DERMATOGLYPHIX

User Manual

Computer program for traditional and new dermatoglyphic analysis

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Dermatoglyphix 1.0

CONTENT

Software Dermatoglyphix 1.0 has been developed by Miroslav Králík, Ondřej Klíma and Lenka Polcerová. It is designed to enhance computer-aided manual/semiautomatic dermatoglyphic analysis of human fingerprints and palmprints.

1 ABOUT THE PROGRAM

Software Dermatoglyphix 1.0 was developed by Miroslav Králík, Ondřej Klíma and Lenka Polcerová. It is designed to enhance computer-aided manual/semiautomatic dermatoglyphic analysis of human fingerprints and palmprints. An update of the program is planned according to the users' feedback and other development in the field. The software was supported by the project *Elektronická forma cvičení z dermatoglyfiky* (MUNI/FR/1445/2016) *(Electronic Form of Practice Course in Dermatoglyphics)*.

2 INSTALLATION

2.1 System requirements

The program is available for 64-bit versions of Windows and Linux platforms. The program is distributed as a portable application, without requiring an installation. In case of Windows OS, version 7 or later is recommended. On Windows platform, a prerequisite installation of Redistributable Packages for Visual Studio 2013 is required. The appropriate installation file, `vcredist_x64.exe`, is publicly available at https://www.microsoft.com/en-us/download/details.aspx?id=40784

2.2 Running the program

Download ZIP archive (Dermatoglyphix.zip), extract the files and double click on the `Dermatoglyphix.exe` file in the `bin` folder. The main program window should appear (Fig. 1). The main window consists of a total of twelve fields. The first row is for fingerprints from left hand, the second row is for the right hand fingerprints. The last two fields are for fingerprints of the palms – each field is marked accordingly. Each field has three buttons assigned. The first button ⤶ serves for individual upload of a fingerprint image, the second button ✎ is used for editing the image, and the third button ✖ is used for canceling any changes made in the image.

3 LOADING IMPRINT IMAGE FILES

3.1 Files suitable for loading into the program

The program can read files in following formats: JPG, TIF, and PNG. It is assumed that these images represent digital scans of black fingerprints and handprints (in black ink) on white paper. They should be scanned with sufficient resolution (at least 600 ppi). These image files can be uploaded by main menu

options `File - Import image` and choosing between importing into all fields designated for the right hand, for the left hand or for both. Alternatively, user can import images into each field separately using Import file icon ⬇ below each field in the main window (mentioned in 2.2).

Provided the ink fingerprints on white paper were scanned in 100% size (1:1), the program can *calibrate size dimensions* automatically (see chapter 5.4) and transform measured distances into millimeters.
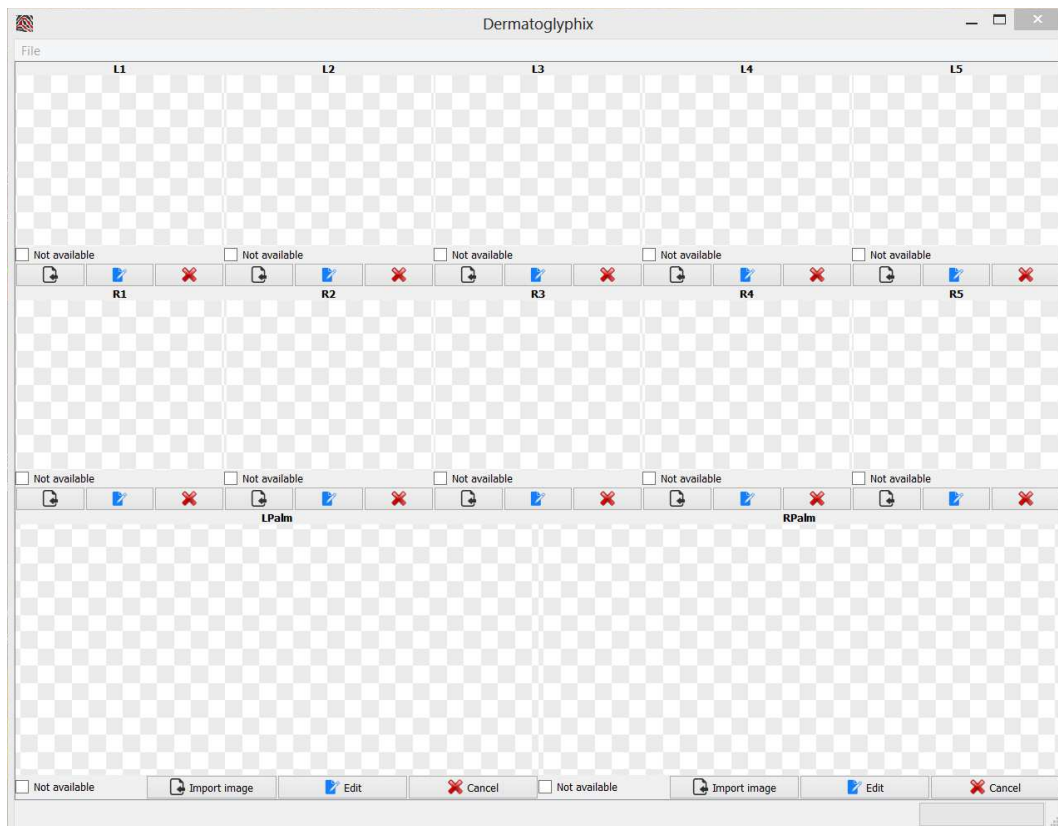
Figure 1 The main program window

3.2 Reloading incorrectly uploaded image

If pictures were uploaded incorrectly, you can either re-upload them

a) All via option `File - Import image` or,

b) Individually by means of an upload icon ⬇.

The originally/previously uploaded images are automatically overwritten and newly uploaded images can be further processed. Be careful, any changes made to the original images will be lost by this procedure.

We strongly recommend not using accents and spaces in the files names.

4 PROJECT SAVING

1.1. Storage format

After uploading all images, save project by menu option `File - Save as`. Storage format is XML which can also be opened in common text or table editors. Make sure you did not use accented characters or spaces in the name of the saved project and in

the file path (names of folders where the project is saved). Generally we recommend using ASCII encoding. After first saving, program will automatically save your data when editing an image – it is not necessary for the user to save data manually. Before closing the program, it opens a dialog asking you for saving or discarding last changes. For extra safety we recommend to use option `File - Save` after each row of images is edited.

5 PROCESSING FINGERPRINTS

5.1 Opening a fingerprint layout

To open editing window (Fig. 2), click on the Edit icon 🖉below the selected field. The editing window (called `Dermatoglyph Editing`) is composed of the central image (image uploaded previously) and left and right tool panels (menus). Expand the window to full screen and optimize the size of the loaded image by clicking on the button 🔍 Magnification.
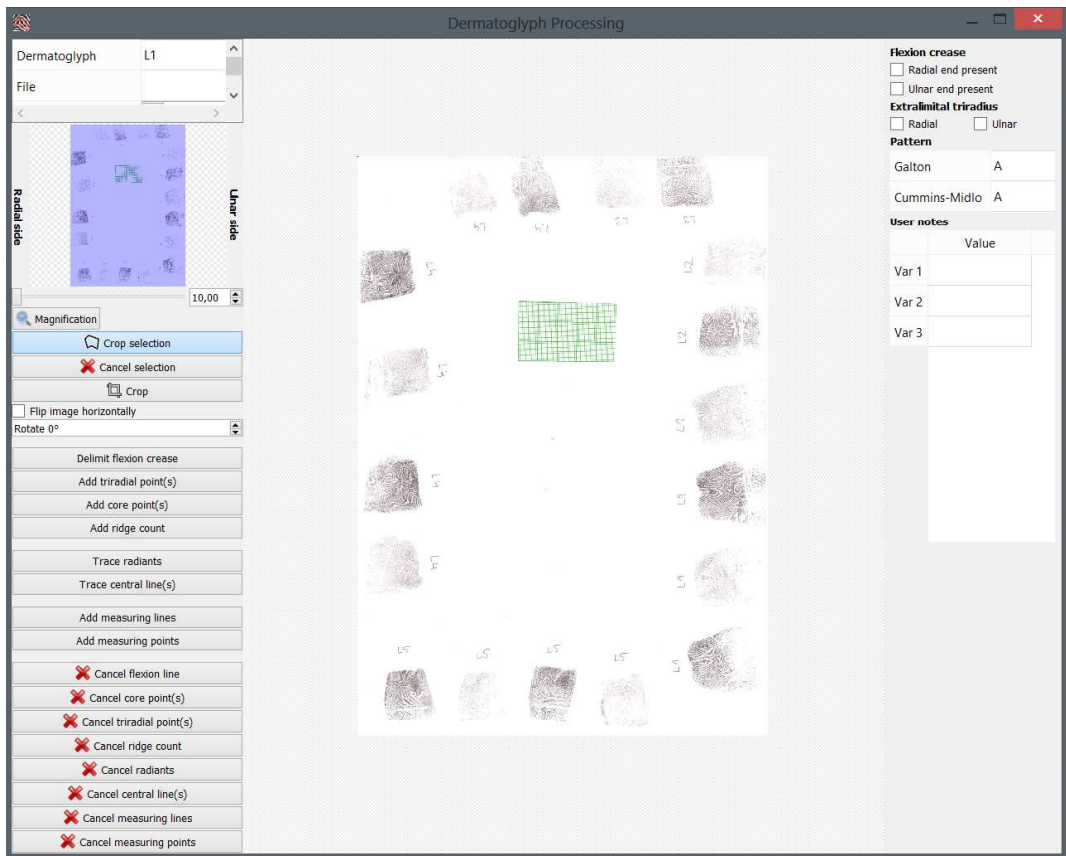
Figure 2 The editing window

5.2 Important processing note: before starting to process images

It should be stressed that in processing of images the user must start on the top of the left menu and proceed from the top to the bottom. It is very important for appropriate sequence/order of calibration, setting proximal border of analyzed region and fixing spatial positions and relationships of the measured points.

5.3 Indication of the file name and dermatoglyphic region

In the Edit window on the top of the left menu, first line/row indicates the dermatoglyphic region that is being edited:

L1 – left thumb;
L2 – left index finger;
L3 – left middle finger;
L4 – left ring finger;
L5 – left little finger;
R1 – right thumb;
R2 – right index finger;
R3 – right middle finger;
R4 – right ring finger;
R5 – right little finger;
LPalm – left palm;
RPalm – right palm.

The second line represents an indication of the filename you saved (where edited data are physically saved), which is the XML file.

5.4 Scale setting

Before measurement, calibrate the size of the measurement (scale). Next two lines in the left menu indicate horizontal and vertical resolution of the uploaded image in PPI. The program calibrates size dimensions automatically according to EXIF metadata, if they are available within the image file. Providing the dimensions of the imprints were scanned in real size (1:1 or 100%), all measured results will be automatically transformed to millimeters correctly. If the image source is not scanned in 100% (unknown source or the source is a photograph), the user can calibrate the size manually. Click on **Distance(mm)** in the upper part of the left menu, establish known real size in mm (e.g. 10), then press the button **calibrate** and click on two subsequent points on the image with the established distance (10 mm). The image will be correctly calibrated in millimeter units.

5.5 Magnifier

Next section of the left menu is magnification (with thumbnail of the image). At any time, the user can change magnification of the viewed part of the edited region which is important for appropriate visualizing of the studied features. By clicking on the button 🔍 **Magnification**, the view is optimized to the screen. By moving the horizontal slider the user can change the magnification that can also be done by positioning the cursor on the slider and scrolling with the scroll wheel. Visualized part is highlighted by a blue shadowed rectangle. The user can also move along the imprint simply by moving the rectangle by mouse along the image thumbnail.

5.6 Cropping

If the image does not represent the studied region only (e.g. all fingers imprint are in one image) the next step of the analysis should be cropping the proper region. Click on the icon *Select crop* ⬦, by the left mouse button select the wanted region of the imprint and click on the *Crop* icon ⬚. If the selection was not correct, the user can cancel the selection and select it again only before using Crop icon ⬚. If the user wants to change the selection after applying the *Crop* icon ⬚, it is necessary to close the editing window and upload the image again in the main window.

5.7 Flipping image

Since visual assessment of dermatoglyphic features can be affected by cognitive biases of the human vision system, right-left differences in the image stimuli should be removed. This is important especially for assessment of dermatoglyphic asymmetry (dermatoglyphic fluctuating asymmetry is a prenatal stress marker). It can be done (and must be done only in this particular step of the image processing) by clicking (yes ✓) on the *Flip image horizontally*. After using it the image converts to its precise mirror image. It should be done with all imprints from the left hand (L1–L5 and LPalm).

By convention that we introduced into the program, radial side (closer to the thumb side of a hand) of imprints is positioned on the left side of the screen and the ulnar side is on the right side of the screen. After flipping all the imprints from the left hand, all imprints will look like they are from the right hand and all imprints will have identical side orientation (radial on the left, ulnar on the right).

5.8 Rotate to the correct position

Final step of the image preparation is rotation of the image to its proper position. Rotation is set only in a clockwise direction. The user should rotate images so each is positioned with its proximal side on the bottom (and the distal side on the top) of the image. After rotation the image is prepared for the subsequent dermatoglyphic analyses.

After preparing all 12 dermatoglyphic regions (properly selected, appropriately cropped, flipped and rotated imprints; those from the left hand are flipped to a pseudo-right view so for each fingerprint and palmprint the radial side is on the left and the ulnar side is on the right side of the image) the user can proceed to the dermatoglyphic assessment.

6 DERMATOGLYPHIC ASSESSMENT OF FINGERPRINTS

Assessment of fingerprints and palm
prints represents a basic procedure of standard dermatoglyphic methodology, as defined by Galton (1892), Henry (1900), Cummins and Midlo (1961, pp 56–60), and Penrose (Penrose, 1968).

6.1 Delimiting of flexion crease

Since subsequent semiautomatic procedures rely on determination of radial-ulnar direction, the first step of dermatoglyphic assessment of dermatoglyphics on distal phalanges of fingers is delimiting of the flexion crease (distal interphalangeal flexion crease between middle and distal phalanx). For this reason it is strongly recommended to follow standard dermatoglyphic methodology (Cummins and Midlo, 1961) and imprint distal phalanges including the whole flexion crease and a part of the middle phalanx, and subsequently, to include this region into the selected region for the analysis. For delimiting flexion crease, click on the **Delimit flexion crease** and then outline the whole flexion region by entering points (simple click). The program highlights the region by blue color and computes an axis of the region (axis of the flexion crease; Fig. 3). The axis represents first principal component from Principal Component Analysis (PC1) of coordinates of all points on the outline of the flexion crease. The axe of the flexion region serves as a base line for several dermatoglyphic procedures, especially automatic assessment of the radial and ulnar side while determining pattern types.
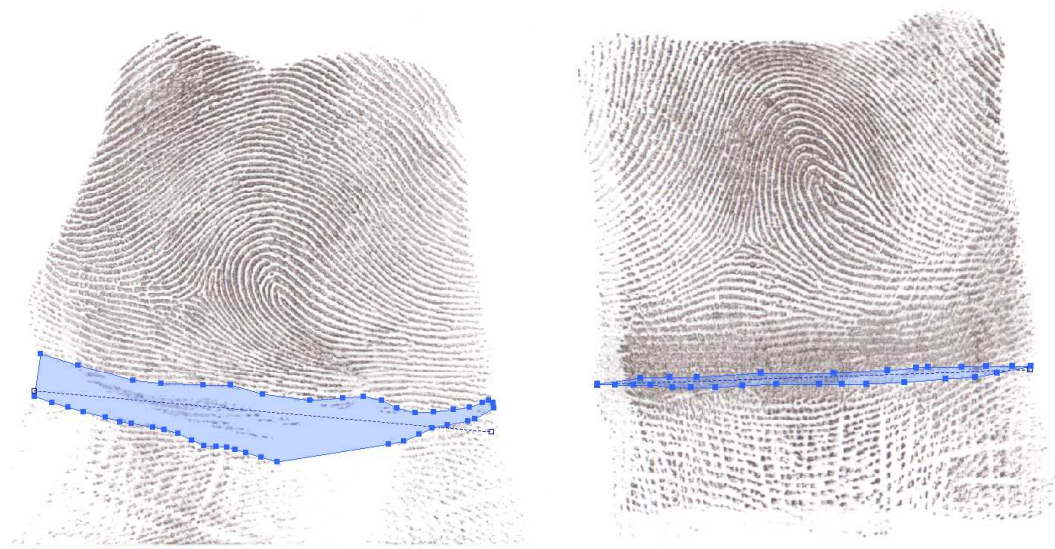
Figure 3 Examples of delimited flexion crease

6.2 Determination of triradial points

After delimiting flexion crease, next step is determination of triradial points. First, check the completeness of the imprint. If it is complete, find all triradia within the imprint. It is crucial because the number of triradial points determines the main pattern type. Select **Add triradial point(s)**, click to the appropriate position on the triradial point and choose **Add triradial point** by left button of a mouse. Triradial point is marked by a red triangle ▲ (Fig. 4). (Note: extralimital triradii are not marked in this step but their presence is recorded in the right tool panel.) Triradial points should be determined by means of standard dermatoglyphic methodology, as described in Cummins and Midlo (1961, pp 56–60). Triradial point is positioned in the middle of the triradial/delta region where

three independent systems of ridges meet. The triradial point can be positioned on the meeting point of three ridges, or on one ridge, or at the end of one ridge, or in the furrow (*sulcus superficialis*) between ridges. Precise position of the triradial point is important for ridge counting.

6.3 Determination of core points

In the next step, core point(s) should be determined. Core point is a point in the center (the innermost point) of the dermatoglyphic pattern around which ridges rotate. Usually, some ridges end/start in the core. The arrangement of the core ridges might be variable. If the number of ridges in the core is odd (1, 3, 5 etc.), the core point lies on the middle ridge, if the number of ridges in the core is even (2, 4, 6 etc.) the core point lies between the two central ridges (i.e. in the middle furrow). By a convention the core point is not placed in the end of the central ridge/furrow but approx. one papillary unit away from the end of the ridge/furrow (Cummins and Midlo, 1961, pp 59–60). Select **Add core point(s)**, click on the appropriate position of the core point and choose **Add core point** by left mouse button. Core point is marked by a yellow diamond ♦ (Fig. 4).

6.4 Ridge Count

"Ridge counting" means counting number of epidermal ridges which cross the line between two defined points in a dermatoglyphic pattern. On fingers it is usually the number of ridges between a triradial point and an adjacent core point. By a convention, ridges on the ends (core and triradial points) are not counted. When triradial points and core points are defined (in the previous steps) the program automatically connects relevant points by a violet line. To count ridges, select **Add ridge count**, click on the first ridge crossing the violet line (cursor changes to a simple cross) and click on the point by left mouse button. The position of the ridge will be marked by a yellow square with red borders. Continue in counting from triradial to core end of the line. Program will show the number of ridges in a red number nearby (Fig. 4).

In Dermatoglyphix, ridge count is also used for automatic pattern type assessment. If one core and one triradius is recorded (in previous steps) but no ridge count is recorded, the pattern is set as a tented arch (T). If one point is placed to the ridge count, the pattern type changes to a loop.

6.5 Tracing radiants

Ridge tracing represents a technique of tracking or following the course of a ridge from a defined point to another. In police fingerprinting, it is/was used for classifying whorls to more detailed categories. In dermatoglyphics, tracing radiants (the three ridges spreading from a triradial point) serves for determining a skeleton of a pattern and the whole shape of a pattern. Select **Trace radiants**, right-click on the position of a triradial point and select **Add radiant** by left mouse button. Then left-click a row of points along the selected ridge and trace it from the

triradial point to the border of the imprint (where the ridge ends). Do it for each of the three radiants (for each radiant right-click on the triradius) and for each triradius of the imprint. The traces will be marked by red squares with yellow borders and red dashed lines (Fig. 4). If a mistake is made while tracing radiants (e.g. a wrong position of a square), use an Esc key to erase squares to the point of the triradius (the beginning of the radiant)

6.6 Tracing central lines

Tracing central lines is used for determining radial or ulnar direction/end of the pattern in loops (radial loop R – has its tail on the radial side of the finger, ulnar loop L – on the ulnar side), determining direction of rotation in true whorls (concentric, clockwise, counterclockwise) and, most importantly, determining tail ends in double-loop patterns for pattern determination as defined by Cummins and Midlo (Cummins and Midlo, 1961, pp 60–70) – in double loop DL each loop ends on the opposite side of the finger, in lateral pocket LP both loops end on the same side of the finger. Select ***Trace central line(s)***, right-click on the position of a core point and select ***Add central line*** by left mouse button. Then click a row of points along the selected ridge and trace it from the core point to the border of the imprint (where the ridge ends). Do it for each of the cores of the imprint. The traces will be marked by brown squares with yellow borders and brown dashed lines. If a mistake is made while tracing a central line (e.g. a wrong position of a square), use an Esc key to erase squares to the point of the core point (the beginning of the central line).
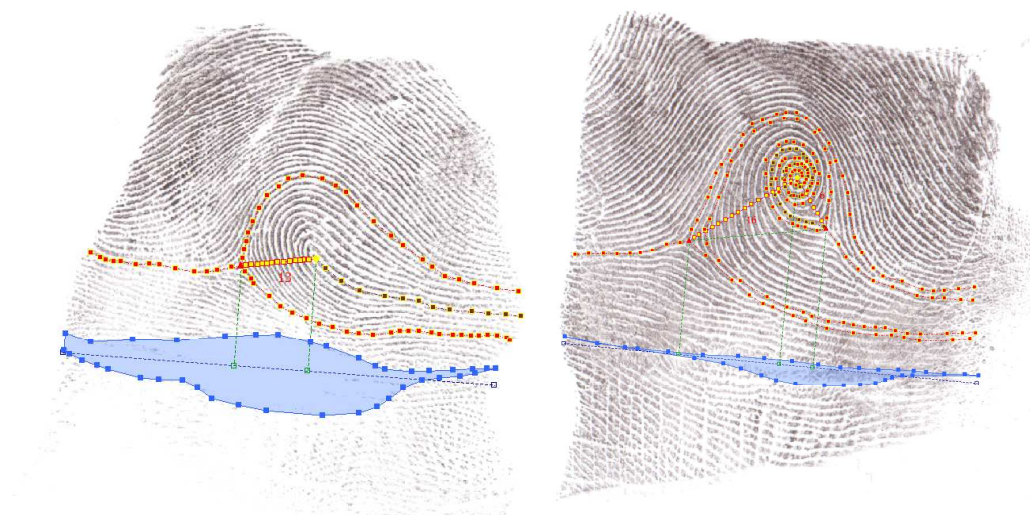
Figure 4 Example of triradial points, core points, ridge count and tracing radiants and central lines

6.7 Ridge breadth measurements

Epidermal ridge breadth represents the distance between the center of a furrow delimiting the ridge in its one side to the center of a furrow on its opposite side measured perpendicularly to the direction of the ridge. Generally, ridge breadth (or density of ridges) is determined as an average value from number of ridges crossed by a segment of a known length. The original method by Schlaginhaufen (1905) used segment of 1 cm length. The method introduced into ***Dermatoglyphix*** allows to use an arbitrary number of segments with any lengths. First, select **Add measuring lines**, place cursor into the middle of one furrow (the white line between two ridges), left-click and select **Add measuring vertex**. Cross several lines and again left-click and select **Add measuring vertex**. After adding the second vertex (orange squares), the segment is marked by a violet dashed line. Then, select **Add measuring points** and mark the midpoints (yellow squares with red borders) of remaining furrows into the segment. Counter nearby the segment presents the number of segments (here: ridges) into which the whole segment is divided (Fig. 5). When exporting the results, the program will export breadths of each individual epidermal ridge measured, while origins of ridges in different segments, as well as order of ridges in each segment will be recoded and saved too.
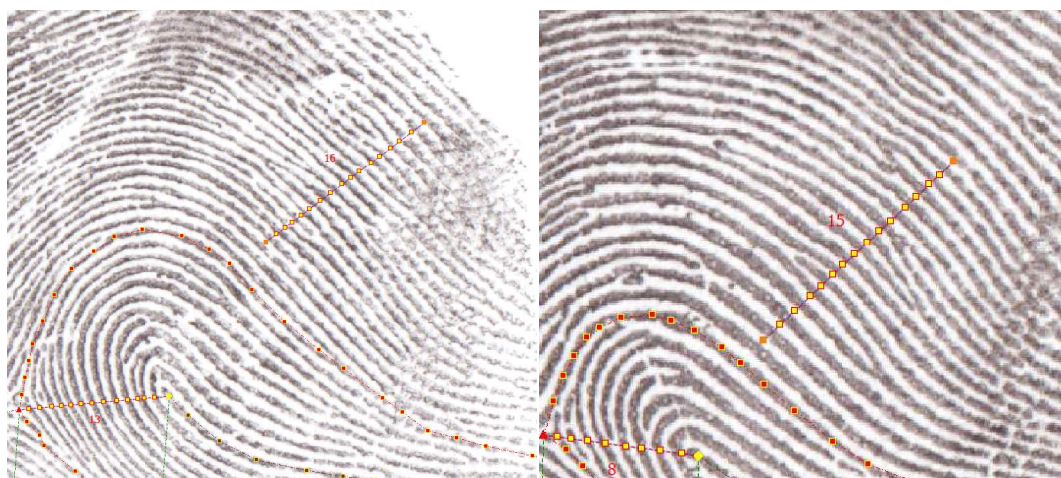
Figure 5 Example of ridge breadth measurements

6.8 Right tool panel menu/right menu

On the top, by clicking (yes ✓) the user records the presence of a border of a flexion crease: **Radial end present** and **Ulnar end present**. If both ulnar and radial side of the interphalangeal flexion crease are present, a rolled fingerprint is regarded as complete.

The next option represents manual recording of presence (yes ✓) of extralimital triradii on radial or ulnar side (or both): **Radial** and **Ulnar**. In the rare cases where no intralimital/present triradii are recorded but the pattern is evidently a whorl, the program cannot automatically assess the pattern type correctly. Without

recording any triradius the pattern is set as an Arch. After manually recording extralimital triradii the assessment of the pattern type is corrected to a loop (with one extralimital triradius) or a whorl (with two extralimital triradii).

Next menu represents recording of pattern assessment which is specific for different pattern types. For loops it is *Central Line Termination* which records the side of the end of the central line: *ulnar side* or *radial side*. For whorls it is *Central line rotation* and *Central Line Termination. Central line rotation* can be divided (by Bhanu (1975)) into *clockwise*, *counterclockwise* and *concentric* for *Inner* (i.e. near core) and *Outer* (distant from core but still inside the patter area) part of the pattern. *Central Line Termination* records the side of the end of the central line: *ulnar side* or *radial side*. For double loop patterns (patterns with two triradii and two cores) it is *Central line rotation* and *Central Line Termination. Central line rotation* can be divided into: *clockwise* and *counterclockwise*, and it is (by definition) identical for both loops. *Central Line Termination* records the side of end of the central line coming from *Radial core* and *Ulnar core* and can be divided into: *ulnar side* or *radial side*. This assessment is a criterion for dividing between double loop DL (terminations in opposite sides) and lateral pocket LP (both terminations on the same side) pattern types.

At the bottom of the right menu results of pattern classification (*Pattern*) are visualized in typologies by Galton (1892) – A, L, W, and Cummins and Midlo (1961) – A, T, U, R, W(s,c), CP, DL, LP, Acc). Make sure that at least determination of cores, triradii, ridge count and central line termination in each of the ten fingerprints are recorded. Finalizing of these procedures is important for automatic pattern assessment. If the user, for instance, forgets to assess the ridge count in case of a loop, the program will classify the pattern as a tented arch (T) since this is the pattern with one core, one triradius and zero ridge count. Another example: if the user does not evaluate central lines terminations in case of a double loop, the program will not be able to differentiate between a double loop and a lateral pocket (both with two cores and two triradii).

7 ANALYSIS OF PALMPRINTS

Assessment of palmprints and their measurement is similar to the previously described assessment of fingerprints. Similarly to fingerprints, the assessment of palmprints should start from top in the left menu and continue to the bottom, than continue with the right menu. Contrary to fingerprints, the presence, the nature and the combinations of triradii, cores and patterns are more complex and, correspondingly, so is the dermatoglyphic assessment of palmprints.

7.1 Processing of images

Manipulating with images of palmprints is almost identical as with fingerprints. First, the user should make a crop selection ⬠ and then crop ⬒ an appropriate region of the image with the whole palm imprint (with the option to cancel the selection). After cropping the picture (similarly to fingerprints), flip the left palm image to its mirrored form and rotate it to the appropriate position (distal direction above, proximal direction below).

For scale setting, rotation and options of magnifying the picture see chapters 5.4., 5.8., and 5.5.

7.2 Determination of triradial points

Check the completeness of the palm print. If it is complete, find all triradia within the imprint. Then click on the **Add triradial point(s)**, find the position of a triradial point (Cummins and Midlo, 1961, pp 85–87), left-click and open menu of a possible triradius, and select one option from the list:

Add triradius a – standard palm triradius a (digital triradius a), localized approx. in the axis of the 2nd finger

Add triradius b – standard palm triradius b (digital triradius b), localized approx. in the axis of the 3rd finger

Add triradius c – standard palm triradius c (digital triradius c), localized approx. in the axis of the 4th finger

Add triradius d – standard palm triradius d (digital triradius d), localized approx. in the axis of the 5th finger

Add triradius t – standard palm triradius t (carpal or axial triradius t)

Add triradius cd – one fused triradius somewhere in the position between space for triradii c and d

Add triradius a1 – accessory digital triradius $a´$, localized near the triradius a

Add triradius b1 – accessory digital triradius $b´$, localized near the triradius b

Add triradius c1 – accessory digital triradius $c´$, localized near the triradius c

Add triradius d1 – accessory digital triradius $d´$, localized near the triradius d

Add triradius tb – borderline triradius in the hypothenar area, usually related to a hypothenar pattern

Add triradius t1 – axial palmar triradius $t´$, localized between position of the triradius t and $t´´$

Add triradius t2 – axial palmar triradius $t´´$, localized approximately in the center of the palm

Add triradius t3 – axial palmar triradius *t´´´*, localized even more distally than triradius *t´´*

Add triradius o1 – another palmar triradius, triradius additional to the triradii specified above

Add triradius o2 – another palmar triradius, triradius additional to the triradii specified above

Add triradius o3 – another palmar triradius, triradius additional to the triradii specified above

Each triradial point is marked by a red triangle ▲ (Fig. 6). (Note: extralimital triradii are not marked in this step but their presence is recorded in the right menu.)

7.3 Determination of core points

In the next step, core point(s) of the patterns (loops or whorls) on the palm should be determined. Location of a core point in a core of a pattern should be determined by the same rules as for fingers. A core point is marked by a yellow diamond ♦ (Fig. 6).

7.4 Ridge counting

As before, the program offers ridge counting. In case of a palmprint, it is the ridge count between two standard triradii, most often between digital triradius *a* and digital triradius *b* – so called *a-b ridge count*. The program also allows counting of ridges between standard triradii ***b*** and ***c***, ***c*** and ***d,*** and ***d*** and ***t***. In case of a joint ***cd*** triradius it is possible to count ridges between ***b*** and ***cd***, and ***cd*** and ***t***.

When counting ridges, the user chooses a button ***Add ridge count*** from left menu and, similarly to assessing fingerprints, by right mouse button counts ridges which the program marks as yellow squares with red border.

Note: when the presence of ***a***, ***t*** and ***d*** triradii is recorded, the program automatically calculates the ***atd*** angle which is shown in right column.

7.5 Tracing main lines

Next option is tracing main lines which are, in fact, radiants of palmar triradii (more precisely: proximal radiants of the riradii ***a***, ***b***, ***c***, ***d***, and a distal radiant of the triradius ***t***). The user can do this by clicking on the button ***Add radiants*** and again, similarly to assessing fingerprints, by right-clicking on the selected triradii and from shown small drop-down menu choosing ***Add radiants*** option (Fig. 6). In case the user wishes to cancel a particular radiant, there is the ***Delete radiants*** option. In case the user wants to cancel all created radiants, there is the ***Cancel radiants*** option in the left column.

7.6 Termination of main lines

Based on tracing main lines (chapter 7.5), the user can mark the end of a particular main line in the right column according to the Penrose (1968) methodology. The

program offers options: `1, 2, 3, 4, 5, 5', 5'', 6, 7, 8, 9, 10, 11, 12, 13, 13', 13''`, and includes also option `0` for missing triradii (most often triradius c) and `X` for abortive lines. The program will automatically add user´s selection to the palm formula (right column, field ***Summary***).

7.7 Axial triradii

Below the field `Termination of Main Lines` there is the `Axial triradii` field in the right column, where the user can indicate the presence of an axial triradius `t`, `t1`, `t2`, `t3`, `tb`, where `t1` represents, according to the Penrose methodology (1968), triradius `t '`, `t2` triradius `t "`, `t3` triradius `t '''`, and `tb` represents the marginal triradius (Fig. 6).

7.8 Palm patterns

The program then allows the user to mark palm patterns based on the Penrose (1968) methodology, separately for each palm area (Fig. 6):

Hypothenar 1: in the first drop-down menu the option `predefined` is selected by default, but it is possible to choose option `custom` or `not available`. In the second drop-down menu the user can select individual patterns: `Au`, `Ar`, `Ac`, `Tu`, `Tr`, `Tc`, `Lu`, `Lr`, `Lc`, `W`, `Ws` or `Wd`, but only if option `predefined` in first drop-down menu is selected. If option `custom` is selected, the user can write custom statement in the white box next to the second drop-down menu. Similarly to `Termination of Main Lines` and `Axial triradii` fields, selected options are immediately and automatically added to palm formula.

Hypothenar 2: in the first drop-down menu the option `not available` is selected by default, but this can be changed by the user the same way as with Hypothenar 1.

Thenar 1: in the first drop-down menu the option `predefined` is selected by default, but it is possible to choose the option `custom` or `not available` similarly to previous palm patterns. In second drop-down menu the user can select individual patterns: `O`, `V`, `Lu`, `Lr` or `W`, but only if option `predefined` in first drop-down menu is selected. If option `custom` is selected, the user can write custom statement in the white box next to the second drop-down menu.

Thenar 2: in the first drop-down menu the option `not available` is selected by default, but this can be changed by the user the same way as with Thenar 1.

I1, I2, I3, I4: in the first drop-down menu the option `predefined` is selected by default, but it is possible to choose the option `custom` or `not available` similarly to previous palm patterns. In the second drop-down menu the user can select individual patterns: `Ld`, `D`, `d`, `L`, `l`, `W`, `O`, `V`, `M`, but only if option `predefined` in first drop-down menu is selected. If option `custom` is selected, the user can write custom statement in the white box next to the second drop-down menu.
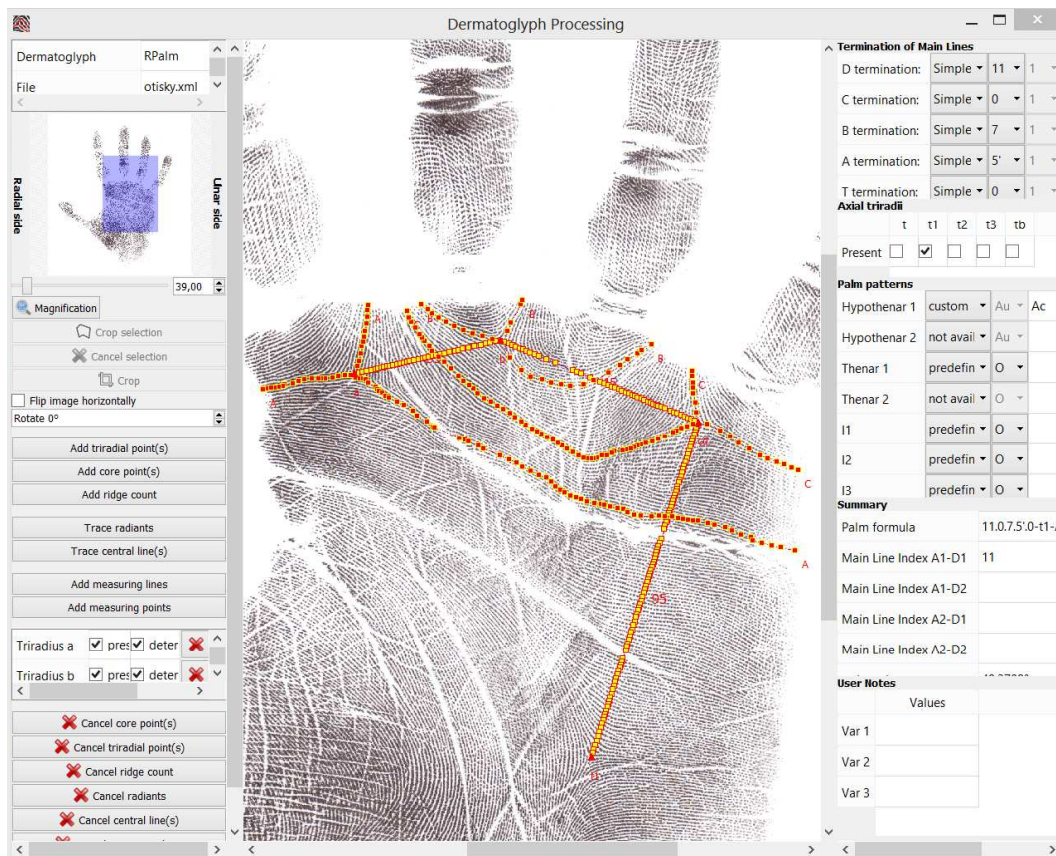
Figure 6 Example of analyzed palm print

7.9 Summary

The `Summary` field represents automatically generated values: `Palm formula`, `MLI` and `atd-angle` based on the previously user-selected parameters.

7.10 User Notes

The last field in the right column represents the option for the user to add notes of his or her choice to three boxes marked `Var 1`, `Var 2` and `Var 2` in column `Values`.

8 DATA EXPORT

Data export is possible by main menu option `File - Export`. This option will save recorded data (i.e. values of the dermatoglyphic features after their assessment as described above) in a csv file. The user can choose from two options of export:

1) `Export patterns` – exports information from the saved `xml` file (the name of the `xml` file is also included in an exported `csv` table). Individually for each fingerprint (which are distinguished by a proper label in front of these variables: `L1 – L5` and `R1 – R5`) following data are exported:

`Avail` – availability of fingerprint (where `1` means available and `0` not available)

`Image` – name of the image that was processed

`Res_w` – resolution width

`Res_h` – resolution height

`nc` – number of cores

`nt` – number of triradii

`trp` – number of radial triradii present

`tup` – number of ulnar triradii present

`RCr` – radial ridge count

`RCu` – ulnar ridge count

`CM.pat` – pattern identification based on the Cummins and Midlo (1961) definition

`G.pat` – pattern identification based on the Galton (1892) definition

`var1` – `var3` – for user's notes

Additionally, the following calculations are also exported:

`AFRC` – absolute finger ridge count

`AFRC.r` – absolute finger ridge count for the right hand

`AFRC.l` – absolute finger ridge count for the left hand

`TFRC` – total finger ridge count

`TFRC.r` – total finger ridge count for the right hand

`TFRC.l` – total finger ridge count for the left hand

`PII` – Pattern Intensity Index

`PII.r` – Pattern Intensity Index for the right hand

`PII.l` – Pattern Intensity Index for the left hand

Moreover, for both hands (where hands are distinguished by an additional letter `r` – for right hand or `l` – for left hand at the end of the particular value):

presence of triradii (`a, b, c, d, t, cd, a1, b1, c1, d1, tb, t1, t2, t3, o1, o2, o3`) where `1` means present and `0` not present

termination of a main line (`A, B, C, D, T`) – based on `type` (if it is not selected, type `NA` values are present)

`MLI` – Main Line Index

`Hy1, Hy2` – patterns on hypothenar

`Th1, Th2` – patterns on thenar

`I1` – `I4` – patterns on interdigital areas

`p.formula` – palm formula

`atd.angle` – atd-angle

`var1` – `var3` – for user's notes

`ab.RC, bc.RC, cd.RC, dt.RC` – ridge counts between present triradii

2) `Export ridge breadths` – exports breadths of each individual epidermal ridge that was measured by the user (6.7). In the xml file the name, the label for the measured finger, the number of the line and the ridge are also presented.

9 REFERENCES

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