

# EVALUATION OF NUMERICAL EVIDENCE IN FORENSIC COMPARISON ANALYSES CRITERIA FOR IDENTITY AND ASSESSMENT OF EVIDENTIAL VALUE

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## ABSTRACT

Two alternative methods of evaluating a discrepancy index are discussed, with a view to match crime/clue material with a comparison/source sample. One is put as  $\theta = \sum_{i=1}^N (Q_i - 1)^2/q_i^2$  (cf. Parker's C) and another,  $\Gamma = \prod_{i=1}^N Q_i (1 - 1/q_i)$  based on the discrepancy quotient  $Q$  and the overall coefficient of variation  $q$ . A simple evaluation of the uniqueness of a crime material is described on the basis of attributes measured in the source and the population, their mean values and the respective standard deviations.

**F**ORENSIC comparison analyses are undertaken to determine if a "crime sample" has originated from an alleged source. The inference drawn from non-numerical analyses like tool marks examination, e.g., in forensic ballistics or hand-in-glove fit of a crime sample with its remnant available elsewhere, can (when good characteristic matches are observed) be interpreted directly without "any reasonable doubt". This however is not possible in (numerical) material analyses<sup>1</sup>. In the former the characteristic match is obvious, but in the latter one has to cautiously interpret the results. Forensic analytical data have been evaluated by Parker<sup>2</sup> (human hair), Hoffman<sup>3</sup> (soils) and Lawson and Framan<sup>4</sup> (general).

Evaluation of analytical data in forensic problems is considered here firstly to establish if the crime and comparison (alleged source) samples match and secondly, that if these do so, then what proportion of the population of such material in question attain the levels of the attributes analysed. The lower it is, the more weighty is the evidence.

## 1. CRITERIA FOR IDENTITY

For matching or otherwise of a crime sample with the source, Parker<sup>2</sup> defined the discrepancy index,  $C$ , as :

$$C = \sum_{i=1}^N D_i^2 = \sum_{i=1}^N (X_i - Y_i)^2/\lambda_i^2 \quad (1)$$

where  $X_i$  and  $Y_i$  are the values for the  $i$ -th attribute measured in the crime sample and the alleged source respectively.  $\lambda_i$  is the combined standard deviation resulting from the standard deviation  $\delta_1$  in the crime sample, due to the measurement errors and the standard deviation  $\delta_2$  in the source, mainly due to the intrinsic variability;  $\lambda^2 = \delta_1^2 + \delta_2^2$ . If  $N$  uncorrelated attributes are measured,  $C$  is distributed as  $\chi^2$  with  $N$  degrees of freedom, if the crime sample originates from the alleged source. The observed  $C$  may be compared with the critical value for  $C$ , viz.,  $C_0$ , from the statistical  $\chi^2$  tables. At a given chosen probability value, say 0.01 (Parker),

if  $C < C_0$  then the crime sample could stem from the alleged source, and if in fact it does, the probability of finding  $C > C_0$  is as low as 0.01.

An alternative to Parker's  $C$  is described here, based on discrepancy quotient (*vide infra*) which is significant to the forensic analyst. Moreover, Parker used  $\ln c$  as against  $c$  (concentration); this is laborious, without making any significant difference in the results using  $c$  conveniently.

Let the values of a given attribute in the crime sample and the alleged source be :  $X_1 \pm \delta_1$  and  $X_2 \pm \delta_2$  respectively, and let  $\delta_1/X_1 = q_1$  and  $\delta_2/X_2 = q_2$ . We define discrepancy quotient,  $Q$ , as  $Q = X_1/X_2$ , we have  $(X_1 \pm \delta_1)/(X_2 \pm \delta_2) = Q \pm k$ , where  $k/Q = \sqrt{q_1^2 + q_2^2} = q$  (let). Parker's element of discrepancy index, viz.,  $D_i^2 = (X_1 - X_2)^2/(\delta_1^2 + \delta_2^2)$  can now be put as :  $D_i^2 = (Q - 1)^2/(Q^2 q_1^2 + q_2^2)$ . Discrepancy quotient,  $Q$ , will be useful in our discussion, if we impose the condition that  $Q \geq 1$ , no matter whether the attribute in the crime sample is greater than that in the source or *vice versa*. It will indicate a  $Q$ -fold discrepancy in the value of the attribute in the crime sample and source and calculations of the discrepancy index (*vide infra*) will be to the benefit of the accused. We now define  $\Delta_i$ , a normal deviate with unit standard deviation as

$$\Delta_i^2 = (1/Q - 1)^2/(k')^2, \text{ where } k'/(1/Q) = q.$$

$\therefore$  if  $(X_2 \pm \delta_2)/(X_1 \pm \delta_1) = (1/Q \pm k')$ , we have  $k'/(1/Q) = q$ . For identity of crime sample and source, we have  $Q \rightarrow 1$ ,  $(1/Q - 1) \rightarrow 0$ . From the above we get

$$\Delta_i^2 = (Q_i - 1)^2/q_i^2 \quad (2)$$

The modified discrepancy index,  $\theta$ , may now be compared with the critical value  $\theta_0$  from  $\chi^2$  tables to test the match.

$$\theta = \sum_{i=1}^N \Delta_i^2 = \sum_{i=1}^N (Q_i - 1)^2/q_i^2. \quad (3)$$

when

$$Q \rightarrow 1, \Delta_i^2 \rightarrow D_i^2.$$

It may appear that when  $X_1$  and  $X_2$  are (presumed to be) normally distributed,  $D^2$  is  $\chi^2$  distributed, then  $\Delta_i^2$  cannot be  $\chi^2$  distributed. In fact "a Gaussian distribution may be inappropriate for measurements, such as chemical composition, which must be always non-negative, a functional transform whereby the new variate is brought into closer alignment with the Gaussian distribution may be used instead. The logarithm of the chemical composition could be used rather than the chemical composition itself<sup>2(a)</sup>. Indeed the log-concentration of elements in human hair has been found to be closely Gaussian<sup>2(b)</sup>. On the first presumption  $X_2 - X_1$  is a Gaussian variate with zero mean and standard deviation  $\sqrt{\delta_1^2 + \delta_2^2}$ . Now, if on the other hand  $\ln X_1$  and  $\ln X_2$  are admittedly better Gaussian distributed, and if the sample could stem from the alleged source,

$$\ln X_2 - \ln X_1 = \ln (X_2/X_1) = \ln \left( 1 + \frac{X_2 - X_1}{X_1} \right) \approx \frac{X_2 - X_1}{X_1} = \left( \frac{1}{Q} - 1 \right)$$

is a Gaussian variate with zero mean and standard deviation  $k' = q \cdot Q$ , and  $\Delta_i^2$  is  $\chi^2$  distributed. The approximation involved is valid at lower discrepancies where the test for matching is sought.

It will now be shown that the use of  $c$  in place of  $\ln c$  (cf. Parker) does not make any significant difference where a critical examination is necessary. For large discrepancies, the difference in the crime sample and the alleged source is obvious; an inspection of data is sufficient. The use of  $c$  units makes evaluation of data less laborious.

Using  $c$  units, we have a series of measurements:  $c_1 = \bar{c} + x_1, \dots, c_n = \bar{c} + x_n$ , where  $x$ 's can be +ve -ve, yielding the result:  $\bar{c} \pm \delta_c$  where  $\delta_c$  is the standard deviation, calculated using  $c$  units directly. To convert the measurements into  $\ln c$  units, we have,  $\ln c_1 = \ln (\bar{c} + x_1) \approx \ln \bar{c} + x_1/\bar{c}$ , etc., showing that  $\delta_{\ln c} \approx \delta_c/\bar{c}$  where  $\delta_{\ln c}$  is the standard deviation calculated using  $\ln c$  units. Parker's discrepancy index element,  $D_i^2$  using  $\ln c$  units, can now be readily shown  $\approx D_i^2$  using  $c$  units, at lower discrepancies.

$D_i^2 = (\ln X_1 - \ln X_2)^2 / [(\delta_{c,1}/X_1)^2 + (\delta_{c,2}/X_2)^2]$  can be shown, at lower discrepancies,  $\approx (X_1 - X_2)^2 / (\delta_{c,1}^2 + \delta_{c,2}^2)$ . Thus in Parker's eqn. (1) whether  $\ln c$  values or  $c$  values are taken, these reduce to the same form and magnitude at lower discrepancies, where the test is necessary.

**Alternative Method for Constructing a Discrepancy Index.**—The discrepancy quotient,  $Q$ , ( $Q \geq 1$ ) may be suitably modified to yield a minimum value,  $Q_{min}$ . Thus at a given chosen probability level

$Q_{min} = Q - t \cdot k$ , where  $t$ —times the standard deviation is subtracted on the basis of Student's  $t$  value for the given desired probability level and for the given degrees of freedom. Thus for a series of 10 measurements (9 degrees of freedom) for  $i$ -th attribute the probability of a chance deviation in  $Q$  not exceeding  $2.26 k$  is 95% ( $t = 2.26$ ). Having obtained  $Q_{min}$  values for each attribute, ( $Q_{min} \geq 1$ ), we have the alternative discrepancy index, which may now be denoted by  $\Gamma$ , simply given by:

$$\Gamma = \prod_{i=1}^N Q_{min, i} = \prod_{i=1}^N (Q_i - t_i k_i) = \prod_{i=1}^N Q_i (1 - t_i \cdot q_i) \quad (4)$$

$Q_{min}$  values  $\geq 1$  only are considered; those working out to  $< 1$  are ignored, as these mean that there

is no significant difference in the values of the given attribute. Ideally,  $\Gamma_0$  for identity between the crime sample and the alleged source should be unity. Values of  $\Gamma$  in excess of unity would therefore indicate the extent of discrepancy between the two.

Application of the above criteria to typical literature data is given in Tables I to III. While  $\Gamma$  is well suited to the evaluation of data on chemical composition it will be apparent that in the evaluation of data on physical properties like density, refractive index, etc., in the event of high discrepancies (owing to very low  $q$ 's),  $\Gamma$  will not suitably reflect these. The discrepancy indexes  $c$  and  $\theta$  have therefore general applicability.

## 2. ASSESSMENT OF EVIDENTIAL VALUE

Once the questioned material is shown indistinguishable from the alleged source, the next consideration arises as to what significance or evidential value this agreement has. Let  $p_i$  be the probability of finding the level of the  $i$ -th attribute in the entire population similar to that in the alleged source then the probability of finding  $N$  uncorrelated attributes (which may be measured) in levels similar to those in the alleged source is  $P_N = \prod_{i=1}^N p_i$ . The smaller the value of  $P_N$ , the more weighty is the evidence. The value of an attribute towards identification depends on "the ratio of the measurement error to the spread of the attribute over the population and also on the value of the sample measurement when referred to the peak of the frequency distribution"<sup>2(b)</sup>. In the case of normal distributions the probability  $p_i$  of finding the level of the attribute  $i$  in the entire population similar



TABLE I

Sample 1 w.r.t. "control" (NAA of human hair)<sup>2(b)</sup>

Attribute	$q$ (estimated)	$D_i^2$		$\Delta_i^2$	$Q \geq 1$	$Q_{min} = 1$	
		Using $\ln c$ units	Using $c$ units			( $P=80\%$ ) $=Q(1-1.38q)$	( $P=95\%$ ) $=Q(1-2.26q)$
Na	0.24	4.1	2.5	6.2	1.60	1.07	—†
Zn	0.10	2.6	2.9	2.9	1.17	1.01	—
		Likewise for Cl, Mn, I, Cu, Br, Au, Hg					
N=9		$\Sigma=15.1$	$\Sigma=12.4$	$\Sigma=22.8$		$\Pi=1.22$	$\Pi=1.0$

† a dash denotes  $Q_{min}=1.00$ .

TABLE II

Summary of analysis of data on samples Nos. 1, 4, 15, 30 w.r.t. "control" (NAA of human hair)<sup>2(b)</sup>

Sample No.	No. of attributes measured	$\sum D_i^2$ using $\ln c$ units	$\sum \Delta_i^2$	$\prod Q_i(1-2.26q_i)$	Remarks
1	9	15.1	(12.4)†	22.8	(12.3)* 1.0 Source similar to control
4	10	42.9	(33.9)†	111.0	(34.0)* 1.28 Source different, significant discrepancy
15	10	209.2		2760	17.2 Source different, large discrepancy
30	9	$2.61_3 \times 10^3$		$2.30_6 \times 10^3$	108.3 Source different, v. large discrepancy

† recalculated values, using  $c$  units, instead of  $\ln c$  units.

$\sum_0^9=27.8$ ,  $\sum_0^{10}=29.6$  (at 0.1% probability level for  $C > C_0$  or  $\theta > \theta_0$ )

\* Calcd. without imposing the condition  $Q \geq 1$ ;  $Q=(X_1/X_2) \geq 1$ .

TABLE III

Soils (F and K-1)—Evaluation of spectrographic (Seidel function) data<sup>5</sup>

Attribute	$q_1$	$q_2$	$q$	$D_i^2$	$\Delta_i^2$	$Q \geq 1$	$Q_{min} = 1$ $=Q(1-2.26q)$
Mn	0.20	0.21	0.29	11.6	92.9	3.79 <sub>5</sub>	1.31
Likewise for Al, Si, Cr, Na, Fe, Mg, Cu, Ca							
Ti	0.25	0.21	0.32 <sub>7</sub>	15.5	259.5	6.26 <sub>7</sub>	1.63 <sub>5</sub>
N=10				$\sum^{10}=108.1$	$\sum^{10}=629.5$		$\Pi=4.10$

Conclusion: Soils from different sources.

to that in the crime material or the alleged source, for which the intrinsic variability of the material and the measurement errors are determined would simply be given by the ratio of areas under the respective distribution curves,  $a/A$ , where  $a$  is that under the source curve and  $A$  is that under the population curve. If the latter is plotted as  $\phi_x$  vs

$\sigma$  curve (Fig. 1) such that the normal distribution is valid:  $\phi_x = (1/\sqrt{2\pi}) \exp(-x^2/2)$  where  $x$  is measured in standard deviation  $\sigma$  units, we have, by definition, area under population curve (PQR, Fig. 1),  $A=1$ . Therefore  $p_i=a$ , the area under the distribution curve for the source (say, ABC or DEF) which is properly constructed within the

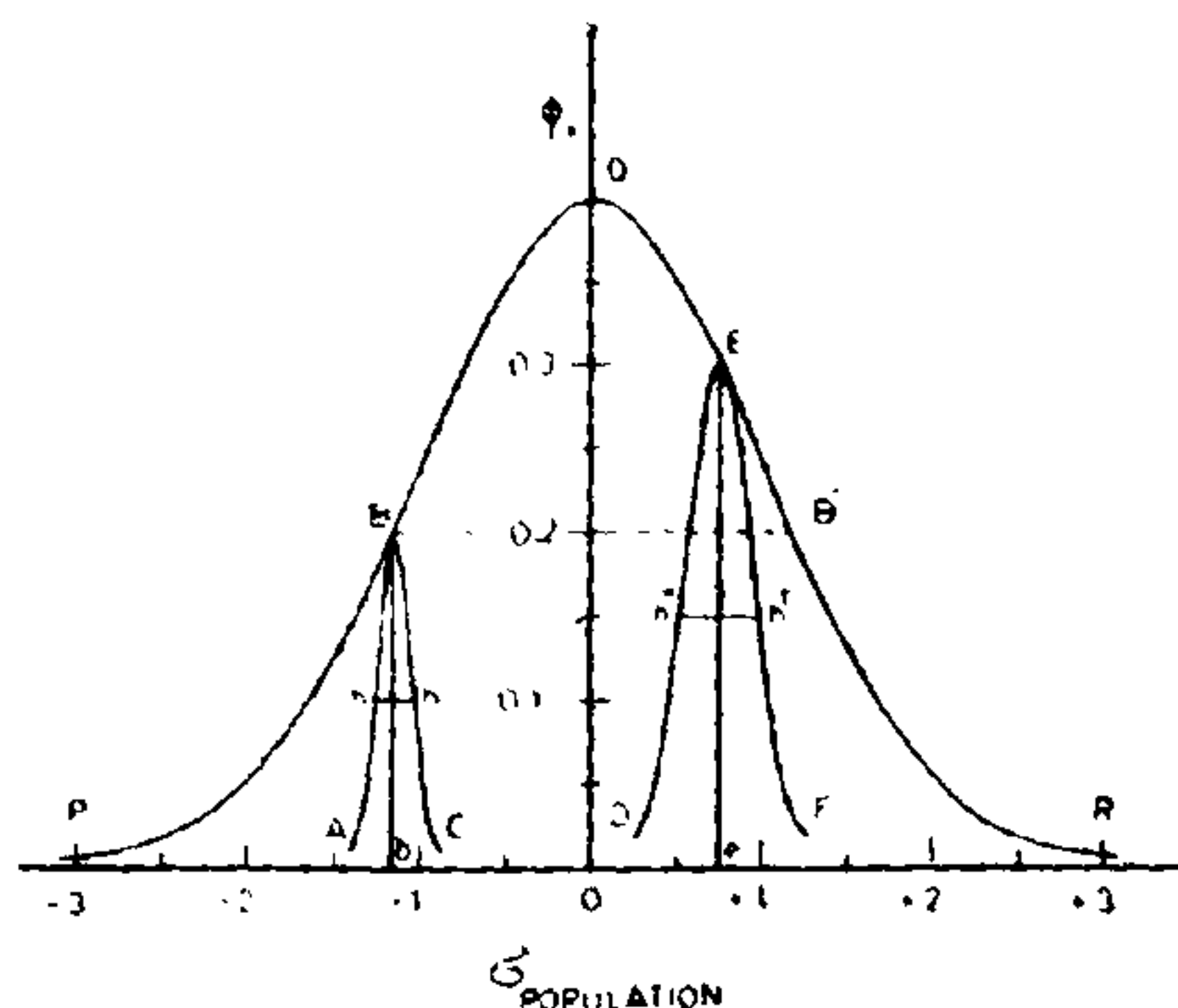


FIG. 1. Construction of a typical normal distribution curve for the alleged source material (ABC or DEF) within that of the population (PQR).  $p_i$ ,  $t$  in  $\sigma_{\text{population}}$  units.  $\sigma_{\text{source}}/\sigma_{\text{population}} = 0.047$ ,  $-1.17$ ,  $0.1$  and  $0.14$ ,  $+0.75$ ,  $0.2$  for curves ABC and DEF respectively.

The approximation in the above equation may be corrected for by utilizing:

$$p_i = 2.51 \phi^*_{x,i} (\sigma_{\text{source}}/\sigma_{\text{population}})_i \quad (5)$$

with benefit to the accused.  $\phi_{x,0}$  ( $\phi$  corresponding to  $\sigma = 0$ ) =  $0.3989$ , is equivalent to area,  $A = 1$  (vide supra). Therefore, area equivalent to  $\phi^*_{x,i} = (1/0.3989) \phi^*_{x,i} (\sigma_{\text{source}}/\sigma_{\text{population}})_i$ , the same as in eqn. (5).

**Illustration.**—The calculation of  $P_N$  for a sample human hair<sup>2(b)</sup> is illustrated in Table IV. The analysis utilizing eqn. (5) would thus reveal, granted that our assumption of (log —) normal distribution over the population is valid and that the attributes are uncorrelated, that there is 1 in  $\sim 10^7$  chance of finding such hair in the population in question, with levels of the ten attributes in question similar to those in the given sample. The magnitude of  $P_N$  is indicative of the uniqueness of the given physical evidence material. It is an attempt to quantitate the evidential value.

TABLE IV

Uniqueness of crime material—Human hair in "control" sample<sup>2(b)</sup>

Attribute	$\frac{\mu_{\text{control}} - \mu_{\text{population}}}{\sigma_{\text{population}} = t}$	$\phi^*_t$ (corresponding to $t$ )	$p_i = 2.36 \phi^*_t \left( \frac{\sigma_{\text{control}}}{\sigma_{\text{population}}} \right)$
Na	0.442	0.362	0.201
Likewise for Cl, Mn, I, Cu, Br, Au, Hg, Zn			
Sb	0.855	0.277	0.284

$$P_N = 1.1 \times 10^{-7} \text{ (Eqn. 5)}$$

$$P_N = \prod p_i = 0.58 \times 10^{-7}$$

population curve. Evaluate  $t = |\mu_{\text{population}} - \mu_{\text{source}}|/\sigma_{\text{population}}$ , where  $\mu$  is the mean value. The crime material or the source is therefore  $t$  units of population-standard deviations removed from the population mean value. Construct a normal curve on the ordinate at  $t$  converting  $\sigma_{\text{source}}$  into  $\sigma_{\text{population}}$  units, by the factor  $(\sigma_{\text{source}}/\sigma_{\text{population}})$ . The area under the source curve,  $a$ , can be evaluated as  $a = \phi^*_t$  (H.I.B.W.) where  $\phi^*_t$  is the ordinate corresponding to the  $t$  value (e.g., Bb or Ee) which can be directly read from the normal error curve tables. The half-intensity band width, H.I.B.W., (e.g.,  $hh'$  or  $h'h''$ ) =  $2.36 (\sigma_{\text{source}}/\sigma_{\text{population}})$  for the source curves. H.I.B.W. =  $2.36 \sigma$  units for any normal curve. We have, therefore,

$$p_i = a_i = 2.36 \phi^*_{x,i} (\sigma_{\text{source}}/\sigma_{\text{population}})_i$$

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