys. We expressed this, first, as the difference between the slopes of the two regression lines (slopeDiffMF), and second, we tested this statistically (Parallel.p-val).

3.2.3 An effect of measuring units on statistical results

Finally, we attempted to address the problem hinted at more extensively in the Introduction: how measuring different numbers of ridges and different numbers and regional selection of segments per individual affects the variance of the groups being compared, and hence our ability to statistically distinguish some age and sex groups based on MRBs of subjects. We distinguished two age categories, the first ranging from 6 to 9 years (younger – y), the second ranging from 12 to 16 years (older – o), in males (m) and females (f) separately. In each of these groups, we then permuted each individual to select a finite number of segments and epidermal ridges on them, distinguishing the following 2 selection variants: small number of units (s) we randomly selected only 1 segment with only 1 triplet of ridges for each individual, and high number of units (h) where we randomly selected 20 segments with all 10 ridges in each of them. Therefore, the combination of all variables (sex, age category and units selection) lead to 8 different groups of data: myh (males-younger-high), mys, moh, mos, fyh, fys foh, fos. These variants were randomly selected from 4 different sampling frames or source sets of segments in our population sample:

A: selection from **all 58 segments** of a given individual
B: Selection only from segments at the **distal positions** of the distal digits (segments: 3, 7, 8, 12, 13, 17, 18, 22, 23, 32, 36, 37, 41, 42, 46, 47, 51, 52).
C: Selection of only the **10 most sexually dimorphic** segments, i.e., those closest to the upper right corner of the graph in *Figure 6B* (segments: 44, 14, 57, 43, 27, 1, 49, 38, 57, 2).
D: Selection only from the **10 least sexually dimorphic** segments, i.e., those closest to the bottom left corner of the graph in *Figure 6B* (segments: 17, 18, 6, 26, 41, 46, 20, 24, 23, 36).

In each of the 4 sampling frames we selected randomly the above mentioned 8 groups of data and tested statistical differences in MRB between the 8 groups by means of nonparametric Kruskal-Wallis type Dunn post-hoc test (Dunn, 1964) available in the R-package *PMCMRplus* (Pohlert, 2021). From the test of all eight groups against each other (48 pairs), we presented only 8 crucial comparisons for the results, which are always groups by sex and selection methods within each age category against each other (male vs. female) and groups by age within each sex selection method against each other (younger *vs.* older). The entire permutation procedure for these random selections was repeated 1000 times and the results then include the percentage of times the Dunn test provided a p-value (H_0 – no difference) of less than 0.05 (i.e., statistically significant).

4 RESULTS

4.1 Variations in individual epidermal ridges

Overall mean of the epidermal ridge breadth (RB) of the whole sample regardless of sex and age was 0.445 mm (SD=0.098, N=49606 ridges, range: from 0.052 mm to 1.010 mm, median=0.435 mm, 5% quantile=0.310 mm, 95% quantile=0.623 mm). A histogram of age distribution for males and females is available in Appendix (*Figure A2*). Complete set of statistical parameters both for males and females is available in the *Table 1*. Statistical tests of normality (Shapiro-Wilk's test and Pearson Chi-square test for normality) rejected the normality of distribution of individual RB values in the whole sample, sexes separately, as well as in sex/class groups separately (*Figure 3*). Estimates of skewness were positive which indicated that the distribution was skewed to the right, with an evident tail in the upper end. Kurtosis values were mostly above the value 0 which indicated slightly leptokurtic distribution (except for several segments with negative values) but the excess was relatively mild.

4.2 Differences between sexes and age categories

Population descriptive statistics for MRBs computed from all 10 ridges for each of the 58 segments separately are available in *Table 2*. A graphical representation of MRB on hand diagrams, categorized by color according to population mean values, is shown in *Figure 4*. Each value is a parameter for children of a given sex of all ages. Although these are predominantly juveniles prior to completion of growth, a number of segments have mean MRB values greater than 0.5 mm. In males, these are the segments on the thenar of the right hand and on both hands on the proximal phalanges of the 1st, 2nd and 3rd fingers

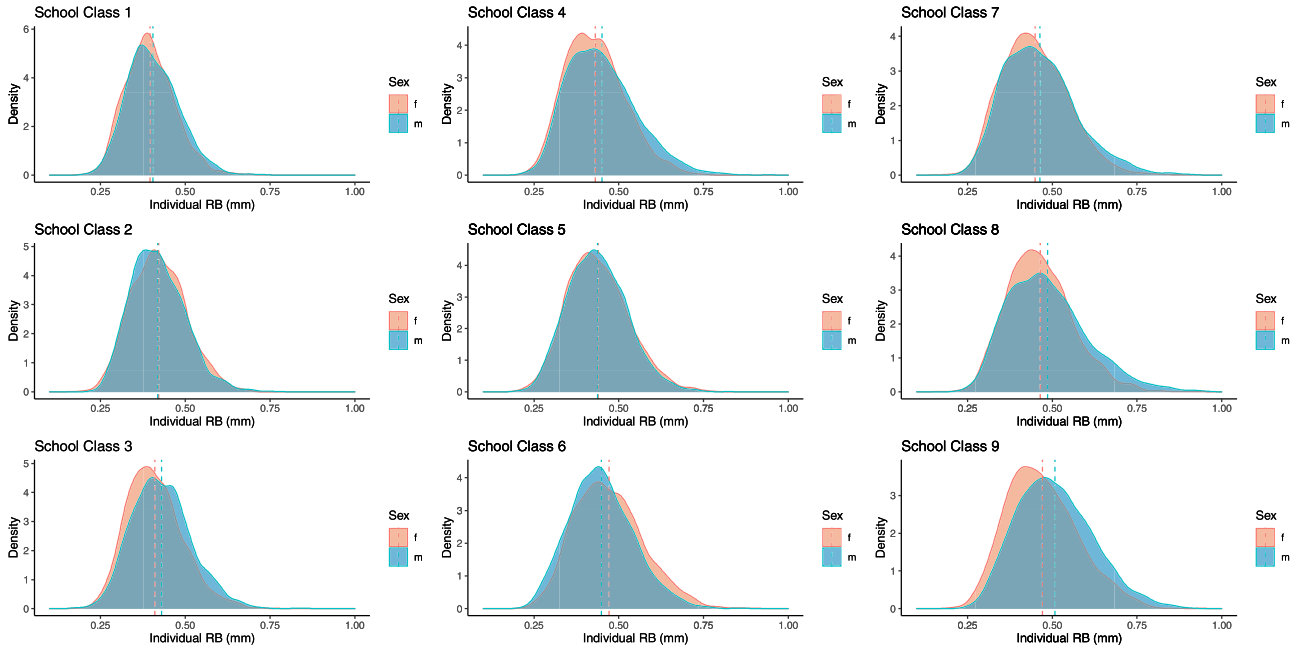

FIGURE 3: Distributions of breadth values of single ridges (see *Table 1* for N values) by sex and school class.

TABLE 1: Descriptive statistics of epidermal ridge breadth (in millimeters) calculated from breadths of individual epidermal ridges for the whole sample, sexes separately and groups by sex and school class.

Sex	School Class	N	Mean	SD	Minimum	Maximum	Median	5% Quant	95% Quant	Skewnes	Kurtosis
combined	combined	49606	0.445	0.098	0.052	1.010	0.435	0.306	0.623	0.67	0.69
females	combined	24369	0.440	0.094	0.159	0.941	0.430	0.303	0.609	0.58	0.44
males	combined	25237	0.450	0.101	0.052	1.010	0.439	0.309	0.636	0.72	0.78
females	1	2450	0.397	0.072	0.184	0.741	0.392	0.289	0.522	0.49	0.55
females	2	2689	0.422	0.080	0.166	0.695	0.418	0.298	0.564	0.26	-0.11
females	3	2840	0.410	0.082	0.169	0.770	0.402	0.291	0.554	0.53	0.33
females	4	2770	0.431	0.087	0.228	0.756	0.424	0.302	0.586	0.46	0.01
females	5	2820	0.439	0.090	0.198	0.787	0.432	0.302	0.597	0.42	0.13
females	6	2770	0.471	0.101	0.213	0.910	0.462	0.324	0.652	0.46	0.11
females	7	2700	0.450	0.096	0.159	0.918	0.441	0.309	0.617	0.51	0.41
females	8	2780	0.465	0.097	0.163	0.938	0.456	0.321	0.640	0.56	0.56
females	9	2550	0.471	0.104	0.199	0.941	0.460	0.319	0.664	0.49	0.04
males	1	2710	0.405	0.075	0.203	0.733	0.398	0.291	0.535	0.45	0.26
males	2	2730	0.419	0.079	0.222	0.780	0.413	0.302	0.553	0.53	0.39
males	3	2670	0.430	0.087	0.170	0.860	0.424	0.301	0.585	0.40	0.31
males	4	2880	0.450	0.102	0.211	1.010	0.438	0.310	0.633	0.69	0.66
males	5	2849	0.438	0.087	0.199	0.824	0.434	0.304	0.585	0.35	0.10
males	6	2869	0.449	0.094	0.206	0.877	0.443	0.303	0.614	0.40	0.17
males	7	2840	0.464	0.107	0.235	0.908	0.452	0.316	0.664	0.69	0.53
males	8	2820	0.486	0.117	0.052	0.961	0.472	0.324	0.700	0.69	0.51
males	9	2869	0.508	0.111	0.236	0.913	0.497	0.342	0.700	0.43	-0.07

and the middle phalanges of the 2nd, 3rd and 4th fingers. In females, it is on the proximal phalanx of the thumb of both hands, and also on the proximal phalanx and middle phalanx of the 2nd finger of the left hand, the middle phalanx of the 3rd finger of the left hand and the middle phalanx of the 4th finger of the right hand. The mean MRB at all distal positions of the distal phalanges of the triphalangeal fingers (2nd to 5th) on both hands is lower than 0.4 mm in both males and females. All values of the slope of the regression lines (*Table 3*) are positive in all segments for both males and females, i.e., MRB increases with age everywhere on the hand, but to different degrees and for different segments differently in males and females.

Percentage sex differences between means are of the positive sign in most segments, i.e., larger means were measured for males (*Figure 5*, upper row). The largest percentage difference was found in four segments: on the proximal 4th finger of the right hand, on the proximal and middle 4th finger of the left hand, and on the thenar of the left hand. The dimorphism in these segments exceeded 5%, and only in these 4 segments did the permutation test reject the agreement of means, and thus the difference between the sexes was statistically significant (*Table 2*). However, in many segments, the dimorphism was small, and in seven segments it was actually numerically negative (i.e., higher means in females, but no test was statistically significant).

The differences between the relationship of MRB to age in men and women are shown in *Table 3* and

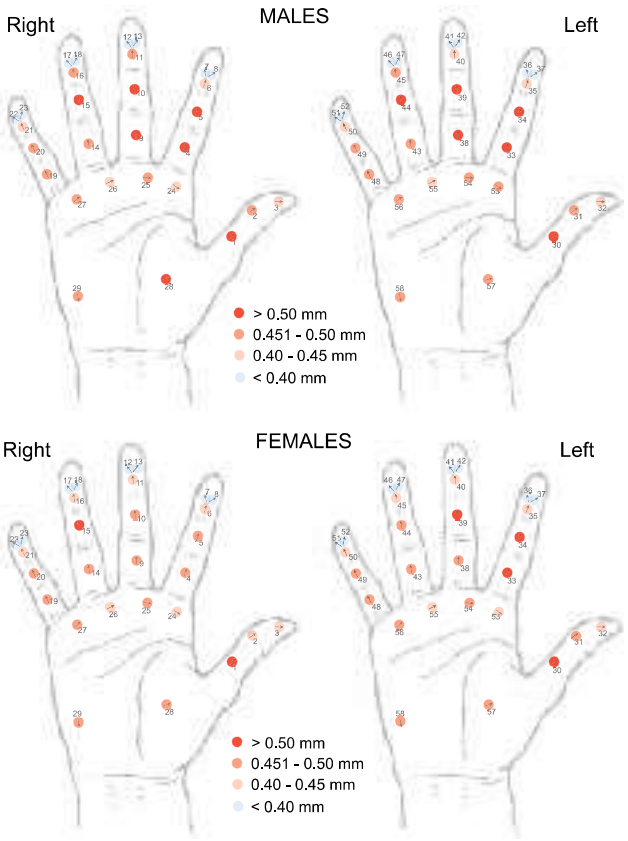

FIGURE 4: Visualizing mean values of MRB10 (categorized into four intervals) in each measured segment for each sex and body side (hand) separately, all age categories combined.

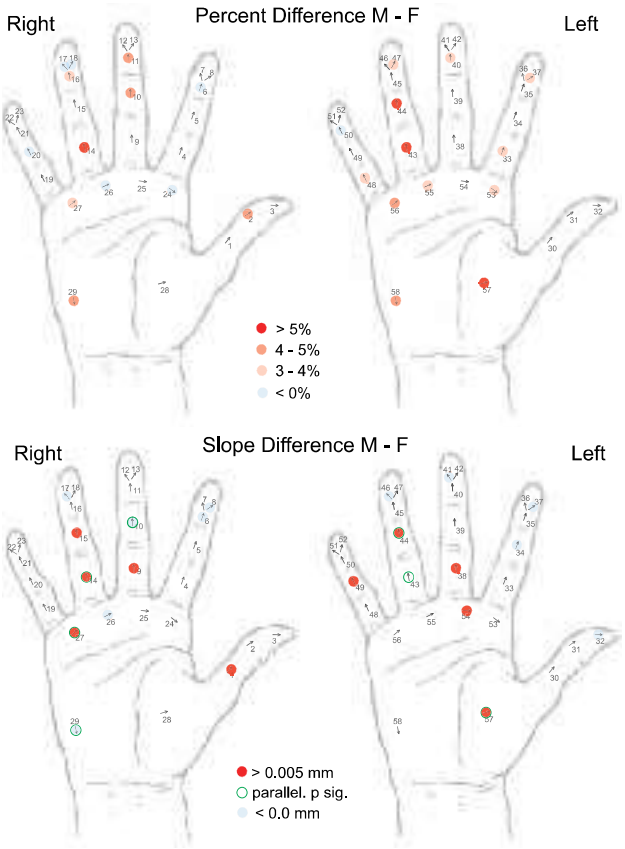

FIGURE 5: Visualizing segments according to percent mean difference between males and females in MRB10 (above), and regression slope differences (MRB10 vs. age) between males and females (below); in the four segments marked most intense red (above) with M – F differences higher than 5% permutation test rejected H_0 of equality of means; in the four segments marked with green circle (below) nonparametric test of parallelism rejected equality of nonlinear change with age for males and females.

TABLE 2: Descriptive statistics and sex differences of MRB10 within the whole sample separately for each segment.

hand	segment	nM	nF	mM	mF	sdM	sdF	DiffMF	PercDiffMF	CohenD	P.p-val
right	1	42	40	0.522	0.509	0.078	0.061	0.013	2.50	0.19	0.40
right	2	45	45	0.462	0.442	0.078	0.054	0.019	4.20	0.29	0.17
right	3	44	44	0.407	0.405	0.045	0.036	0.002	0.47	0.05	0.83
right	4	45	44	0.502	0.488	0.078	0.062	0.013	2.69	0.19	0.37
right	5	45	45	0.504	0.489	0.069	0.065	0.015	2.91	0.22	0.30
right	6	45	45	0.437	0.439	0.055	0.053	-0.002	-0.42	-0.03	0.87
right	7	45	45	0.392	0.385	0.052	0.043	0.007	1.80	0.15	0.48
right	8	43	42	0.398	0.387	0.038	0.038	0.011	2.86	0.30	0.17
right	9	45	44	0.503	0.499	0.067	0.066	0.004	0.86	0.06	0.76
right	10	45	45	0.518	0.495	0.061	0.066	0.023	4.39	0.36	0.09
right	11	45	45	0.459	0.440	0.072	0.059	0.020	4.26	0.30	0.16
right	12	44	45	0.371	0.363	0.034	0.035	0.008	2.09	0.22	0.29
right	13	41	35	0.371	0.365	0.035	0.027	0.006	1.60	0.19	0.41
right	14	45	45	0.494	0.467	0.062	0.064	0.027	5.50	0.43	**0.045**
right	15	45	44	0.520	0.514	0.081	0.067	0.006	1.15	0.08	0.70
right	16	44	45	0.460	0.443	0.062	0.058	0.017	3.65	0.28	0.19
right	17	44	39	0.359	0.370	0.031	0.034	-0.012	-3.23	-0.36	0.11
right	18	41	36	0.355	0.366	0.035	0.033	-0.011	-3.03	-0.32	0.17
right	19	42	35	0.472	0.463	0.048	0.049	0.009	1.84	0.18	0.43
right	20	45	44	0.483	0.485	0.065	0.060	-0.002	-0.34	-0.03	0.90
right	21	45	43	0.423	0.418	0.064	0.054	0.005	1.14	0.08	0.70
right	22	43	44	0.387	0.380	0.046	0.033	0.008	2.05	0.20	0.36
right	23	35	35	0.367	0.367	0.032	0.028	0.000	0.11	0.01	0.95
right	24	45	44	0.442	0.446	0.053	0.047	-0.003	-0.77	-0.07	0.75
right	25	45	45	0.491	0.481	0.057	0.053	0.009	1.93	0.17	0.41
right	26	45	44	0.443	0.443	0.041	0.045	0.000	-0.01	0.00	1.00
right	27	45	44	0.485	0.467	0.065	0.050	0.018	3.70	0.31	0.15
right	28	45	42	0.500	0.485	0.064	0.057	0.015	2.97	0.25	0.25
right	29	45	45	0.477	0.456	0.056	0.063	0.021	4.40	0.35	0.10
left	30	45	39	0.524	0.515	0.078	0.068	0.009	1.70	0.12	0.58
left	31	45	45	0.464	0.451	0.067	0.058	0.013	2.91	0.22	0.31
left	32	43	43	0.412	0.403	0.037	0.035	0.009	2.11	0.24	0.27
left	33	45	43	0.519	0.502	0.075	0.062	0.017	3.21	0.24	0.26
left	34	45	45	0.511	0.502	0.064	0.065	0.009	1.79	0.14	0.50
left	35	45	44	0.437	0.431	0.059	0.044	0.006	1.46	0.12	0.56
left	36	42	45	0.380	0.374	0.041	0.043	0.006	1.61	0.14	0.50
left	37	40	42	0.390	0.377	0.044	0.040	0.013	3.44	0.32	0.15
left	38	45	44	0.505	0.491	0.068	0.070	0.014	2.83	0.21	0.33
left	39	45	45	0.516	0.503	0.069	0.064	0.013	2.46	0.19	0.37
left	40	45	44	0.455	0.438	0.063	0.053	0.016	3.60	0.28	0.19
left	41	42	39	0.362	0.358	0.034	0.040	0.004	0.98	0.10	0.67
left	42	39	36	0.375	0.366	0.036	0.032	0.008	2.26	0.25	0.29
left	43	44	42	0.491	0.454	0.060	0.042	0.036	7.39	0.72	**0.002**
left	44	45	45	0.526	0.493	0.086	0.065	0.033	6.28	0.44	**0.043**
left	45	43	45	0.455	0.445	0.066	0.065	0.010	2.28	0.16	0.45
left	46	38	38	0.360	0.359	0.028	0.031	0.001	0.31	0.04	0.87
left	47	41	36	0.366	0.354	0.035	0.027	0.011	3.13	0.36	0.12
left	48	42	32	0.466	0.450	0.061	0.036	0.016	3.54	0.34	0.18
left	49	45	40	0.482	0.469	0.069	0.053	0.013	2.72	0.21	0.33
left	50	40	41	0.421	0.422	0.062	0.040	-0.001	-0.18	-0.01	0.95
left	51	43	37	0.382	0.374	0.040	0.026	0.008	2.12	0.25	0.29
left	52	37	30	0.370	0.361	0.044	0.029	0.009	2.50	0.25	0.32
left	53	44	44	0.455	0.440	0.058	0.047	0.014	3.15	0.27	0.20
left	54	45	43	0.495	0.482	0.060	0.043	0.013	2.72	0.26	0.23
left	55	44	41	0.447	0.434	0.054	0.038	0.014	3.07	0.30	0.18
left	56	44	42	0.477	0.457	0.063	0.057	0.020	4.22	0.34	0.12
left	57	45	44	0.494	0.466	0.075	0.051	0.028	5.74	0.45	**0.040**
left	58	45	45	0.476	0.456	0.061	0.062	0.020	4.29	0.33	0.12

TABLE 3: Regression parameters, predictions and tests of sex differences of relationships between MRB10 and age within the whole sample separately for each segment.

hand	segment	interceptM	interceptF	slopeM	slopeF	slopeDiffMF	PredM.y6	PredF.y6	PredM.o15	PredF.o15	PredDiffMF.y6	PredDiffMF.o15	PredictChange.y6o15	equal.p-val	parallel.p-val
right	1	0.291	0.374	0.021	0.012	0.008	0.414	0.448	0.600	0.558	-0.033	0.042	0.075	0.12	0.20
right	2	0.280	0.303	0.016	0.012	0.004	0.377	0.378	0.523	0.490	-0.001	0.033	0.034	0.24	0.17
right	3	0.313	0.341	0.008	0.006	0.003	0.363	0.376	0.438	0.427	-0.013	0.011	0.023	0.40	0.62
right	4	0.337	0.363	0.015	0.011	0.003	0.425	0.431	0.557	0.533	-0.006	0.025	0.031	0.58	0.51
right	5	0.316	0.328	0.017	0.014	0.002	0.417	0.415	0.567	0.544	0.002	0.022	0.021	0.68	0.27
right	6	0.319	0.316	0.011	0.011	0.000	0.382	0.382	0.477	0.481	0.000	-0.004	-0.004	0.71	0.98
right	7	0.279	0.308	0.010	0.007	0.003	0.339	0.349	0.430	0.411	-0.010	0.019	0.028	0.36	0.44
right	8	0.308	0.289	0.008	0.009	-0.001	0.356	0.341	0.427	0.418	0.015	0.009	-0.006	0.81	0.20
right	9	0.328	0.381	0.016	0.011	0.005	0.421	0.445	0.562	0.541	-0.023	0.021	0.045	0.33	0.53
right	10	0.338	0.312	0.016	0.016	0.000	0.434	0.410	0.579	0.558	0.024	0.020	-0.003	0.79	**0.025**
right	11	0.254	0.268	0.018	0.015	0.003	0.364	0.360	0.528	0.499	0.004	0.030	0.026	0.40	0.13
right	12	0.327	0.321	0.004	0.004	0.000	0.350	0.344	0.385	0.378	0.007	0.008	0.001	1.00	0.66
right	13	0.324	0.323	0.004	0.004	0.000	0.348	0.345	0.385	0.379	0.003	0.007	0.004	0.75	0.70
right	14	0.330	0.391	0.015	0.007	0.008	0.418	0.432	0.550	0.493	-0.014	0.056	0.070	0.11	**0.013**
right	15	0.288	0.353	0.021	0.015	0.006	0.412	0.440	0.598	0.571	-0.028	0.027	0.055	0.19	0.35
right	16	0.270	0.299	0.017	0.013	0.004	0.371	0.376	0.522	0.492	-0.005	0.030	0.035	0.37	0.19
right	17	0.306	0.291	0.005	0.007	-0.002	0.334	0.333	0.377	0.395	0.001	-0.018	-0.020	0.44	0.22
right	18	0.289	0.303	0.006	0.006	0.000	0.325	0.336	0.378	0.386	-0.011	-0.008	0.003	0.27	0.40
right	19	0.364	0.378	0.010	0.008	0.002	0.422	0.425	0.509	0.494	-0.002	0.016	0.018	0.58	0.58
right	20	0.319	0.336	0.015	0.013	0.001	0.407	0.417	0.539	0.538	-0.010	0.001	0.011	1.00	0.93
right	21	0.235	0.279	0.017	0.013	0.004	0.336	0.354	0.487	0.466	-0.018	0.020	0.038	0.32	0.42
right	22	0.317	0.354	0.006	0.002	0.004	0.354	0.368	0.410	0.388	-0.014	0.022	0.036	0.32	0.38
right	23	0.313	0.342	0.005	0.002	0.002	0.341	0.355	0.383	0.375	-0.014	0.008	0.022	0.40	0.70
right	24	0.307	0.336	0.012	0.010	0.002	0.379	0.395	0.488	0.484	-0.016	0.004	0.020	0.50	0.66
right	25	0.349	0.350	0.013	0.012	0.001	0.425	0.421	0.539	0.526	0.004	0.012	0.008	1.00	0.60
right	26	0.339	0.333	0.009	0.010	0.000	0.394	0.392	0.478	0.479	0.003	-0.001	-0.004	0.73	0.98
right	27	0.317	0.382	0.015	0.008	0.007	0.407	0.428	0.541	0.496	-0.021	0.046	0.066	0.054	**0.047**
right	28	0.371	0.368	0.012	0.011	0.001	0.440	0.432	0.544	0.528	0.008	0.015	0.008	0.73	0.52
right	29	0.366	0.289	0.010	0.015	-0.005	0.425	0.379	0.515	0.513	0.046	0.001	-0.045	0.09	**0.033**
left	30	0.326	0.361	0.018	0.014	0.004	0.432	0.444	0.591	0.569	-0.012	0.021	0.034	0.56	0.69
left	31	0.289	0.311	0.016	0.013	0.003	0.383	0.386	0.524	0.499	-0.004	0.025	0.028	0.37	0.26
left	32	0.332	0.314	0.007	0.008	-0.001	0.374	0.362	0.437	0.433	0.012	0.004	-0.008	0.51	0.54
left	33	0.371	0.386	0.013	0.011	0.003	0.450	0.449	0.568	0.544	0.001	0.024	0.023	0.76	0.53
left	34	0.333	0.319	0.016	0.016	0.000	0.428	0.417	0.571	0.564	0.011	0.006	-0.004	1.00	0.64
left	35	0.291	0.340	0.013	0.008	0.005	0.369	0.389	0.487	0.463	-0.020	0.024	0.044	0.25	0.41
left	36	0.309	0.304	0.006	0.006	0.000	0.346	0.341	0.402	0.397	0.005	0.005	0.000	1.00	0.84
left	37	0.319	0.267	0.006	0.010	-0.003	0.356	0.326	0.413	0.413	0.031	0.000	-0.031	0.23	0.09
left	38	0.404	0.470	0.009	0.002	0.007	0.458	0.482	0.540	0.499	-0.023	0.041	0.064	0.26	0.25
left	39	0.318	0.339	0.018	0.015	0.003	0.424	0.427	0.582	0.560	-0.003	0.023	0.026	0.48	0.28
left	40	0.307	0.332	0.013	0.010	0.004	0.386	0.389	0.504	0.475	-0.004	0.029	0.033	0.45	0.26
left	41	0.324	0.261	0.003	0.008	-0.005	0.344	0.312	0.373	0.387	0.032	-0.014	-0.046	0.15	0.29
left	42	0.305	0.351	0.006	0.001	0.005	0.341	0.359	0.395	0.371	-0.018	0.024	0.042	0.16	0.15
left	43	0.372	0.368	0.010	0.008	0.003	0.435	0.414	0.529	0.483	0.021	0.047	0.026	0.58	**0.0004**

TABLE 3: Continued.

left	44	0.307	0.368	0.020	0.011	0.008	0.424	0.435	0.600	0.536	-0.011	0.064	0.075	0.13	**0.013**
left	45	0.286	0.294	0.015	0.013	0.001	0.375	0.375	0.509	0.496	0.000	0.012	0.012	0.72	0.73
left	46	0.326	0.324	0.003	0.003	0.000	0.343	0.342	0.370	0.369	0.001	0.001	-0.001	1.00	0.96
left	47	0.308	0.299	0.005	0.005	0.000	0.339	0.329	0.384	0.372	0.010	0.012	0.002	1.00	0.31
left	48	0.323	0.350	0.013	0.009	0.004	0.400	0.404	0.516	0.486	-0.004	0.030	0.034	0.44	0.24
left	49	0.310	0.383	0.015	0.008	0.008	0.402	0.429	0.540	0.498	-0.027	0.042	0.069	0.09	0.09
left	50	0.279	0.326	0.012	0.008	0.004	0.354	0.377	0.466	0.453	-0.023	0.013	0.036	0.36	0.70
left	51	0.318	0.351	0.006	0.002	0.004	0.352	0.363	0.404	0.381	-0.011	0.023	0.034	0.21	0.17
left	52	0.305	0.305	0.006	0.005	0.000	0.338	0.336	0.388	0.382	0.002	0.007	0.004	1.00	0.88
left	53	0.326	0.339	0.011	0.009	0.002	0.395	0.394	0.498	0.475	0.001	0.023	0.022	0.62	0.27
left	54	0.312	0.373	0.016	0.010	0.006	0.410	0.432	0.557	0.521	-0.022	0.036	0.058	0.06	0.06
left	55	0.337	0.364	0.010	0.006	0.004	0.396	0.402	0.485	0.459	-0.006	0.026	0.032	0.46	0.31
left	56	0.342	0.336	0.012	0.011	0.001	0.414	0.400	0.523	0.497	0.014	0.026	0.012	1.00	0.12
left	57	0.340	0.387	0.014	0.007	0.007	0.422	0.430	0.546	0.494	-0.007	0.053	0.060	0.19	**0.021**
left	58	0.347	0.332	0.012	0.011	0.000	0.416	0.399	0.520	0.498	0.017	0.022	0.004	0.54	0.19

Figure 5 (lower row). Again, the differences in the slope of the regression lines are mostly positive (i.e., MRB increases more with age in males than in females). The largest differences were found in five segments on the right and five segments on the left hand, where the slope of the regression line was more than 0.005 mm per year higher in males than in females). List of these segments partially overlaps with the segments with the greatest percentage dimorphism mentioned above, which was particularly true for the proximal and middle 4th finger segments. Some of these positive differences (segments 14, 27, 43, 44, 57) were also found to be statistically significant using a nonparametric test for parallelism of nonlinear relationship (green circles in *Figure 5* bottom row). Some of the sex differences in the regression slope had a negative sign (i.e., higher slope in females than in males), and, comparing to the above mentioned percentual differences, in this case some of these differences (segment 10 and 29) were even statistically significant.

In *Figure 6*, we have shown the relationships between some of the descriptive and inferential parameters of each segment (numbers denoting segments are shown in the plots instead of points) for convenience. The relationship of the mean MRB values of each segment is similar in males and females (*Figure 6A*), with the higher mean value in males being higher also in females. However, it can be seen that the female mean values increase less as the male means increase and most segments in the plot are below the equivalence line, with only a few segments directly on it (e.g., 3, 50, 6, 24) and two segments even significantly above it (17, 18), indicating a markedly higher female mean compared to male mean. *Figure 6B* shows how broad is the cloud expressing the relationship between the dimorphism of the means and the dimorphism of the regression slope of the MRB – age relationship. While we find segments indicating a clear and strong positive relationship of the two dimorphism indicators (e.g., segment 44 with high values of both indicators and segment 17 with low values of both indicators), we also find segments that have a relatively high value in one, but an average or even low value in the other (e.g., segment 29 and 15). The relationship between the dimorphism of the prediction from the linear model at 6 years and at 15 years (*Figure 6C*) is similar to the previous plot (the cloud is only slightly counterclockwise rotated comparing to *Figure 6B*). However, we find a few segments with significantly higher dimorphism at 6 than at 15 years (segments 29, 37, 41). Another comparison is the relationship between the change in

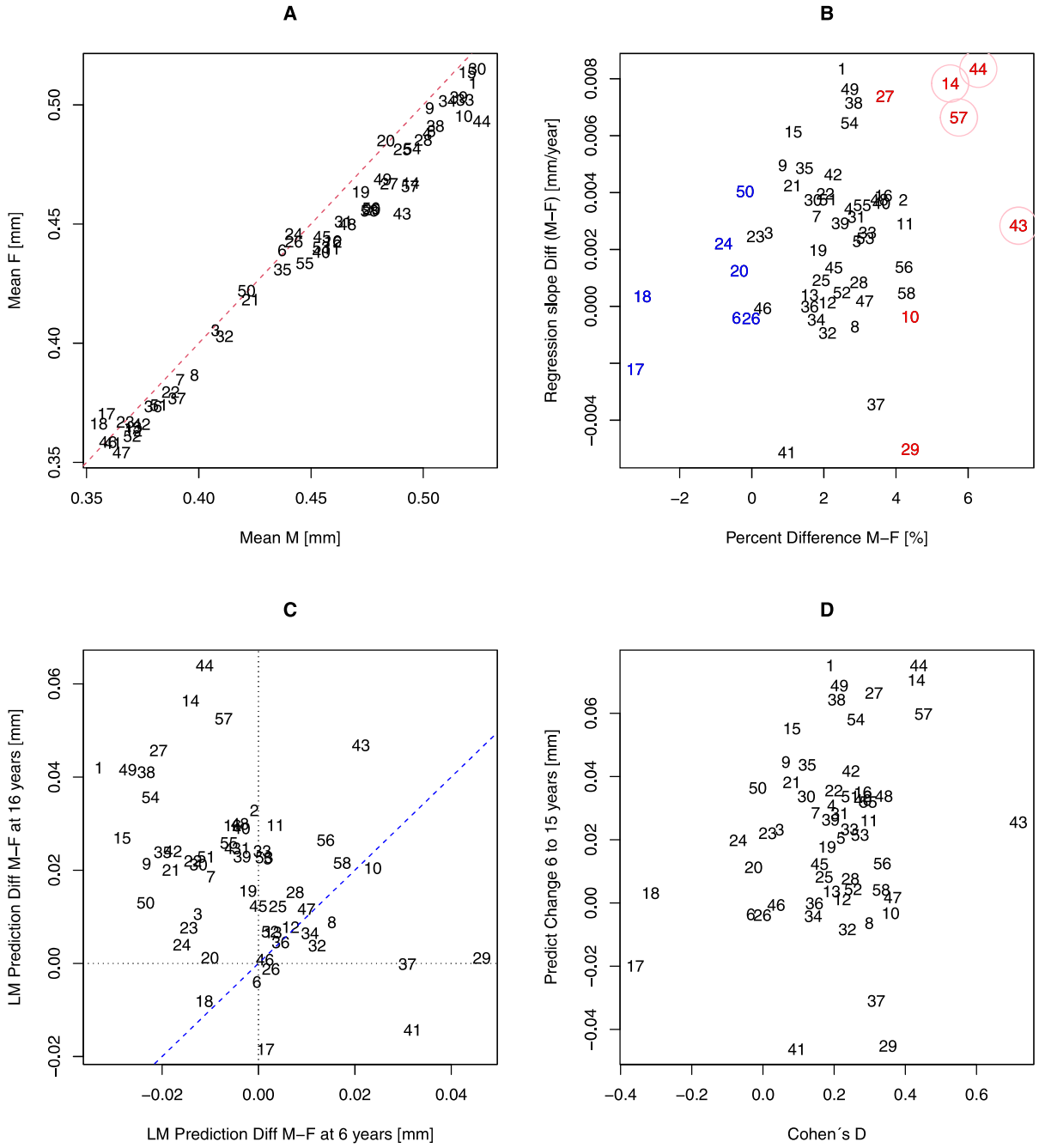

FIGURE 6: MRB10 statistics in various relationships in each segment (numbers in plots) separately: (A) relationship between mean MRB10 for males and females (red dashed line is the line of equivalence – with identical means for males and females); (B) regression slope differences (MRB10 vs. age) between males and females against percent difference (red – segments with significant test of rejecting parallelism of age trends for males and females, circles – segments with significant permutation test of mean values for males and females, blue – segments with negative percent differences M – F, i.e., with higher mean MRB10 values in females than in males); (C) differences between LM prediction of MRB10 for males and females in 15 years plotted against differences between LM prediction of MRB10 for males and females in 6 years (blue dashed line is the line of equivalence – were is identical prediction change between 6 and 15 years in males and females; (D) change in LM prediction difference in males and females against Cohen's D.

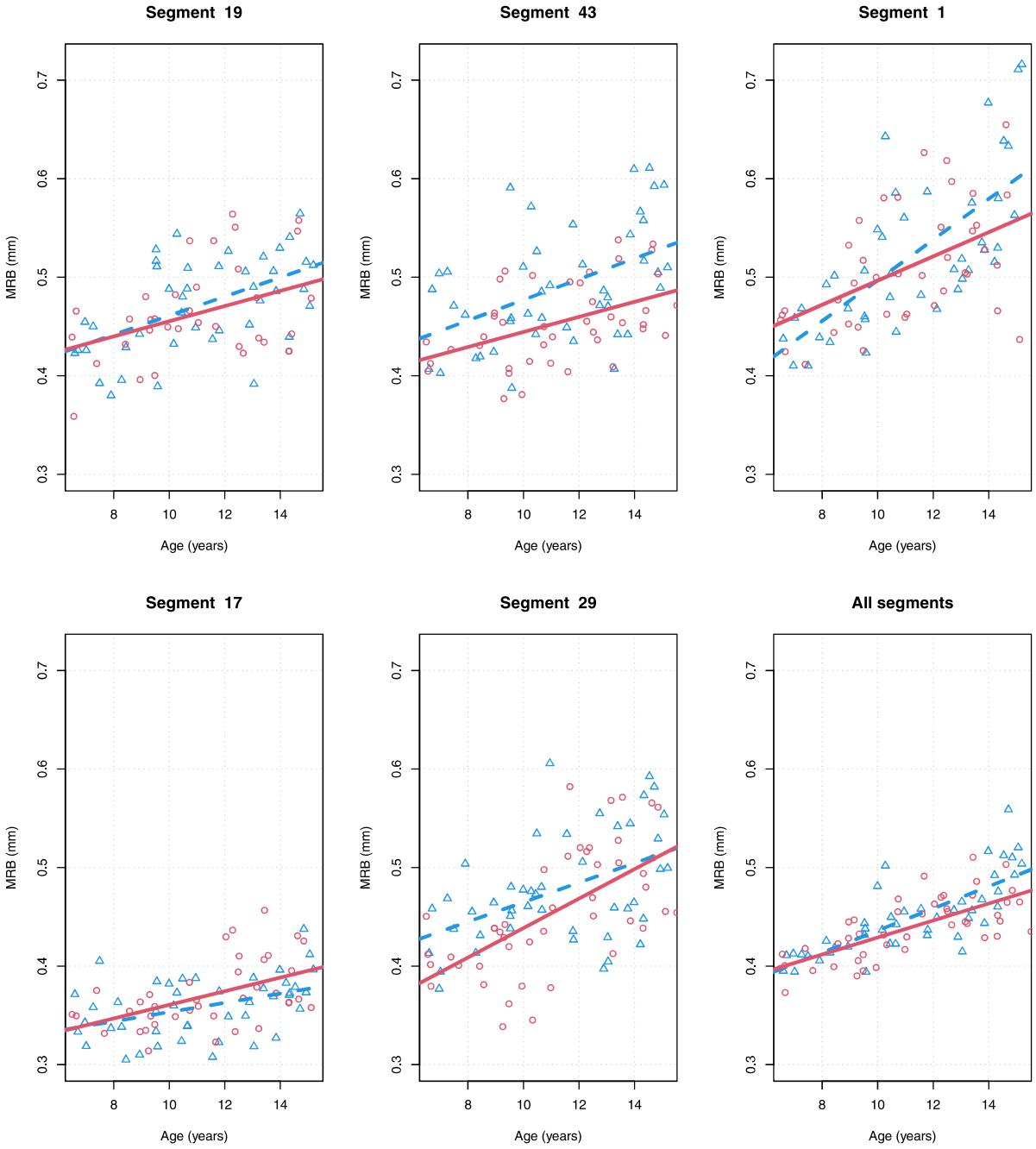

FIGURE 7: Examples of varying relationships between MRB10 in selected segments and age (red circles and red solid line – females, blue triangles and dashed lines – males): Segment 19 – typical segment (center position in *Figure 6B*), segment 43 – relatively mild increase with age and mild difference in increase between sexes, but highest percent difference between sexes (all over the age range), segment 1 – moderate percent difference between sexes but relatively high difference in regression slope in advance of males, segment 17 – an example of low overall MRB and reversed (negative) dimorphism both in percent difference and regression slopes, segment 29 – an example of typical (positive) percent dimorphism but negative difference in regression slopes, all segments – an average computed from all segments, lower residuals around regression lines are evident but the sex differences are relatively moderate in absolute terms both in percent differences and regression slopes.

dimorphism from the linear prediction between 6 and 15 years and the effect size of the average dimorphism expressed by Cohen's D (*Figure 6D*) – providing again a very similar distribution of segments to the two previous plots.

As can be seen from *Tables 2 and 3*, the individual segments differ substantially not only in the mean MRB value and percentage dimorphism, but also in the slope of the regression line of MRB versus age and slope dimorphism. In *Figure 7*, we have selected five segments that differ significantly in these parameters (MRB from all 10 ridges of a given segment vs. age) and added a plot of MRB from all 58 segments (these regression lines for all 58 segment separately are available in *Figure A3* in Appendix). Perhaps most importantly, these plots show very well the fundamental differences between MRBs in different hand regions (with this variability not affected in any way by differences in averaging; they were all obtained using the same procedure). We can see, for example, that the mean MRB of segment 17 at age 16 (i.e., in terms of hand size, practically in adulthood) is similar (or even smaller!) than the mean value of segment 29 at 6 years. The differences between the mean MRB values at different locations of the hand may be comparable to, or even greater than, the full real range of change during postnatal growth from 6 to 16 years!

But the differences between the hand regions are not only in the absolute value of MRB, but also in its change with age and the nature of sex differences during this change. We have selected just a few distinct types for illustration here. We first selected segment 19 (*Figure 7*), which is quite average in terms of several indices of dimorphism (see its position in *Figure 6B*). Segment 43 is shown as the second, which is among the most dimorphic of all in terms of percentage dimorphism, but only average in terms of the difference between the slopes of the regression lines. Next shown is segment 1, which has only average percentage dimorphism but a significant difference between the regression lines in favour of males. Segment 17 is presented as the fourth graph, where the percentage dimorphism between the averages is small but negative, and so is the negative difference between the regression slopes in favour of females. Last is the segment 29, where the dimorphism is positive, in favour of males, but the difference of the regression lines is negative (in favour of females). The MRB plot of all segments, presented as the sixth, shows significantly lower variance (and hence residuals of the regression models) but also lower slope and dimorphism than most of the individual segments (*Figure 7*).

4.3 Effect of measuring units selection on statistical differences between age and sex groups

The results of the permutation procedure used to test the effect of ridge and segment selection on statistical differences between groups by sex and age are shown in *Table 4*. This represents the percentage of statistically significant results (p-value less than 0.05) from Dunn's post-hoc test of the difference between these groups in a set of 1000 permutation results. In *Figure 8*, we can then see 1 particular instance of random selection from these 1000 permutations of random selections. The sample sizes in each group in the plots (*Figure 8*) ranged from 8 to 11 in the younger age category (6–9 years) and from 17 to 19 in the older age category (12–16 years); the differences between the samples were due to the fact that some segments were missing in the raw data for some subjects, and if this segment was randomly selected for a given subject by the randomization procedure, the resulting (non-existent) value was then missing and the sample size was lower. In all 4 sampling frames ("A"–"D"), calculating the MRB from a random selection of 20 segments and 10 ridges on each of them leads to a much smaller variance in MRB values within each group than calculating the MRB from only a single random segment and a single randomly selected triplet of ridges on it.

The results of the permutation procedure are fairly unambiguous as far as differences between age groups are concerned. Despite the relatively small sample sizes compared, statistical differences between age groups are unambiguous (100%) when selected from a large number of units ("h"); differences were statistically significant in all sampling frames ("A"–"D") for both males and females. When only a small number of units ("s") were randomly selected, the percentage of statistically significant tests was significantly lower, and the decrease was much greater for females than for males. In addition, then, there are also differences between sampling frames, with the variant selecting from the ten most dimorphic segments ("C") yielding the highest percentage of statistically significant tests, while selecting from the most distal ("B") and least dimorphic ("D") segments yielded significantly worse results, with selection from all segments ("A") somewhere in between. In addition, there is a sex difference here, with a significantly higher percentage of males than females distinguishing between age

groups. When we tested for differences in pairs of age groups with different unit selection method (i.e., mixing "h" vs. "s"), the results varied in the sense that the percentage success is somewhere between the results for "s" and "h" selection methods. It does not appear that the differentiation of the groups depended on which age group was "h" and which was "s", but there still remained a difference between the sexes. For both variations of the combination of "s" and "h" from sampling frame C (the most dimorphic segments), the

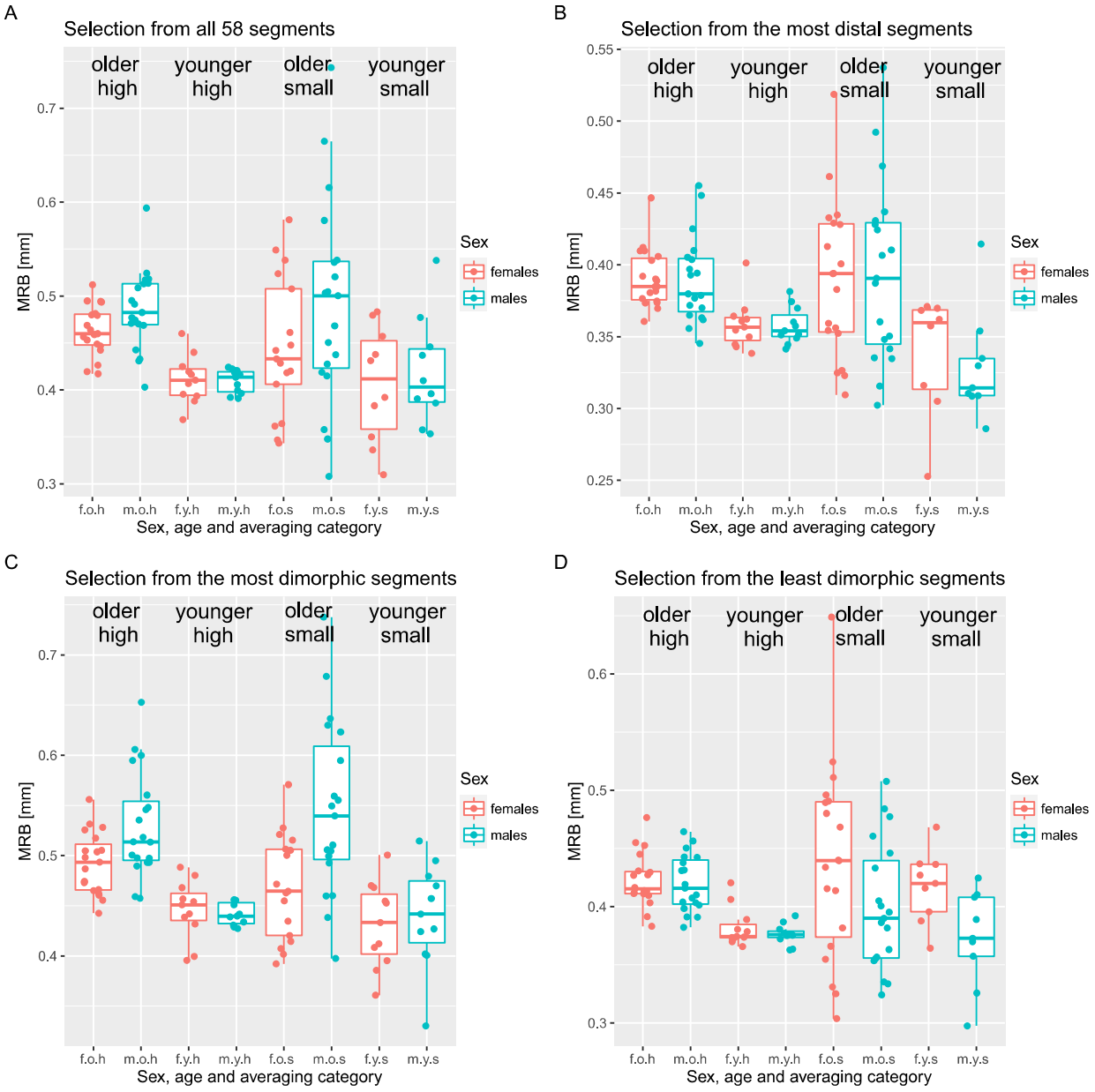

FIGURE 8: Visualization of one of 1000 permutes of the procedure testing the effect of a random ridge and segment selection on statistical differences between groups by sex and age in four different sampling frames: A – selection of all 58 segments, B – selection from distal positions on distal phalanges of fingers, C – selection from the 10 most dimorphic segments, D – selection from the 10 least dimorphic segments; f – female, m – male, y – younger category, o – older category, s – selection of small number of units (ridges and segments), h – selection of high number of units.

TABLE 4: Results of permutation procedure testing statistical differences between age and sex categories by means of nonparametrics post-hoc Dunn's test; numbers represent percentages of statistically significant results ($p<0.05$) out of 1000 permutes of sample selection in four different sampling frames; A – selection from all 58 segments, B – selection from distal positions on distal phalanges, C – selection from the 10 most sexually dimorphic segments, D – selection from the 10 least sexually dimorphic segments, in abbreviations of the compared groups: m – males, f – females, y – younger category (6–9 years), o – older category (12–16 years), s – random selection from small number of ridges and segments (1 segments with 1 triplet of ridges per individual, with replacement), h – random selection of 20 segments (with replacement) and all 10 ridges on each of them.

			Within one statistical analysis				Separate analyses of "h" and "s"			
			A	B	C	D	A	B	C	D
Within the same selection										
Sex categories	moh	vs. foh	0	0	0.4	0	0	0	1.3	0
	mos	vs. fos	13.4	5.1	24	10	6.2	2.9	16.3	3.6
	myh	vs. fyh	0	0	0	0	0	0	0	0
	mys	vs. fys	5.2	5.7	2.9	5.3	2.2	2.2	1.4	2.2
Age categories	moh	vs. myh	100	100	100	100	100	100	100	100
	mos	vs. mys	61.8	43.8	89.7	43.6	49.2	33	86.4	30
	foh	vs. fyh	100	100	100	100	100	100	100	100
	fos	vs. fys	39.7	34.2	40	38	26.9	24.3	30.3	24.4
Between different selections										
Sex categories	moh	vs. fos	24.1	4.7	59.1	10.1				
	mos	vs. foh	3.8	5.3	3.3	25.2				
	myh	vs. fys	3.3	3.8	1.9	4.3				
	mys	vs. fyh	1.9	1.1	0.8	1.3				
Age categories	moh	vs. mys	87.3	67.1	99.1	76.9				
	mos	vs. myh	84.9	66	99.6	62.6				
	foh	vs. fys	66	58.8	68.4	75.9				
	fos	vs. fyh	61	53.2	57.3	50.9				

success rate for distinguishing age groups is above 99% for males.

Completely different success rates are achieved by statistical differentiation of groups by sex (tests presented here are only between sexes within the same age category). When sampling the "h" variant, the test was unable to distinguish the sexes at all (mostly 0%, except for 0.4% for sampling frame C in the older age category). When sampling the "s" variant, the success rate was surprisingly higher, ranging from a few to several tens of percent (24% for sampling frame "C"). When males and females selected by a different sampling method ("h" vs. "s") were combined, the proportion of significant tests increased in both age categories, but clearly only for the combination where males are selected by the "h" method and females by the "s" method. The opposite combination of the sex groups (women "h" and men "s") led to different changes in the different sampling frames.

Finally, we tested the effect of the total variance of the data on the ability of the test to detect differences between groups. In the previous post-hoc tests, all eight groups ("h" and "s" methods together) were always part of the test sample, so that we could determine the result for the combination of the "h" and "s" selection methods. We have now tested the same (on the same data from the identical 1000 permutations) in separate post-hoc tests for the "h" and "s" methods (right part of *Table 4*). Regarding the age groups, the results are the same for the "h" method (always 100%) and always slightly worse for the "s" method. Regarding the differentiation of the groups by sex, the results are again similar, but for the "s" method they again provide a slightly lower percentage of significant results than when combining both methods in one test.

5 DISCUSSION

In the present study, we tested the differences between age and sex groups in a sample of school-aged children with an equal representation of age groups and the effect of selection of number and location of epidermal ridges on mean (MRB). The results show that both the number of ridges selected and the locations from which they are selected on the hand affect the resulting representations of individuals and thus statistical comparisons. We attempt to discuss and explain our main findings here.

The distribution of individual ridge breadth (RB) values across the whole sample is skewed to the right with a clear tail at higher values. Initially, we thought that the skew of RB values would be reversed (at the lower end of the distribution) due to occasional segment crossing over the ridge near the minutia, where the ridges taper significantly. For this reason, we tried to ensure that these ends of the ridges were intercepted by the segments as little as possible during the measurements. While some outliers are present at the lower end and can be explained in this way, the overall skew of the distribution is at the upper end. We speculated that this may be due to the distinctly "ontogenetic" nature of the sample and the presence of some individuals growing more strongly at puberty, but the RB distributions by school class (*Figure 3*) have similar skewness at the upper end, as the majority of the children in each of the classes were in prepubertal developmental stages. Thus, it is not clear what mechanism is involved in the formation of this skew. One possible explanation is that in our method of measurement (using a manually laid segment), an incorrectly placed segment that is not exactly perpendicular to an epidermal ridge to be measured cannot bias the RB towards lower values, but only towards higher values (if the segment is exactly perpendicular, the RB measurement is correct, if it is turned other than perpendicular, the RB will always and only be higher than the correct value). In this paper we cannot decide to what extent this mechanism contributes to the skewed distribution of RB values, but it would be possible to test this hypothesis in some way. If this were the case, it would be useful to somehow treat the situation methodologically.

We also found that even in children, individual sites on the hand differed significantly in the epidermal ridge breadth. Thus, it is not just a matter of final status in adulthood, as previous studies have found (Cummins *et al.* 1941, Ohler, Cummins 1942, Gutiérrez-Redomero, Alonso-Rodríguez 2013), but intraindividual variability between hand positions is already observable in childhood. To the best of our knowledge, our study is the first to demonstrate this, as previous growth studies in children and adolescents have measured only limited areas on the hand (Loesch, Czyżewska 1972, Loesch, Godlewska 1971). With regards to the application of epidermal ridge measurements in forensic investigation and archaeology, it is therefore of great importance to assess the differences in these hand positions in relation to their preservation in prints commonly available in forensic and archaeological finds. If the reference samples (comparison data) do not match the case being evaluated in their region on the hand, it is very easy to make a completely wrong estimate from the epidermal ridge breadth measurements.

Our findings allow us to be more specific about the next focus of method development for these estimates in terms of appropriate regions on the hand. However, it will be crucial whether we will be able to distinguish them among others or find the detailed place of its origin on the hand (i.e., so-called fingerprint localization (Králík, Novotný 2005)). As in adults (Cummins *et al.* 1941, Ohler, Cummins 1942), the epidermal ridges on the fingertips (distal positions of the distal phalanges) were found to be the thinnest of the whole hand and showed the lowest level of dimorphism and age differences during childhood. Thus, these areas are probably not the best choice (when there is a choice from the whole hand) if we want to differentiate individuals or groups by age and sex. Interestingly, most measurement methods (see *Figure 3, D–G*) and published studies, with some exceptions (Gutiérrez-Redomero, Alonso-Rodríguez 2013), have largely focused on these finger locations, which is probably not fortunate. While these areas are of eminent importance in the forensic field, as these are the parts of the fingers that frequently touch surfaces and are therefore imprinted on them, they will not be the best in terms of the result expected from their analysis. Fingerprints on archaeological ceramics will then depend heavily on what proportion these fingertip impressions make up the total set of impressions on a given object—the MRB of the same person can only vary substantially depending on the proportion of these locations in their set of impressions. Therefore, when comparing fingerprints on ceramics, it may be highly desirable to strictly control modeling techniques, which may just vary in the proportion of use of individual regions on the hand and fingers, and to move towards methods of localizing all the prints on the hand. Our

results clearly show the relevance and need to develop methods for localizing (cf. Králík, Novotný 2005) the imprint to the original region on the hand as accurately as possible. To do this, however, we need to evaluate both the 3D shape of the surface of the imprints on ceramics in relation to the original region on the hand, and to know the regional variability of individual ridges and their local clusters/streams in terms of their divergence, curvature, gradients in RB, gradients in *minutiae* frequency, presence of incipient ridges, tendencies to "dotting" and so on. However, these data are not sufficiently available. We therefore hope that our results will stimulate new detailed research in this area.

Biologically quite interesting is the finding that among the most dimorphic locations on the hand in terms of epidermal ridge breadth are the proximal and middle phalanges of the 4th finger (especially proximal phalanx of the left 4th finger). It is the 4th finger that should be more strongly influenced prenatally by prenatal testosterone in boys than in girls. It would be interesting to see if similar effects as have been found in the ratio between finger lengths (2D:4D ratio) (Králík *et al.* 2017, 2019, Manning 2002), midphalangeal hair *(*Harnádková *et al.* 2021) and finger ridge counts (Jantz 2022, Polcerová *et al.* 2022) are manifested also in the MRB ratio between fingers, and if it is already manifested in childhood.

It should be noted that our sample consisted of children from one narrowly defined area of the Czech Republic and, in addition, children of parents with different than long-term local origins were excluded from the sample. Thus, our results are in no way indicative of interpopulation differences, nor of the suitability of any palm regions for distinguishing different human populations on the basis of RB. It may well be that distal finger regions are suitable for interpopulation comparisons, but we cannot comment on this based on our results.

Under the assumptions mentioned in the Introduction, we found that mean values per individual (MRB) are strongly influenced by both the number of ridges averaged (i.e., segment length or number of ridges per measurement) and the number of segments averaged per individual. While the overall mean of these averages for a population group does not change significantly, the variance of individual values around this population mean does change significantly. The fewer of these units at each of the two levels that are used to calculate the average for an individual, the more the individual representations then vary around the mean. If we do not take into account methodologically the effect of the number of averaging units (i.e., if, for example, we measure a different number of ridges for each subject and use a different number of segments), this is unlikely to change much the *inductive* descriptive results for a large set of individuals in terms of *mean* MRBs, but it will change the variance at each level of averaging substantially, and the resulting MRB values for each individual will each belong to a different "population" of MRB values with a predictably different variance. This will then affect *deductive* statistical results, e.g., statistical differentiation of two or more groups from each other—larger number of measured units (ridges, measurement segments) allow us to detect smaller differences among groups. This can be seen very well in our results for tests of age group differences: averaging 20 segments resulted in a sample of MRB values that could always (100%) statistically distinguish the two age groups (6–9 years vs. 12–16 years) from each other, for both males and females. However, this cannot be said for MRB values that were calculated from a small number of ridges.

Certainly, our attempt to permutationally compare the effect of the number of averaged units on the outcome of tests of age and sex differences represents some extreme limits of possible real-world scenarios. The differences between the variances of MRB samples from a small number of units (only a single triplet from all segments, "s") and a large number of units (all 10 ridges from 20 segments, "h") are enormous (*Figure 8*). We can clearly see that a MRB value obtained by the "s" procedure cannot be compared with the reference set that would have been generated by the "h" procedure (and *vice versa*). If we have the number of measurement units defined uniformly, we at least know which reference set to compare the unknown case with. If we do not know the number of units measured, we have no assurance that our comparison is correct, even if the differences in the number of units averaged will not be this large. However, our comparison shows that the problem needs to be addressed and the effect of the number of averaged units on the reliability of estimates in real situations needs to be tested in detail.

From the point of view of deductive methods (estimating new cases based on inductive rules from reference samples), these trivial findings have important implications, mainly: the number and provenance of the averaged units affects the variance of the average values. One possible solution is to standardize the number of measurement units, where the MRB of each evaluated case would be calculated by averaging over similar numbers of units as the MRB of the reference set value

that is used for comparison. If we do not move in the direction of standardizing the number of measurement units, we will never be sure that the probabilities with which we distinguish between two groups are correct, i.e., that we classify an unknown evaluated case correctly into a group. It is hard to imagine that in an archaeological fingerprint application (but easier in forensic context) it will be possible to measure the same large number of ridges and make the same large number of measurements (segments) for all cases (fingerprints on archaeological ceramics). For these applications, it will probably be suitable to have some "dynamic reference sample" of fingerprints on ceramics measured in detail on a ridge-by-ridge basis (as in this study), and to create an *ad hoc* reference sample of MRBs for each evaluated case, generated by averaging setting that corresponds to the number of averaged units of the evaluated case (that is, instead of conforming the unknown case to the nature of the reference sample, which is difficult in principle, we adjust the reference sample to each case evaluated).

LIMITATIONS OF THE STUDY

One limitation of this study is the number of children, with only 5 girls and 5 boys selected from each class, and even this was at the limit of humanly acceptable capacity to perform the sheer amount of manual measurements. Certainly, the ideal would be to have several hundred individuals, i.e., at least many dozens in each age group. We currently have this number but will need to develop a reliable method of automatic measurement.

The main limitation of this study is its cross-sectional nature; it is a cross-sectional sample where we do not observe actual growth with age, but only differences between individuals of different ages. These undoubtedly differ in their age and biological development, but they also differ in other characteristics that may also influence their ridge breath, and we do not control for these factors.

Another limitation of our study is the yet incomplete growth of the children in our sample. While most of the girls will no longer experience significant growth at older ages, some of the boys are likely to have grown further at ages not in our data. Thus, we are missing the period till full adulthood, so we do not capture adult values of epidermal ridge breadth and adult sexual dimorphism at the oldest ages.

Breadth of individual epidermal ridges varied substantially also within each segment. This aspect of intra-individual variability was also recorded, and we even have the possibility to study the direction of the possible systematic change (a gradient) in ridge breadth within each segment due to the methodology used (see arrows in *Figure 2*), but these results are not included in this this paper and will be part of a future study.

FUTURE DEVELOPMENTS

Based on the findings of this study, we venture to suggest that a desirable development in the measurement and application of epidermal ridge dimensions should be towards some semi-automatic or automatic measurement of individual ridges across large regions of the hand (or the whole hand), which would then be subject to subsequent averaging operations and analyses, or directly to some multilevel/hierarchical method of analysis of variance. If our assumption about the reasons for the asymmetric distribution of RB values is correct (the result of slight deviations in the orientation of the measurement line), automatic and unbiased measurement of individual ridges could relieve us of this deviation from data normality. Then, we could consider the use of Mixed Effect Linear Models in the statistical analysis of the measured RB data.

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APPENDIX

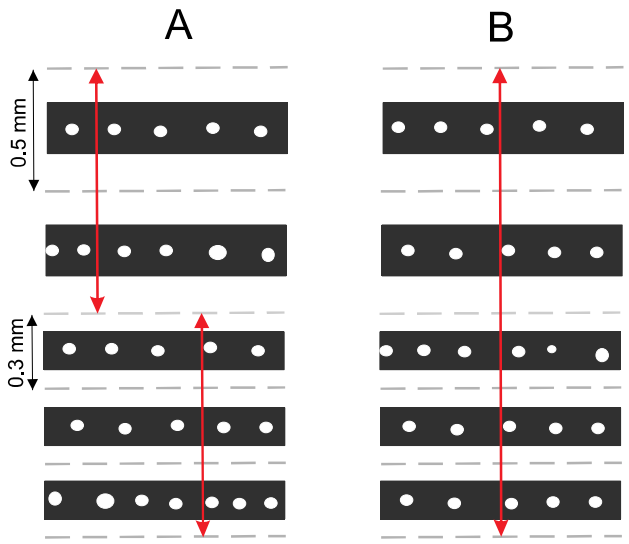

FIGURE A1: Two ways of performing epidermal ridge breadth measurements on a small region of papillary terrain. We have 2 ridges each 0.5 mm in breadth along with 3 ridges each 0.3 mm of breadth. If we use two segments(A), one for 2 and the second for 3 ridges, and obtain the resulting MRB as their average, the result is an average ridge breadth of 0.40 mm. If we use one segment (B) that spans all 5 ridges, the result is an average value of 0.38 mm. The number of ridges to be measured, or the length of the segments and the number of segments, are determined by the researcher's decision when measuring manually. The imprints on archaeological ceramics are so varied in terms of extent and preservation that differences in the number and length of segments cannot be avoided, and therefore neither can these numerical effects associated with them.

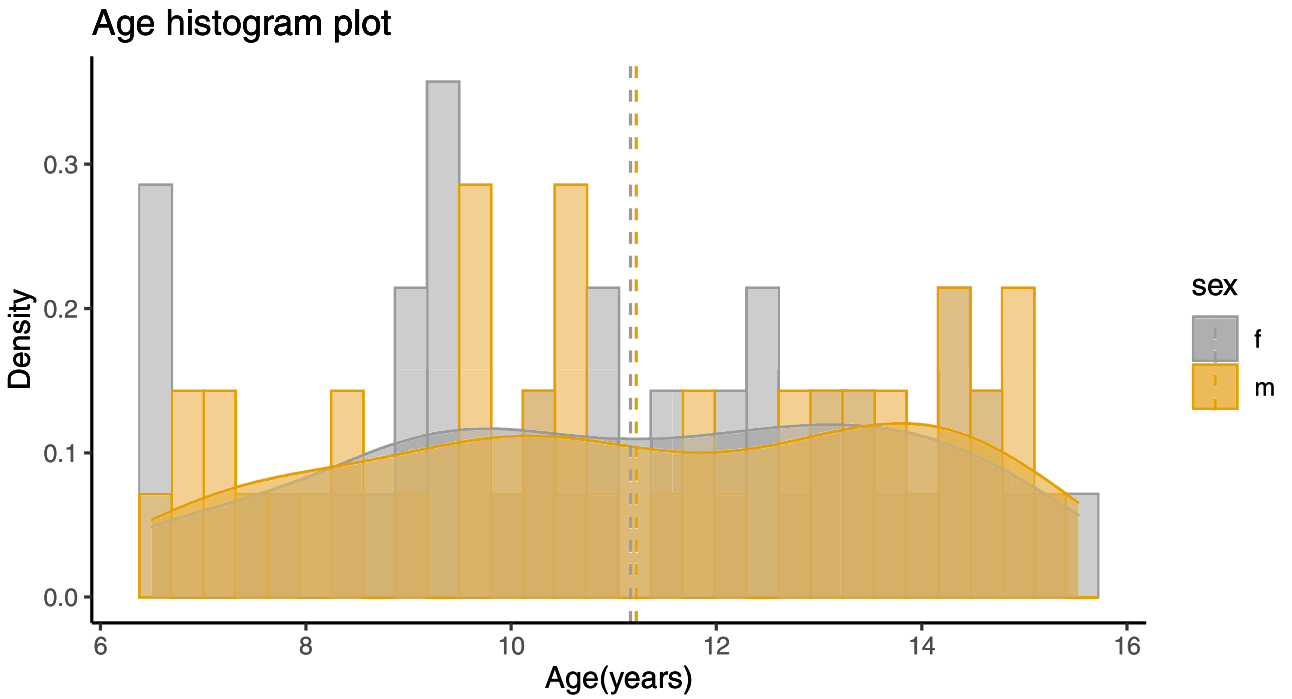

FIGURE A2: Distributions of age values within the studied sample of children (N=90); dashed verticals represent mean values for males and females.

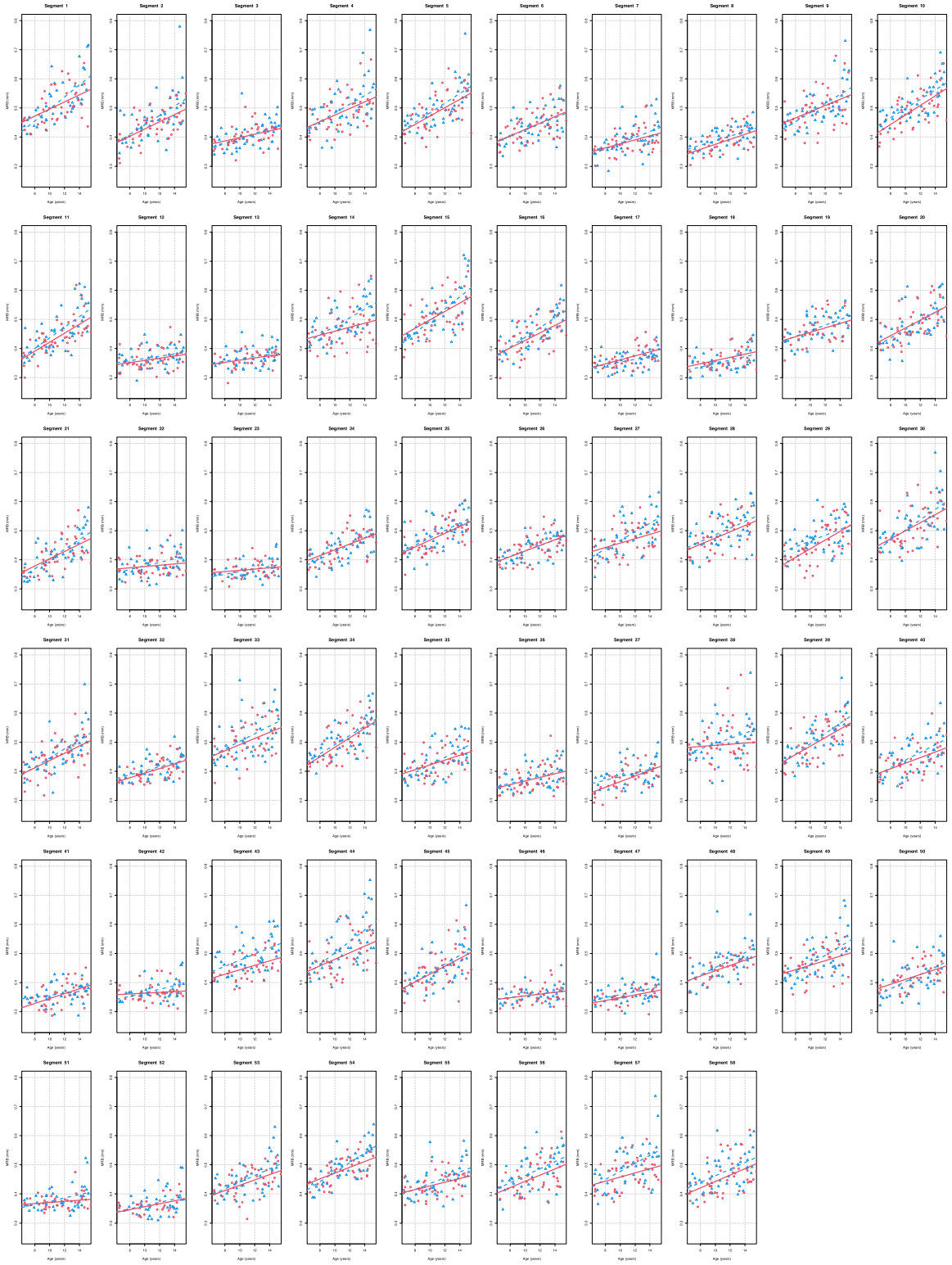

FIGURE A3: Relationships between MRB10 and age (red circles and red solid line – females, blue triangles and dashed lines – males) in all 58 segments separately.