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Fingerprints and the Diagnosis of Zygosity in Twins *

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I. Design of the Work

I.1. Introduction

Bibliographic references, aim, material and methods of the present study, as well as the methodology especially worked out for the qualitative analysis, have already been largely described in a previous introductory note (Parisi and Di Bacco, 1967). A few minor variations having been introduced, and for the sake of completeness, essential data shall be now referred to again, before describing and discussing the results.

This research was designed with two complementary aims:

a) To apply the twin method to the study of the hereditary behaviour of digital dermatoglyphic traits, both at the qualitative and quantitative level;

b) To apply the results thus obtained to work out a method for discriminating MZ and DZ twins by means of fingerprints.

I.2. Material and Methods

A sample of 100, apparently healthy, same-sexed twin pairs, only selected as to sex combination and zygosity (25 ♂ + 25 ♀ MZ, and 25 ♂ + 25 ♀ DZ), was drawn from the Mendel Institute's large twin file and fingerprinted.

Zygosity was determined on account of the following data (cf recommendations of the WHO report on the methodology of twin studies, 1966, and Hauge et al, 1968): (*a*) number of choria; (*b*) ABO, MN and Rh blood groups; (*c*) eye and hair colour, according to the apposite anthropological scales; (*d*) information about the twins ever having been mixed up by parents, friends or relatives; (*e*) subjective judgements on the basis of the twins' general aspect, direct medical examination, anamnestic data etc.

Fingerprints were examined with respect to both qualitative and quantitative

* With an Appendix on Automatic Procedure by M. Umani.

Tab. I. Standardized procedure for the collection of data: pattern/ridge count

(Dx = right; Sn = left; 1a and 2a nata = 1st and 2nd born)

5736: F. ANTONINA E PAOLA - MZ

	DX						SN						DX + SN
	I	II	III	IV	V	RFRC	I	II	III	IV	V	LFRC	TFRC
1a nata	W/21	Lu/15	Lu/13	Lu/5	Lu/6	60	S/23	Lu/10	Lu/5	Lu/5	Lu/7	50	110
2a nata	Lu/20	Lu/11	Lu/10	Lu/12	Lu/9	62	Lu/18	Lu/10	Lu/11	Lu/10	A/0	49	111

traits (cf Tab. I), i.e. to the five fundamental papillary patterns [W = whorl; Lu = ulnar loop; Lr = radial loop; S = twin loops (S figure); A = arch], and to ridge counts, both single for each finger and cumulative for one or both hands (RFRC = right finger ridge count; LFRC = left finger ridge count; TFRC = = total finger ridge count).

II. Methodology of the Analysis

II.1. Qualitative analysis

A judgement on the similarities existing for each finger between cotwins' papillary patterns will be based upon the probability of obtaining *at random and conditional upon the distribution of the five papillary patterns observed in the sample* a number of concordances (namely, of coinciding patterns between cotwins' corresponding fingers) not lesser than the number observed in the sample.

The calculation of this probability is not easily done: it may however be summed up as follows.

Let us order the five papillary patterns arbitrarily. Let then ${}_{D}Z_{i}$ ($i = 1; \ldots; 5$) be the aggregate number of the i^{th} type observed on the D finger in the two members of the n twin pairs observed. Let also ${}_{D}f_{ii}$ be the number of pairs in which the finger D of both members has the pattern i, and ${}_{D}f_{ij}$ the number of pairs in which one of the two members has the pattern i on his finger D while the other has the pattern j ($j = 2; \ldots; 5$. In general, $j > i$).

The observed sample of n pairs may be represented by a sample configuration which is a vector formed by fifteen non-negative integer numbers:

$$[1.1] \qquad {}_{D}F_{r} \equiv ({}_{D}f_{11}; \ldots; {}_{D}f_{55}; \quad {}_{D}f_{12}; \ldots; {}_{D}f_{15}; \ldots; \quad {}_{D}f_{34}; {}_{D}f_{35}; \quad {}_{D}f_{45})$$

and the number of observed concordances is ${}_{D}r = \Sigma_{i}{}_{D}f_{ii}$.

In the previous, already cited, introductory note, it has been shown that the probability

$$P_{r}\{{}_{D}F_{r} \mid {}_{D}Z_{1}; \ldots; {}_{D}Z_{5}\}$$

to obtain the sampling configuration at random, is:

$$[1.2] \qquad P_r\{{}_DF_r \mid {}_DZ_1;\ \ldots;\ {}_DZ_5\} = \frac{n!}{\prod\limits_{i\leq j} {}_Df_{ij}!} \cdot \frac{\prod\limits_{i=1}^{5} {}_DZ_i!}{(2n)!}\, 2^{n-{}_Dr}.$$

However, [1.2] *is not* the probability of obtaining ${}_Dr$ concordances at random, conditional upon the frequencies. This may be obtained, instead, by setting up all the sampling configurations that may be obtained from [1.1] by causing ${}_Df_{ii}$ and ${}_Df_{ij}$ to vary in the class of non-negative integer numbers under the conditions:

$$[1.3] \qquad \begin{cases} \sum\limits_{i=1}^{5} {}_Df_{ii} = {}_Dr \\ 2\,{}_Df_{ii} + \sum\limits_{j=2}^{5} {}_Df_{ij} = {}_DZ_i. \end{cases}$$

The probability of each such configurations may be calculated by means of [1.2]. Then,

$$[1.4] \qquad P_r\{{}_Dr \mid {}_DZ_1;\ \ldots;\ {}_DZ_5\} = \Sigma\, P_r\{{}_DF_r \mid {}_DZ_1;\ \ldots;\ {}_DZ_5\}$$

(being the summations extended to all the configurations obtained under the conditions [1.3]) is actually the probability required.

Finally, if also the probability values under [1.4] are calculated for all possible values of r greater than ${}_Dr$ (on putting r instead of ${}_Dr$ in [1.3] and [1.4]), then:

$$[1.5] \qquad P_r\{r \geq {}_Dr \mid {}_DZ_1;\ \ldots;\ {}_DZ_5\} = \sum_{r={}_Dr}^{{}_DR} P_r\{r \mid {}_DZ_1;\ \ldots;\ {}_DZ_5\},$$

where ${}_DR = \sum\limits_{i=1}^{5} {}_DS_i$, with ${}_DS_i = \frac{{}_DZ_i}{2}$ or ${}_DS_i = \frac{{}_DZ_i - 1}{2}$, according to ${}_DZ_i$ being even or odd.

The [1.5] is the required probability of obtaining at random a number of concordances greater than, or equal to, that observed on the D finger, conditional upon the frequencies ${}_DZ_1;\ \ldots;\ {}_DZ_5$ of the five types of patterns referring to the D finger.

The difficulty of this procedure lies in the constructions of configurations similar to [1.1] under the conditions [1.3]. A method which makes this construction possible has already been explained (Parisi and Di Bacco, 1967: II.2), while in the Appendix to the present work details of the Fortran program are given. By employing this method it was possible to entrust to a 7044/K32 IBM computer the search for the sampling configurations. Having fixed the critical value 0.01 of the probability

https://doi.org/10.1017/S1120962300012750 Published online by Cambridge University Press

of an error of the first kind, it may be said that there is a similarity with respect to the finger D between the twins, if the probability $P_r \{r \geq {}_Dr | {}_DZ_1; \ldots; {}_DZ_5\}$ calculated by means of [1.5] is lesser than, or equal to, 0.01. If the probability is greater than 0.01, the hypothesis is rejected.

The results of this test are shown in Tab. II, together with a synthetical judgement on the hypothesis of similarity, i.e.: " + " if it is true, " — " if it is false.

Since sex did not appear to play any relevant role, the same analysis has been carried out on the two samples of 50 MZ and 50 DZ twin pairs, irrespective of sex (third section of the table). The results of this analysis by zygosity only are quite similar to those by sex and zygosity, except that for finger II only the upper or lower probability limits are given, instead of the precise probability value [1.5]. Actually, as explained in the Appendix, an accurate computation of these four values would have required an enormous load of work, practically unnecessary for the purposes of our conclusion: in fact, also in this particular case the preassigned probability value of an error of the first kind is 0.01.

II.2. Quantitative Analysis

Cumulative ridge counts, i.e. RFRC, LFRC and TFRC values, have been considered, and their correlations estimated in the four types of twin pairs (MZ ♂, MZ ♀, DZ ♂ and DZ ♀) by computing, for each sample and for each count, the intra-class correlation coefficient. The twelve values of the latter are shown in the upper part of Tab. III. Their general coefficient will be indicated as r_{ijt} ($i \equiv$ MZ, DZ; $j \equiv$ ♂, ♀; $t \equiv$ R for RFRC, L for LFRC, T for TFRC), which is an unbiased and consistent estimator of the " true " coefficient of intra-class correlation, ρ_{ijt}.

We may reasonably assume that the bivariate random variable associated with the sample values of RFRC, LFRC and TFRC in twin pairs is fairly well approximate to a bivariate normal distribution. It is then possible to set up also a confidence interval for the coefficient ρ_{ijt}.

In fact, if $1 - \alpha$, where $0 < \alpha < 1$, is the confidence coefficient, the upper [lower] confidence limits for the coefficient of correlation are*:

$$[2.1] \qquad \operatorname{tngh}\left\{\operatorname{tngh}^{-1} r_{ijt} + \frac{\lambda}{n - \frac{3}{2}}\right\} \left[\operatorname{tngh}\left\{\operatorname{tngh}^{-1} r_{ijt} - \frac{\lambda}{n - \frac{3}{2}}\right\}\right],$$

* The justification for [2.1] lies in the following property: if the parent-population, from which the sample is obtained, is bivariate-normally distributed, then the transformation $Z_{ijt} = \operatorname{tngh}^{-1} r_{ijt}$ is asymptotically normally distributed with mean $= \operatorname{tngh}^{-1} \rho_{ijt}$ and variance $= \frac{1}{N - 3/2}$ (cf Fischer, 1921).

where n is the number of pairs making up the sample (i.e. 25) and λ is the root of the equation $G(-x) = \frac{\alpha}{2}$ if $G(x)$ is the distribution function of the normal random variable with mean 0 and variance 1.

By choosing $1 - \alpha = 0.95$, hence $\lambda = 1.96$, we obtain the twelve confidence intervals at 95% level. They are shown in the lower part of Tab. III.

The following questions have then been examined:

(*A*) Is the coefficient of intra-class correlation higher in MZ than in DZ twin pairs?

(*B*) Is the coefficient of intra-class correlation significantly different in ♂ and ♀ twin pairs?

(*C*) Is there any significant interaction between sex and zygosity for the characteristics under consideration? In other words, are sexual differences significantly diverse according to the pairs being MZ or DZ? Or, conversely: are differences due to zygosity significantly diverse according to the pairs being ♂ or ♀?

Answers to these questions have been provided (only with respect to the TFRC, because of its wider use and probably more limited random variability, as the general cumulative value) by applying the comparative orthogonal design to the two "factors", zygosity and sex, each having two "levels": MZ; DZ, and ♂; ♀ respectively.

In our particular case, once selected the value of the probability of an error of the first kind, tests * have to be set up in order to verify the three hypotheses:

[2.2]
$$u_A = \frac{(Z_{MZ,\sigma,T} + Z_{MZ,\varphi,T}) - (Z_{DZ,\sigma,T} + Z_{DZ,\varphi,T})}{\sqrt{\frac{4}{23 \cdot 5}}}$$

$$u_B = \frac{|(Z_{MZ,\sigma,T} + Z_{DZ,\sigma,T}) - (Z_{MZ,\varphi,T} + Z_{DZ,\varphi,T})|}{\sqrt{\frac{4}{23 \cdot 5}}}$$

$$u_C = \frac{|(Z_{MZ,\sigma,T} - Z_{MZ,\varphi,T}) - (Z_{DZ,\sigma,T} - Z_{DZ,\varphi,T})|}{\sqrt{\frac{4}{23 \cdot 5}}}$$

where $Z_{ijt} = \text{tngh}^{-1} r_{ijt}$.

The three questions, A; B; C, will be given positive answers, respectively if $u_A \geq -\lambda(\alpha)$; $u_B \geq -\lambda\left(\frac{\alpha}{2}\right)$; $u_C \geq -\lambda\left(\frac{\alpha}{2}\right)$.

* The justification for the three tests here applied is given in detail by Naddeo (1960).

Since $-\lambda(\alpha)$ and $-\lambda\left(\frac{\alpha}{2}\right)$ are the roots of the two equations, respectively $G(x) = \alpha$ and $G(x) = \frac{\alpha}{2}$ [where $G(x)$ is the distribution function of the normal random variable with mean 0 and variance 1], if we choose $\alpha = 0.05$ we have $-\lambda\left(\frac{\alpha}{2}\right) = 1.96$ and $-\lambda(\alpha) = 1.649$.

The following values are thus obtained*:

$$u_A = 8.3438;\ u_B = 0.4023;\ u_C = 1.0427.$$

Our conclusion will therefore be that the TFRC correlation is significantly higher in MZ than in DZ pairs. On the other hand, sex does not seem to play any relevant role, nor does it appear to exist any interaction between sex and zygosity.

On the basis of these latter two results, sexes have been pulled within zygosities, and sample intraclass correlation coefficients, and respective confidence intervals (with $1 - \alpha = 0.95$), have been estimated for MZ and DZ twin pairs, irrespective of sex (cf Tab. IV).

Correlation values were then estimated for each finger. Sex having already been shown not to play any relevant role, the analysis was directly carried out on the two samples of 50 MZ and 50 DZ twin pairs, irrespective of sex. The results are shown in Tab. V.

Although, because of methodological problems, the previously described test could not be applied in this case, correlation values for single fingers appear to be much higher in MZ than in DZ twin pairs, and altogether similar to those obtained for cumulative values.

* The values of u_A; u_B; u_C; are based on the following valus of Z_{ijt}:

$$Z_{MZ\,♂\,T} = \text{tngh}^{-1}(0.988) = 2.555$$
$$Z_{MZ\,♀\,T} = \text{tngh}^{-1}(0.983) = 2.3796$$
$$Z_{DZ\,♂\,T} = \text{tngh}^{-1}(0.381) = 0.4013$$
$$Z_{DZ\,♀\,T} = \text{tngh}^{-1}(0.633) = 0.7465$$

III. Results

III.1. Qualitative analysis

The results of the qualitative analysis are summarized into the six sections of Tab. II, the upper three being referred to the MZ sample and the lower three to the DZ one.

Tab. II. Qualitative analysis

	Finger	♂			♀			♂ + ♀		
		N. of concordances	Probability	Judgement	N. of concordances	Probability	Judgement	N. of concordances	Probability	Judgement
					a. MZ sample					
RIGHT	I	13	0.00876	+	17	0.00164	+	30	0.00004	+
	II	10	0.14430	—	16	0.00010	+	26	<0.01*	+
	III	18	0.00003	+	22	0.00004	+	40	0.00000	+
	IV	19	0.00002	+	20	0.00001	+	39	0.00000	+
	V	20	0.00053	+	21	0.00112	+	41	0.00000	+
LEFT	I	14	0.00742	+	18	0.00021	+	32	0.00000	+
	II	13	0.00219	+	18	0.00000	+	31	<0.01*	+
	III	21	0.00000	+	18	0.00060	+	39	0.00000	+
	IV	18	0.00016	+	21	0.00000	+	39	0.00000	+
	V	19	0.05554	—	22	0.00008	+	41	0.00004	+
					b. DZ sample					
RIGHT	I	17	0.00200	+	12	0.20378	—	29	0.00294	+
	II	11	0.06805	—	12	0.21797	—	23	>0.01*	—
	III	17	0.05479	—	22	0.01114	?	39	0.00133	+
	IV	19	0.00701	+	11	0.65506	—	30	0.03899	—
	V	20	0.01031	—	18	1.00000	—	38	0.05542	—
LEFT	I	19	0.00429	+	13	0.12494	—	32	0.00291	+
	II	13	0.01174	—	13	0.00812	+	26	<0.01*	+
	III	14	0.48860	—	17	0.09283	—	31	0.14686	—
	IV	17	0.02076	—	18	0.00765	+	35	0.00061	+
	V	20	0.07184	—	19	0.48427	—	39	0.08177	—

* Only upper or lower probability limits are given, instead of the precise probability [1.5] the calculation of which would have required a practically unnecessary, enormous load of work (cf Appendix).

https://doi.org/10.1017/S1120962300012750 Published online by Cambridge University Press

III.2. Quantitative analysis

The results of the quantitative analysis are summarized in Tables III, IV and V, respectively referred to the analysis of cumulative ridge counts by sex and zygosity, to the analysis of TFRC values by zygosity only, and to the analysis of single ridge count values, also by zygosity only.

Tab. III. Quantitative analysis: Cumulative ridge counts

Sample	RFRC	LFRC	TFRC
	a. Estimates of the intraclass correlation coefficient (ρ)		
MZ ♂	0.960	0.975	0.988
MZ ♀	0.928	0.955	0.983
DZ ♂	0.398	0.323	0.381
DZ ♀	0.687	0.565	0.633
	b. Confidence intervals of ρ (confidence coefficient = 0.95)		
MZ ♂	$0.912 \leq \rho \leq 0.965$	$0.946 \leq \rho \leq 0.989$	$0.973 \leq \rho \leq 0.994$
MZ ♀	$0.849 \leq \rho \leq 0.967$	$0.908 \leq \rho \leq 0.977$	$0.962 \leq \rho \leq 0.993$
DZ ♂	$0.019 \leq \rho \leq 0.679$	$0.073 \leq \rho \leq 0.627$	$0.004 \leq \rho \leq 0.666$
DZ ♀	$0.417 \leq \rho \leq 0.849$	$0.225 \leq \rho \leq 0.777$	$0.326 \leq \rho \leq 0.815$

Tab. IV. Quantitative analysis: TFRC irrespective of sex

Sample	ρ	Confidence interval of ρ
MZ	0.985	$0.966 \leq \rho \leq 0.993$
DZ	0.533	$0.189 \leq \rho \leq 0.760$

Tab. V. Quantitative analysis: Estimates of ρ for single ridge counts

	Finger	MZ	DZ
RIGHT	I	0.853	0.258
	II	0.796	0.380
	III	0.842	0.547
	IV	0.907	0.528
	V	0.904	0.436
LEFT	I	0.893	0.122
	II	0.867	0.212
	III	0.888	0.454
	IV	0.932	0.535
	V	0.893	0.332

https://doi.org/10.1017/S1120962300012750 Published online by Cambridge University Press

IV. Application of Fingerprints to the Diagnosis of Zygosity

IV.1. Introduction

The utmost importance of the twin method in human genetic studies makes the diagnosis of zygosity to be a fundamental problem of research. In fact, a large number of methods have been introduced, in the past fifty years, to meet this problem. A recent, authoritative analysis of the main ones has been provided by a WHO report on the methodology of twin studies (1966), which concludes, however, that " there is a great need for further research ". Such a need is especially felt in the study of large groups, where more economic and simpler procedures are to be taken into account.

Fingerprints appear to very well meet this need; actually, they started being used for the diagnosis of zygosity in twins around 1930, and many methods have been, and keep being proposed since then. Except for the pattern score worked out by Wendt (1955), the main ones have been proposed by two British biometric schools (Maynard-Smith and Penrose, 1955; and Nixon, 1956; Slater, 1963; Slater et al, 1964) and are generally based on ridge counts.

They all consist in score methods, in which the probability of monozygosity is indirectly proportional to the difference in the cotwins' ridge counts; i.e.: the probability is higher when the difference is lower. For the sake of simplicity, as well as for methodological reasons, we have preferred to work out a method aiming to finding out a general discriminant function between MZ and DZ twin pairs, i.e. based on the classic principles of nonparametric classificatory analysis, with fixed values and probability of error. According to the results obtained in the present study, the search for the discriminant function was based on TFRC differences.

IV.2. TFRC discriminant method

The intraclass correlation coefficient may be interpreted " as a simple linear transformation of a ratio of variances between classes and within classes in the Analysis of Variance " (Kendall and Stuart, 1962).

It has been ascertained (II.2) that the value of the intraclass correlation coefficient is higher in MZ than in DZ twin pairs, and fails to show any sex difference or interaction between sex and zygosity. The modulus Δ of the difference * between

* The use of the absolute difference, instead of the relative one, is advisable, among other things, also in view of the fact that the identification of the cotwins as first and second born is purely conventional. Of course, Δ^K, with K even, could be chosen instead of Δ, but this, as will be plain at a later stage, would be an unnecessary complication.

As it is implicit in the inductive techniques employed in the preceding section, we deem it reasonable to assume that the pairs of TFRC values be approximate determinations of a two-dimensional normal random variable. However, this assumption apparently fails to be very useful in attempting to establish a discriminant function of zygosity, so that we have applied a more general procedure (cf Stoller, 1954).

the two TFRC values observed on the two members of a same-sexed twin pair of unknown zygosity, may be reasonably assumed for the purpose of classifying the pair as either MZ or DZ.

The problem is then to choose a value δ_0 of the variable Δ, such that, if δ is the observed value of Δ:

[3.1] $\delta \leq \delta_0$ leads to classify the pair as MZ; whereas

[3.2] $\delta > \delta_0$ leads to classify the pair as DZ.

The choice of the discriminant value δ_0 may be based on the following considerations derived from Stoller (1954) with a few modifications.

Let us suppose we know the probabilities p (δ) and q (δ) for Δ to assume a value $\delta = 0; 1; 2; \ldots; n$, in MZ and DZ twins, respectively.

Let us further suppose we know the probability π for a same-sexed pair to be MZ.

Then: $$\pi \sum_{\delta=0}^{\bar{\delta}} p(\delta)$$

is the probability that a same-sexed pair be MZ *and* that a δ value of Δ, lesser than, or equal to $\bar{\delta}$, be observed thereon.

Similarly, the probability for a same-sexed twin pair to be DZ, *and* for a δ value, lesser than, or equal to $\bar{\delta}$, to be observed thereon, is:

$$(1 - \pi) \sum_{\delta=0}^{\bar{\delta}} q(\delta).$$

Then the probability:

[3.3] $$P(\bar{\delta}) = \pi F(\bar{\delta}) + (1 - \pi)\,[1 - G(\bar{\delta})],$$

where $$F(\bar{\delta}) = \sum_{\delta=0}^{\bar{\delta}} p(\delta) \text{ and } G(\bar{\delta}) = \sum_{\delta=0}^{\bar{\delta}} q(\delta),$$

refers to the event of observing a value $\delta \leq \bar{\delta}$ on a MZ, or a value $\delta > \bar{\delta}$ on a DZ same-sexed pair.

If $P(\bar{\delta})$, considered as a function of $\bar{\delta}$, is maximized for $\bar{\delta} = \delta_0$, then the criterion of classification under [3.1] and [3.2] possesses the desirable property of maximizing the probability of making a correct diagnosis of zygosity of a twin pair under observation. As a result, δ_0 shall be chosen so that

[3.4] $$P(\delta_0) = \text{maximum.}$$

The solution to the problem under [3.4] implies the prior knowledge both of the two distribution functions, p(δ) and q(δ), and of the probability of monozygosity (π).

At present, in Italy, the latter may be estimated at 0.30 (Gedda and Brenci, 1961). Hence, we may insert in [3.3]:

$$\pi \simeq \frac{0.30}{0.30 + 0.70 + 0.50} = 0.46.$$

The distribution functions p (δ) and q (δ) are unknown, and we cannot estimate them by means of the Δ values observed in the four samples under consideration.

The following estimators may therefore be set up:

$$\hat{p}(\delta) = \frac{m♂(\delta) + m♀(\delta)}{50} \qquad \hat{q}(\delta) = \frac{n♂(\delta) + n♀(\delta)}{50},$$

$m_K(\delta)$ and $n_K(\delta)$ (where K ≡ ♂; ♀) being the number of pairs which, respectively in the ♂ and ♀ MZ and ♂ and ♀ DZ samples, have $\Delta = \delta$.

Then, the probability in [3.3], when inserting $\pi = 0.46$, is estimated by means of:

[3.5] $$0.46\ \hat{F}(\bar{\delta}) + 0.54\ [1 - \hat{G}(\bar{\delta})] = \hat{P}(\bar{\delta}),$$

where $\hat{F}(\bar{\delta}) = \sum_{\delta=0}^{\bar{\delta}} \hat{p}(\delta)$ and $\hat{G}(\bar{\delta}) = \sum_{\delta=0}^{\bar{\delta}} \hat{q}(\delta)$.

These quantities are obviously determinations of two random variables whose variances are $F(\bar{\delta})\ [1 - F(\bar{\delta})]\ 50^{-1}$ and $G(\bar{\delta})\ [1 - G(\bar{\delta})]\ 50^{-1}$, respectively. It follows that the standard deviation of the random variable described by the [3.5] estimate is not greater than 0.05.

Let us now consider the sequence generated by [3.5] when $\delta = 0; 1; \ldots; n$. If for $\bar{\delta} = \delta_0$ the sequence reaches its absolute maximum, δ_0 will be chosen according to the criterion of classification [3.1]; [3.2]. The probability of correctly classifying a twin pair under observation will be estimated by $\hat{P}(\delta_0)$ and its standard deviation will not exceed 0.05.

It should finally be noted that, in the application of this method, r values $\delta_0^{(j)}$ ($j = 1; 2; \ldots; r$), which maximize the sequence, are likely to be obtained. If these r values, arranged in increasing order according to the index (j) are contiguous, the following procedure may be used.

For any $\delta \leq \delta_0^{(1)}$, the observed pair will be classified as MZ, while for any $\delta > \delta_0^{(r)}$ the pair will be classified as DZ. No classification shall be assigned if $\delta_0^{(1)} < \delta \leq \delta_0^{(r)}$, but in our experience the unique value $\delta_0 = 11$ has been obtained, being

$$P(11) = 0.86.$$

On the basis of these results, we suggest that a twin pair be classified as follows:

$$\text{MZ, if } \Delta \leq 11 \qquad \text{DZ, if } \Delta > 11.$$

The error of classification may be estimated in the range of 0.14.

https://doi.org/10.1017/S1120962300012750 Published online by Cambridge University Press

V. Discussion and Conclusions

The qualitative analysis has shown:

1. A significantly higher concordance in MZ than in DZ twin pairs. The hypothesis of genetic conditioning thus appears fully supported.
2. A remarkable variability of single finger concordance values. Individual genetic conditioning, for single finger patterns, may thus be inferred.
3. Absence of significant influence of handedness and sex. The analysis by zygosity only, irrespective of sex, thus appears justified.

The quantitative analysis on cumulative values has shown:

1. Significantly higher correlations in MZ ($\sim$ 1) than in DZ ($\sim$ 0.3-0.7) twin pairs. The hypothesis of genetic conditioning thus appears fully supported.
2. Much more limited confidence intervals in MZ than in DZ twin pairs. Almost complete genetic conditioning may thus be inferred.
3. Absence of significant influence of handedness and sex. The analysis of TFRC irrespective of sex thus appears justified.

The quantitative analysis on single values, although less extensive, has apparently yielded quite similar results to the ones of cumulative values. Also taking into account the fact that random variability must obviously be higher in single than in cumulative values, individual genetic conditioning, for single finger values, may thus be inferred.

In conclusion, our results clearly support the view of a practically complete genetic conditioning of digital dermatoglyphics. Rather than at a cumulative level for the ten fingers, as is largely believed, the latter appears to act, however, on single finger quali-quantitative traits. Actually, TFRC would hardly appear to be a trait as such, and should rather be considered as a useful, but artificial cumulative value, with a reduced random variability, and summarizing the single finger actual traits. As such we have used it in our discriminant method, which, yielding a single discriminant value between MZ and DZ twins, may provide a useful and simple tool for the diagnosis of zygosity, especially in large twin samples.

Summary

A twin study was undertaken with the twofold aim (a) of studying the hereditary behaviour of digital dermatoglyphic traits both at the qualitative and quantitative level, and (b) of working out a method for discriminating MZ and DZ twins by means of fingerprints.

Fingerprints of 50 MZ (25 ♂ and 25 ♀) and 50 DZ (25 ♂ and 25 ♀) twin pairs were thus examined and analyzed by means of a special methodology and of a 7044/K32 IBM computer.

The *qualitative* analysis has shown a significantly higher concordance in MZ than

in DZ twin pairs, with a certain variability of single finger concordance values. The *quantitative* analysis has shown significantly higher correlation values in MZ than in DZ twin pairs, with very limited confidence intervals in the former. Single ridge counts apparently behave as cumulative counts on the five or ten fingers, although with an obviously higher random variability.

Digital dermatoglyphics thus appear to show practically complete genetic conditioning, which, rather than at a cumulative level for the ten fingers, as is largely believed, appears to act on *single finger* quali-quantitative traits. The total finger ridge count, rather than a trait, only appears to be a useful, but artificial cumulative value. Actually, applied to the diagnosis of zygosity, it provides, by itself, a fairly high, general probability (0.86) of a correct diagnosis.

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APPENDIX *

Automatic procedure for testing the qualitative hypotheses

From a numerical point of view the test of the qualitative hypothesis proposed in II.1 can be split up into the following phases:

A. Input operation and initialization of auxiliary quantities;

B. Search for the configurations [1.1] subject to the restrictions [1.3];

C. Computation of [1.2] for each configuration and cumulation of its successive values for obtaining [1.4];

D. Cumulation of the [1.4] values, comparison with the significance level and output operation, which are however closely interdependent one with the other as evidenced by Fig. 1.

A. The following boxes of Fig. 1 are concerned with this phase:

Box 1: Control for end of data.

Box 2: The following input quantities are required (the corresponding symbols used in II.1 are to be found, if any, in the second member):
N1 = number of attributes. In our own case it is 5;
K(I) = $_{D}r$ number of concordances observed with respect to finger D;
ALPHA = level of significance;
SINT = logical variable conditioning the output;
= T synthetic output;
= F analytical output;
Z(I) = $_{D}Z_{I}$ number of fingerprints possessing the i^{th} attribute.
The variable FORMAT to read-in the above quantities must be expressed by means of the variables FRM and FOR.

Box 3: The main auxiliary quantities are:
NC = n number of twin pairs examined;
KSUP = $_{D}R$ maximum number of concordances for finger D;
NC2 = number of individuals examined.
F = $_{D}F_{r}$ vector containing the configurations [1.1]

Box 4: Subroutine PRIM generates all I prime numbers not greater than NMAX and stores them into the NP vector. They will be utilized later in phase C. More details are given in Fig. 2.

B. In order that the application of the program should not be confined only to populations whose members exhibit five attributes provision has been made for N1 to be assigned any integer value greater than 1 during the input phase. This has substantially affected the translation of this phase into FORTRAN IV language as such generalization does not permit us to know at the programming stage the number of routines which are nec-

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essary for describing the search process of the configurations ${}_{D}F_{r}$ (Parisi and Di Bacco, 1967, II.2).
The problem has been solved by means of only one routine to be performed at the different levels which are necessary for searching one individual configuration and to be repeated again and again for as many cycles as are the configurations satisfying [1.3].
For a better understanding of the above procedure and for enphasizing its salient aspects, the operations indicated in Boxes 5, 6 and 7 of Fig. 1 have been represented in detail on Figs. 3 and 4.

C. It is useful for computational purposes to consider [1.2] as the quotient of P_1 by P_2, where

$$P_1 = \frac{n!}{(2n)!}\, 2^n - {}_{D}r \prod_{i=1}^{5} {}_{D}Z_i!$$

and

$$P_2 = \prod_{i \leq j} f_{ij}!$$

in that only P_1 varies as a function of the configuration ${}_{D}F_{r}$ under consideration. Bearing in mind that P_1 and P_2 may always be expressed as products of powers of distinct positive integers not greater than 2n and n respectively, the value of the exponent of the generic base i has been assigned, for each power belonging to P_1 to the i^{th} element of vector INIZ. Subsequently, for each configuration ${}_{D}F_{r}$ generated in phase B, the elements of vector IFACT have been equated to the corresponding ones of INIZ and the exponent of the power of the generic base i in P_1 has been subtracted from the i^{th} element of the former vector. Hence, in order to minimize the loss of significant digits in the computation of the product of powers represented by IFACT, the latter vector has been simplified by transferring (with the aid of the prime numbers generated by the PRIM subroutine) the value of its elements whose serial number is not prime to those indicated by factoring the latter.
In this manner, all non-prime elements of IFACT are set to zero and will not be considered for the purpose of the computation of [1.2].
The operations described in boxes 8 and 9 of Fig. 1, whose details are explained by Fig. 5, refer to the present phase.

D. The following boxes of Fig. 1 belong to this phase:
Box 10: Cumulation of [1.4] values as ${}_{D}r$ increases from its initial value to ${}_{D}R$;
Box 11: Comparison between ${}_{D}r$ and its maximum value;
Box 12: Comparison between [1.5] and ALPHA;
Box 13: If SINT = T in output only a judgement on the significance of the test performed is obtained. Furthermore, in the event of non-significant concordances, there will be a saving in the performance time.
If SINT = F in addition to the judgement as above, the probabilities relative to each ${}_{D}r$ considered and their successive cumulation are obtained;
Box 14: Step up of ${}_{D}r$.

The statistical tests of the random association hypothesis have been carried out by an IBM 7044/32K computer.

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This experience has revealed that the execution time is, for each test, a non-decreasing function of n and a non-increasing one of both $_{D}r$ and d, the latter being a dispersion measure of the papillary patterns frequencies. This measure is given by

$$d = \frac{\sum_{1}^{5} \left| {}_{D}Z_1 - m \right|}{5}$$

where m is the arithmetic mean of the $_{D}Z_1$.

The memory space required is approximately of $\frac{5}{2}$ (N1 + 1) N1 + 3 N1 + 5n + 3150 words.

In the following pages the source program has been entirely reported in Fortran IV language.

```
C         PRIM                                                    PRIM0001
C         SUBROUTINE FOR GENERATING PRIME NUMBERS                 PRIM0002
C                                                                 PRIM0003
      SUBROUTINE PRIM(NMAX,NP,I)                                  PRIM0004
      DIMENSION NP(1)                                             PRIM0005
      NP(1)=2                                                     PRIM0006
      NP(2)=3                                                     PRIM0007
      NP(3)=5                                                     PRIM0008
      I=2                                                         PRIM0009
      NN=1                                                        PRIM0010
   10 DO 50 K=4,6,2                                               PRIM0011
      NCOM=NN+K                                                   PRIM0012
      COM=NCOM                                                    PRIM0013
      NS=SQRT(COM)                                                PRIM0014
      J=3                                                         PRIM0015
   20 IF(NP(J).GT.NS) GOTO 40                                     PRIM0016
      IF(MOD(NCOM,NP(J)).EQ.0) GOTO 50                            PRIM0017
   30 J=J+1                                                       PRIM0018
      GOTO 20                                                     PRIM0019
   40 IF(NCOM.GT.NMAX) RETURN                                     PRIM0020
      I=I+1                                                       PRIM0021
      NP(I)=NCOM                                                  PRIM0022
   50 CONTINUE                                                    PRIM0023
      NN=NCOM                                                     PRIM0024
      GOTO 10                                                     PRIM0025
      END                                                         PRIM0026
```


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```
C       FPBT                                                                FPBT0001
C       PROGRAM FOR THE STATISTICAL TEST OF THE HYPOTESES OF CONCORDANCE    FPBT0002
C       BETWEEN THE PAPILLARY PATTERNS OF MZ AND DZ TWINS                   FPBT0003
C                                                                           FPBT0004
     1 FORMAT(12A6)                                                         FPBT0005
     3 FORMAT(/////////12X,9HNUMBER OF,31X,10HCUMULATIVE/)                  FPBT0006
     4 FORMAT(1H1///1X,12A6///)                                             FPBT0007
     5 FORMAT(10X,12HCONCORDANCES,9X,13HPROBABILITIES,7X,13HPROBABILITIESFPBT0008
      *////)                                                               FPBT0009
     7 FORMAT(12X,I5,14X,F11.8,9X,F11.8/)                                   FPBT0010
     8 FORMAT(//////1X,34HSIGNIFICANT CONCORDANCES AT LEVEL ,F5.2////)      FPBT0011
     9 FORMAT(//////1X,38HNOT SIGNIFICANT CONCORDANCES AT LEVEL ,F5.2///)FPBT0012
       LOGICAL SINT                                                         FPBT0013
       INTEGER Z(99),F(999),G(999)                                          FPBT0014
       DIMENSION N(99),J(99),K(999),INIZ(999),IFACT(999),LS(999),L(999),NFPBT0015
      *P(99),NOME(12),FRM(12),FOR(12)                                       FPBT0016
C                                                                           FPBT0017
C                          PHASE A                                          FPBT0018
C                                                                           FPBT0019
       READ(5,1) (FRM(I),I=1,12)                                            FPBT0020
       READ(5,1) (FOR(I),I=1,12)                                            FPBT0021
  . 10 READ(5,1) (NOME(I),I=1,12)                                           FPBT0022
       READ(5,FRM) N1,K(1),ALPHA,SINT                                       FPBT0023
       READ(5,FOR) (Z(I),I=1,N1)                                            FPBT0024
       WRITE(6,4) (NOME(I),I=1,12)                                          FPBT0025
       IF(SINT) GOTO 12                                                     FPBT0026
       WRITE(6,3)                                                           FPBT0027
       WRITE(6,5)                                                           FPBT0028
C                                                                           FPBT0029
    12 NC2=0                                                                FPBT0030
       KSUP=0                                                               FPBT0031
       DO 14 I=1,N1                                                         FPBT0032
       NC2=NC2+Z(I)                                                         FPBT0033
       L(I)=Z(I)/2                                                          FPBT0034
    14 KSUP=KSUP+L(I)                                                       FPBT0035
       N(1)=N1                                                              FPBT0036
       NC=NC2/2                                                             FPBT0037
       NC1=NC+1                                                             FPBT0038
       NT=(N1*N1+N1)/2                                                      FPBT0039
       PRR=0.                                                               FPBT0040
       CALL PRIM(NC2,NP,NTP)                                                FPBT0041
C                                                                           FPBT0042
C                          PHASE C                                          FPBT0043
C                                                                           FPBT0044
       DO 16 I=3,NC2                                                        FPBT0045
       INIZ(I)=0                                                            FPBT0046
    16 IF(I.GE.NC1) INIZ(I)=-1                                              FPBT0047
       INIZ(2)=NC-K(1)+1                                                    FPBT0048
       DO 20 I=1,N1                                                         FPBT0049
       IF(Z(I).LT.2) GOTO 20                                                FPBT0050
       LV=Z(I)                                                              FPBT0051
       DO 18 JL=2,LV                                                        FPBT0052
    18 INIZ(JL)=INIZ(JL)+1                                                  FPBT0053
    20 CONTINUE                                                             FPBT0054
    22 INIZ(2)=INIZ(2)-1                                                    FPBT0055
       PROB=0.                                                              FPBT0056
C                                                                           FPBT0057
C                          PHASE B                                          FPBT0058
C                                                                           FPBT0059
       DO 24 I=1,NT                                                         FPBT0060
    24 F(I)=0                                                               FPBT0061
       M=1                                                                  FPBT0062
```


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```
   26 J(M)=0                                                        FPBT0063
      NN=N(M)                                                       FPBT0064
      MI=(M-1)*N1-(M-1)*(M-2)/2                                     FPBT0065
      MII=MI+1                                                      FPBT0066
      MM=MII+1                                                      FPBT0067
      NNN=NN+MI                                                     FPBT0068
      NS=NNN-1                                                      FPBT0069
      LS(MII)=L(MII)                                                FPBT0070
C                                                                   FPBT0071
   28 J(M)=J(M)+1                                                   FPBT0072
      JM=J(M)+MI                                                    FPBT0073
   30 JJ=JM+1                                                       FPBT0074
   36 K(JJ)=K(JM)-F(JM)                                             FPBT0075
      IF(K(JJ).GE.L(JJ)) GO TO 40                                   FPBT0076
      LS(JJ)=K(JJ)                                                  FPBT0077
      GO TO 50                                                      FPBT0078
   40 LS(JJ)=L(JJ)                                                  FPBT0079
   50 IF(JM.LT.NS) GO TO 28                                         FPBT0080
      KL=K(NNN)-L(NNN)                                              FPBT0081
      IF(KL.GT.0) GOTO 90                                           FPBT0082
      IF(F(JM).LE.LS(JM)) GO TO 70                                  FPBT0083
   60 F(JM)=0                                                       FPBT0084
      J(M)=J(M)-1                                                   FPBT0085
      JM=J(M)+MI                                                    FPBT0086
      IF(JM.GT.MI) GOTO80                                           FPBT0087
      M=M-1                                                         FPBT0088
      IF(M.LE.0) GO TO 250                                          FPBT0089
      NN=N(M)                                                       FPBT0090
      MI=(M-1)*N1-(M-1)*(M-2)/2                                     FPBT0091
      MII=MI+1                                                      FPBT0092
      MM=MII+1                                                      FPBT0093
      NNN=NN+MI                                                     FPBT0094
      NS=NNN-1                                                      FPBT0095
      JM=J(M)+MI                                                    FPBT0096
      GO TO 80                                                      FPBT0097
   70 F(NNN)=K(NNN)                                                 FPBT0098
C                                                                   FPBT0099
      ISUM=0                                                        FPBT0100
      DO 110 I=MII,NNN                                              FPBT0101
      G(I)=L(I)-F(I)                                                FPBT0102
      IF(M.EQ.1) G(I)=Z(I)-2*(L(I)-G(I))                            FPBT0103
      IF(I.EQ.MII) GOTO 100                                         FPBT0104
      IF(G(I).LE.ICOM) GO TO 110                                    FPBT0105
  100 INDEX=I                                                       FPBT0106
      ICOM=G(I)                                                     FPBT0107
  110 ISUM=ISUM+G(I)                                                FPBT0108
      IF(2*ICOM-ISUM) 130,150,80                                    FPBT0109
  130 G(INDEX)=G(MII)                                               FPBT0110
      DO 140 I=MM,NNN                                               FPBT0111
      II=I+NN-1                                                     FPBT0112
  140 L(II)=G(I)                                                    FPBT0113
      K(NNN+1)=ICOM                                                 FPBT0114
      M=M+1                                                         FPBT0115
      N(M)=NN-1                                                     FPBT0116
      GO TO 26                                                      FPBT0117
  150 G(INDEX)=G(MII)                                               FPBT0118
      DO 160 I=MM,NNN                                               FPBT0119
      II=I+NN-1                                                     FPBT0120
  160 F(II)=G(I)                                                    FPBT0121
C                                                                   FPBT0122
C                          PHASE C                                  FPBT0123
C                                                                   FPBT0124
```

```
      DO 190 I=2,NC2                                                    FPBT0125
  190 IFACT(I)=INIZ(I)                                                  FPBT0126
      DO 210 I=1,II                                                     FPBT0127
      IF(F(I).LT.2) GOTO 210                                            FPBT0128
      LV=F(I)                                                           FPBT0129
      DO 200 JL=2,LV                                                    FPBT0130
  200 IFACT(JL)=IFACT(JL)-1                                             FPBT0131
  210 CONTINUE                                                          FPBT0132
C                                                                       FPBT0133
      PR=1.                                                             FPBT0134
      DO 230 JL=1,NTP                                                   FPBT0135
      IP=NP(JL)                                                         FPBT0136
      RIP=IP                                                            FPBT0137
      IP2=IP+IP                                                         FPBT0138
      JS=NC2/IP*IP                                                      FPBT0139
      IF(IP2.GT.JS) GOTO 230                                            FPBT0140
      DO 220 I=IP2,JS,IP                                                FPBT0141
      JI=JS-I+IP2                                                       FPBT0142
      JD=JI/IP                                                          FPBT0143
      IFACT(IP)=IFACT(IP)+IFACT(JI)                                     FPBT0144
      IFACT(JD)=IFACT(JD)+IFACT(JI)                                     FPBT0145
  220 IFACT(JI)=0                                                       FPBT0146
  230 PR=PR*RIP**IFACT(IP)                                              FPBT0147
      PROB=PROB+PR                                                      FPBT0148
C                                                                       FPBT0149
C                          PHASE B                                      FPBT0150
C                                                                       FPBT0151
      DO 170 I=MM,NNN                                                   FPBT0152
      II=I+NN-1                                                         FPBT0153
  170 F(II)=0                                                           FPBT0154
   80 F(JM)=F(JM)+1                                                     FPBT0155
      IF(F(JM)-LS(JM))30,30,60                                          FPBT0156
   90 F(JM)=F(JM)+KL                                                    FPBT0157
      GO TO 36                                                          FPBT0158
C                                                                       FPBT0159
C                          PHASE D                                      FPBT0160
C                                                                       FPBT0161
  250 PRR=PROB+PRR                                                      FPBT0162
      IF(SINT) GOTO 254                                                 FPBT0163
      WRITE(6,7) K(1),PROB,PRR                                          FPBT0164
      GOTO 260                                                          FPBT0165
  254 IF(PRR.LT.ALPHA) GOTO 260                                         FPBT0166
  256 WRITE(6,9) ALPHA                                                  FPBT0167
      GOTO 10                                                           FPBT0168
  260 K(1)=K(1)+1                                                       FPBT0169
      IF(K(1).LE.KSUP) GOTO 22                                          FPBT0170
      IF(PRR.GE.ALPHA) GOTO 256                                         FPBT0171
      WRITE(6,8) ALPHA                                                  FPBT0172
      GOTO 10                                                           FPBT0173
      END                                                               FPBT0174
```


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Flow Charts

(Figs. 1-5)

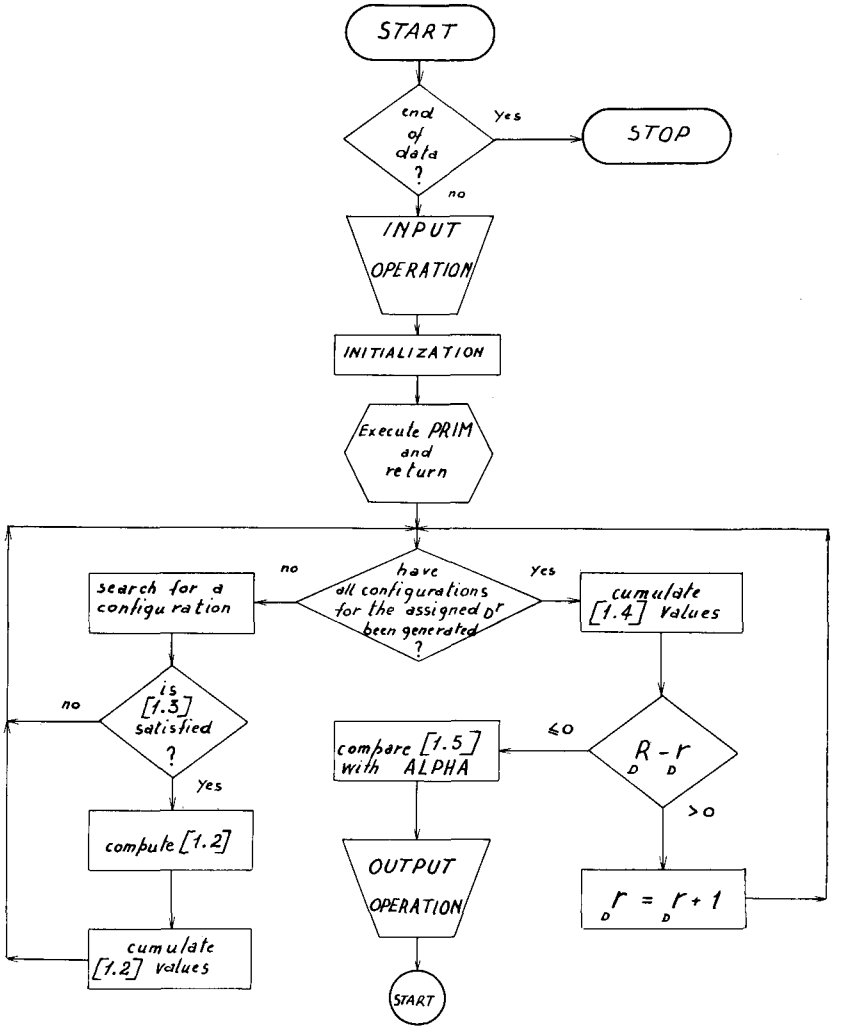

Fig. 1

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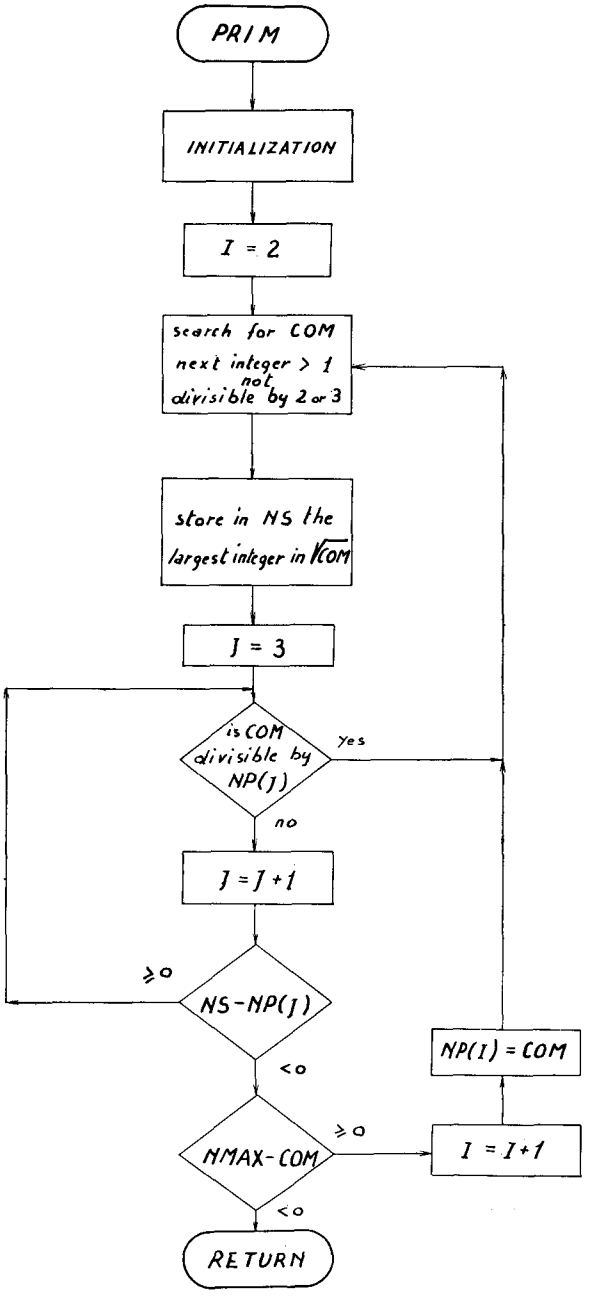

Fig. 2

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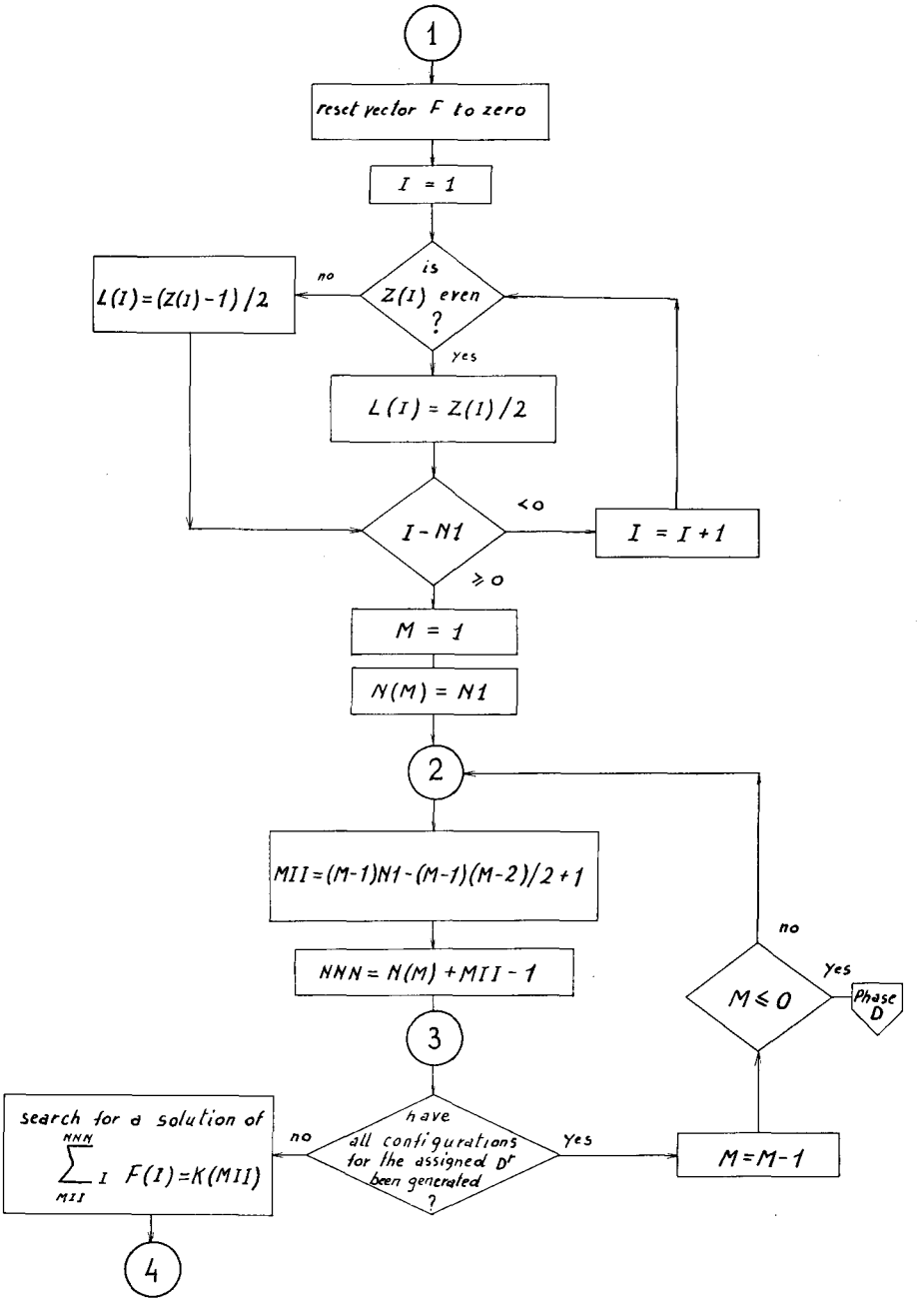

Fig. 3

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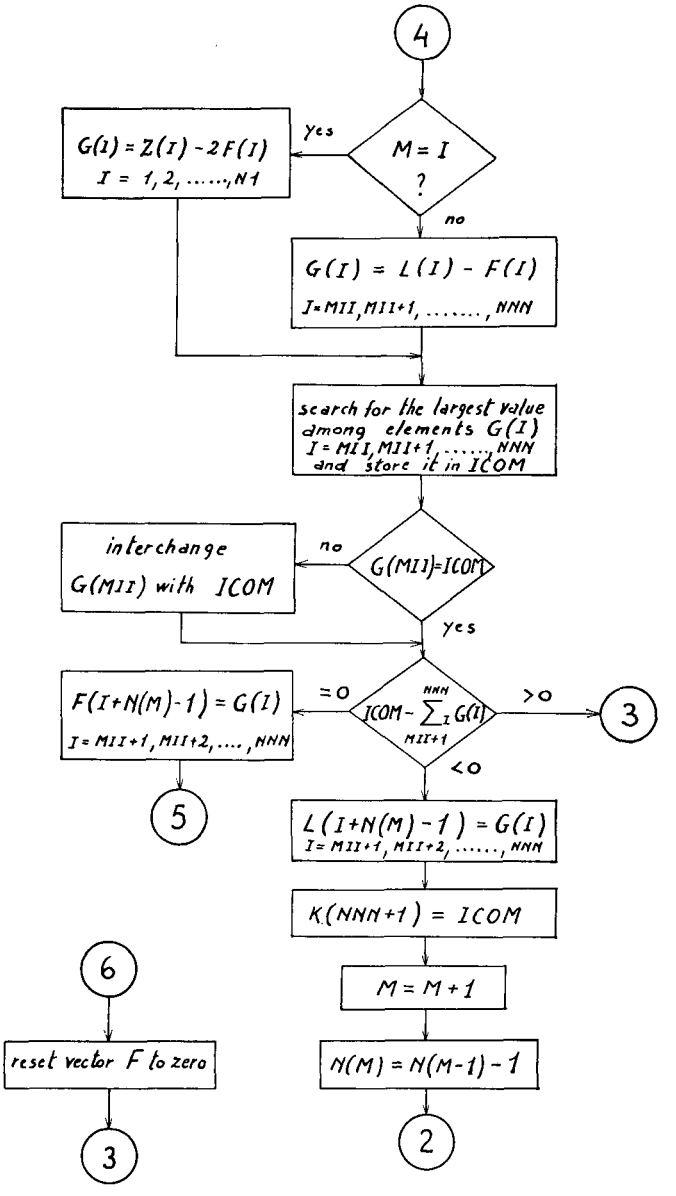

Fig. 4

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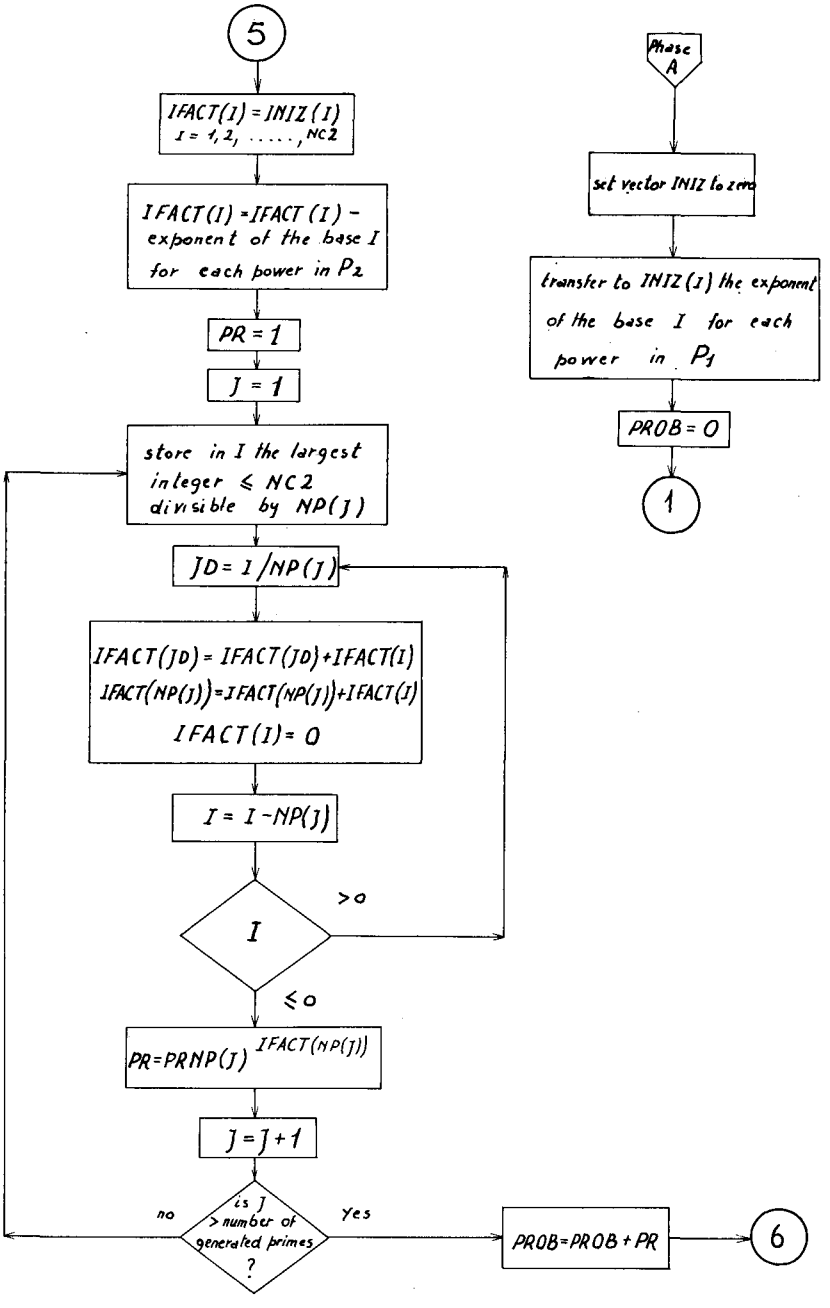

Fig. 5

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RIASSUNTO

È stato condotto uno studio gemellare con il duplice scopo: 1. di studiare il comportamento ereditario dei dermatoglifi digitali a livello sia qualitativo che quantitativo, e 2. di elaborare un metodo per distinguere i gemelli MZ dai DZ mediante le impronte digitali.

Le impronte digitali di 50 coppie MZ (25 ♂ e 25 ♀) e 50 DZ (25 ♂ e 25 ♀) sono dunque state esaminate ed analizzate con una metodologia originale e un calcolatore IBM 7044/K32.

L'analisi *qualitativa* ha indicato una concordanza significativamente più elevata nelle coppie MZ che nelle DZ, con una certa variabilità fra i valori di concordanza di ogni singolo dito. L'analisi *quantitativa* ha indicato delle correlazioni significativamente più elevate nelle coppie MZ che nelle DZ, con intervalli di confidenza molto limitati nel primo caso. I conteggi singoli presentano un comportamento analogo a quello dei conteggi cumulativi compiuti sulle 5 o 10 dita, pur con una variabilità casuale ovviamente più elevata.

I dermatoglifi digitali risultano dunque presentare un condizionamento genetico praticamente completo che più che a un livello cumulativo per le 10 dita, come generalmente si ritiene, sembra agire a livello dei caratteri quali-quantitativi delle singole dita. Il numero totale delle creste, più che un carattere, sembra essere un valore cumulativo utile ma artificiale; applicato alla diagnosi di zigotismo, esso fornisce da solo una probabilità generale di una giusta diagnosi relativamente elevata (0.86).

RÉSUMÉ

Une étude gémellaire a été conduite avec le but 1. d'étudier l'hérédité des dermatoglyphes digitaux au point de vue qualitatif et quantitatif, et 2. de développer une méthode pour séparer les jumeaux MZ et DZ moyennant les empreintes digitales.

Les empreintes digitales de 50 couples MZ (25 ♂ et 25 ♀) et 50 DZ (25 ♂ et 25 ♀) ont été examinées et analysées par une méthodologie originale et un computer IBM 7044/K32.

L'analyse *qualitative* a indiqué des valeurs de concordance significativement plus élevées chez les MZ vis-à-vis des DZ, avec une certaine variabilité parmi les différentes valeurs pour chaque doigt. L'analyse *quantitative* a indiqué des valeurs de corrélation significativement plus élevées chez les MZ vis-à-vis des DZ, avec des intervalles de confiance très limités chez les premiers. Le numéro des crêtes sur chaque doigt a un comportement similaire aux numéros complexifs pour 5 ou 10 doigts, tout en présentant une variabilité casuelle évidemment plus élevée.

Les dermatoglyphes digitaux présentent donc un conditionnement génétique pratiquement complet qui, plutôt qu'à un niveau cumulatif pour les 10 doigts (ainsi que l'on croit généralement), paraît agir sur les caractères quali-quantitatifs de chaque doigt. Le numéro total des crêtes, au lieu qu'un caractère, paraît être une valeur complexive utile, mais artificielle, qui, appliquée au diagnostic de zygotisme, donne une probabilité générale relativement élevée (0.86) d'un diagnostic correct.

https://doi.org/10.1017/S1120962300012750 Published online by Cambridge University Press

ZUSAMMENFASSUNG

Verf. führten eine Zwillingsuntersuchung durch, die folgende Ziele verfolgte: 1. die Vererbung der Fingerleisten sei es qualitativ als quantitativ gesehen zu untersuchen und 2. eine Methode auszuarbeiten, die es gestattet, auf Grund der Fingerleisten EZ von ZZ zu unterscheiden.

Es wurden daher mit Hilfe einer 7044/K32 IBM-Büromaschine und nach einer besonderen Methode die Fingerleisten von 50 EZ und 50 ZZ-Paaren (jeweils 25 ♂ und 25 ♀) untersucht und analysiert.

Die *qualitative* Analyse zeigte eine wesentlich höhere Konkordanz der EZ gegenüber den ZZ mit einigen Schwankungen in den Konkordanzwerten der einzelnen Finger. Die *quantitative* Analyse wies auf bedeutend höhere Korrelationen bei den EZ- als bei den ZZ-Paaren hin mit sehr beschränkten « Confidence-Intervals » bei den ersteren. Die Auszählungen an den einzelnen Fingern ergaben ähnliche Werte wie diejenigen, die sich über 5 oder 10 Finger erstreckten, wenn auch die Zufallsschwankungen dabei natürlich höher sind.

Die Fingerhautleisten scheinen somit praktisch voll und ganz erbbendingt zu sein. Während allgemein angenommen wird, dass sich die Erblichkeit kumulativ auf die 10 Finger auswirkt, so scheint sie hingegen eher an den qualitativ-quantitativen Merkmalen der einzelnen Finger zum Ausdruck zu kommen. Die Gesamtleistenzahl (total finger ridge count) würde demnach weniger ein Merkmal als einen nützlichen jedoch künstlichen Kumulativwert darstellen: wenn man ihn auf die Eiigkeitsdiagnose anwendet, so liefert er in der Tat allein schon eine relativ hohe allgemeine Wahrscheinlichkeit für eine richtige Diagnose (0.86).