Letters to the Editor

Further Discussion on Discussion of "Hair Analysis for Drugs of Abuse"

Dear Sir:

The comments of Dr. Frederick C. Sauls in the July 1990 issue of the *Journal of Forensic Sciences* (Vol. 35, No. 4, p. 778) regarding the inadequacy of the article by Baumgartner, Hill, and Blahd on "Hair Analysis for Drugs of Abuse" (Vol. 34, No. 6, Nov. 1989, pp. 1433–1453) prompted me to add my own views on this subject.

I, too, was very disappointed to find the *Journal of Forensic Sciences* willing to accept for publication an article in which the very core of the scientific method is hidden behind the veil of "proprietary secret." This has been a persistent ploy of Dr. Baumgartner for several years in his attempts to evade proper scientific scrutiny of his method.

I had the pleasure of offering testimony opposing that of Dr. Baumgartner late in 1987 in a court trial in North Carolina, in which the military judge held that the method did not meet minimal criteria for introduction as evidence. This trial followed, by over a year, an earlier trial in California, in which the military judge reached similar conclusions based on the lack of open testing and the alleged "proprietary" nature of the details of the procedure.

As is perhaps implied in Dr. Saul's comments, the manuscript serves more to further the advertising purposes of Psychemedics Corp. than to advance scientific knowledge. (The opinions expressed are not necessarily those of the U.S. Department of Defense nor of the U.S. Department of the Navy, but are solely the opinion of the author.)

> Saul B. Needleman, Ph.D. Navy Drug Screening Laboratory Building 38-H Great Lakes, IL 60088-5223

Author's Response

Dear Sir:

Dr. Saul Needleman, in his letter to the editor, misinterprets my reluctance to disclose Psychemedics Corporation's [patent pending] proprietary technology for hair analysis and the central issue of two court-martial proceedings in which hair analysis was used.

I can assure Dr. Needleman that the patent status of our technology is not "a ploy ... to evade proper scientific scrutiny." As was pointed out in my first letter to the editor (*Journal of Forensic Sciences*, Vol. 35, No. 4, July 1990, pp. 778–779), in response to Dr. Frederick C. Sauls, the advantage of the proprietary hair analysis technology lies mainly in its commercial viability for mass screening. For isolated forensic cases, one of several published methods, including those from our own laboratory, can be and are used. Furthermore, Psychemedics and eight other laboratories are currently collaborating with the National Institute of Standards and Technology for further evaluation of the published and proprietary methods.

With respect to the two court-martials, I would like to remind Dr. Needleman that the evidence which I presented at those proceedings was, for obvious reasons, obtained by my published methods. Therefore, the alleged "lack of open testing" never became an issue in these court-martials. Instead, the central issue was whether defendants who tested positive by urine and negative by hair analysis could be given the benefit of the doubt. I pursued this argument on the basis of the superior performance of hair analysis over urine analysis for identifying drug users.

Werner A. Baumgartner, Ph.D. Scientific Director Psychemedics Corporation 1807 Wilshire Blvd., Suite B-2 Santa Monica. CA 90403

Discussion of "Analysis Protocol for Discrimination of Automotive Paints by SEM-EDXA Using Beam Alignment by Current Centering"

Sir:

I read with interest the article by Teresa Beam and Dr. William Willis titled "Analysis Protocol for Discrimination of Automotive Paints by SEM-EDXA Using Beam Alignment by Current Centering" (*Journal of Forensic Sciences*, Vol. 35, No. 5, September 1990, pp. 1055–1063) and applaud the authors' statistical evaluation of this type of data. I would like to address several statements in this article.

The peak-to-background (P/B) ratio is defined as $(I_i - I_b)/I_b$, where I_i is the intensity of the peak of interest and I_b is the intensity of the background [1]. P/B measurements have been shown to be insensitive to detector efficiency, beam current fluctuations, and live-time correction inaccuracies, which makes them useful first approximations of elemental concentrations in particulate or rough surface samples [2]. Since spectral resolution is dependent on the count rate, and since as resolution decreases, the P/B ratio becomes lower for a given energy [1], the authors' statement that "the greater the count rate, the greater the peak-to-background ratio" is incorrect. The decline in P/B ratio occurs because, to obtain a significant net count intensity for a peak, it is necessary to sample a wider energy range containing more background counts [1].

The authors display a common misconception when they claim that "excessive dead time necessitates longer acquisition times, as does very low dead time." Dead time, which occurs when the system cannot process an incoming X-ray signal, is in contraposition to live time, the actual period during which the system can accept new X-ray signals. When live time is calculated adjusting for dead time, real time, the actual elapsed clock time, is the result. The authors' statement is misleading because, to achieve the same number of counts in a spectrum, an acquisition with high dead time will take proportionately longer (more clock seconds) than one with a low dead time, which will require an absolutely longer live time (more time spent sampling the specimen) to achieve the same number of counts. On two spectra acquired in our laboratory, the times required to achieve 100 000 counts in a spectrum were the following:

Counts/s	Dead Time, %	Real Time, s	Live Time, s
2700	20	72	58
9400	50	25	12

As can be seen, an obvious difference exists in real time between very high and very low dead time acquisitions.

Finally, a note on beam alignment by current centering (BACC). While it is true that using an optical microscope to columnate and align the beam before the objective lens is critical for microanalysis, it is only true for certain methods. In wavelength-dispersive spectroscopy (WDS), beam alignment and specimen focusing are crucial because the X-rays must impinge the detector precisely on the Rowland circle to be admitted into it—geometry is everything. BACC is also critical to high-resolution (high-magnification) scanning electron microscopy (SEM) imaging to reduce astigmatism in the electron beam. I submit, however, that for energy-dispersive spectroscopy (EDS), which has less stringent geometrical requirements than WDS, BACC would add no perceptible precision or accuracy to the analysis. It would be far more important to reduce the probe current fluctuations to less than $\pm 1\%$, so that the acquisition parameters would be consistent. Also, since the authors are working at $\times 200$, any BACC alignment would not be significant or even noticeable at that comparatively gross scale.

These points aside, I commend Beam and Willis for the main thesis of their article, that statistically oriented, quantitative analysis of paint chips by EDS can produce far more credible evidentiary reports than simplistic and highly subjective qualitative comparisons.

> Max M. Houck Manager, Midwest Applications Link Analytical Old Sauk Trails Park 8017 Excelsior Drive Madison, WI 53717

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Author's Response

Dear Sir:

Thank you for the opportunity to respond to Mr. Houck's letter, which contains some incorrect interpretations and extrapolations of our work. I would like to address the following three points.

Spectrometers for energy-dispersive X-ray analysis (EDXA) have lower peak-to-background (P/B) ratios and wider peaks than do wavelength-dispersive instruments. This ratio should be maximized for the best analytical EDXA work. Up to the point where bremsstrahlung and fluorescence become excessive, the peak intensity (I_i) increases more rapidly with accelerating voltage than does the background intensity (I_b) over the energy range of interest, and so the P/B ratio, defined as $(I_i - I_b)/I_b$, increases as the total count rate increases [1]. It is in this context that we made the statement that the P/B ratio increases with the count rate, with the common and implicit understanding that a constant energy range is being used. Mr. Houck evidently uses a different basis for comparison.

Large dead-time corrections in the case of high count rates are usually made by extending the acquisition time to compensate for lost counts. For low count rates, which have smaller associated dead times, longer counting periods are required to obtain statistically significant results [2]. As Mr. Houck points out, there is a difference between real time and live time for the two situations, but operationally, the results is the same for both cases: a longer data acquisition period is required, as we stated. We made no statement, implied or otherwise, that the causes were the same for both. Compensation

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for high dead times during high count rates and compensation for low dead times during low count rates both require longer acquisition times (real time) to achieve the same statistical reliability. As is discussed in the sentence in our article following the one quoted by Houck, we chose 33% dead time as a compromise between dead time and acquisition time considerations, once the sample-to-detector distance was chosen in our instrument. This distance also affects the P/B ratio, and must be optimized as well.

The inhomogeneities of painted automobile surfaces have been well documented by several investigators (see Ref 3, for example). These and other studies on various coatings have shown that larger spot sizes (that is, lower magnifications) are necessary to achieve the desired discrimination between similar paints. The reasons for this are complex and involve much more than beam alignment by current centering (BACC) considerations alone [4]. We studied the effects of beam magnification on the overall ability of EDXA to discriminate between similar automobile paint samples and found that a magnification of $\times 200$ was the best compromise in our instrument. Contrary to Mr. Houck's submission, we have found that BACC *does* improve the accuracy and precision of the analysis [5]. BACC is less critical for modern paints, which have particles between 0.5 and 1.0 μ m in size, provided the beam scan covers at least 150 μ m², as reported by others. For other types of samples with gross inhomogeneities, BACC becomes much more critical, so our efforts were directed toward developing a generally useful protocol.

William V. Willis, Ph.D. Professor of Chemistry California State University at Fullerton Fullerton, CA 92634

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Discussion of "Role of Forensic Science in a Democracy"

Dear Sir:

In his letter to the editor (*Journal of Forensic Sciences*, Vol. 35, No. 5, Sept. 1990, p. 1021), Barry Fisher wished every success to our Soviet, Eastern European, and Central American colleagues in their efforts to bring about democracy in their own countries. He also endorsed mutual cooperation in efforts to advance the forensic sciences.

No doubt, well-wishes and endorsements are important parts of any undertaking. However, practical application of the principles and assistance in their implementation are even more important elements in the long process of democratization.

Bearing this in mind, about two years ago, Forensic Scientist's Services contemplated an Educational Exchange Program for Forensic Scientists. After much planning and negotiating with the Soviet Ministry of Justice and with Soviet and American colleagues, a program to benefit both Western and Soviet forensic scientists was established. As a first step in this program, the All-Union Scientific-Research Institute of Forensic Expertise (AUSRIFE) of the Ministry of Justice in Moscow, USSR, extended an invitation to forensic specialists from the United States and other countries to visit the institute in July 1990.

The first group of 30 specialists in various areas of forensic sciences from the United States and Finland completed the inaugural trip. In November 1990, in accordance with our program, several Soviet specialists visited the Central Police Crime Laboratory in Helsinki, Finland. Hopefully, this May and June, Soviet forensic scientists will visit several crime laboratories in the United States.

It is necessary to emphasize that our trips are not like many other tour packages. Participants in our groups study and work side by side with our counterparts, present technical and scientific papers, and exchange experience and expertise in various areas of the forensic sciences. We visited with our colleagues in their homes, had prolonged professional discussions, enjoyed Russian hospitality, and made quite a few friends.

We hope this sort of exchange will not only benefit Western forensic specialists but will also expose our Soviet colleagues to Western values and life-styles and will help them on the very bumpy and difficult road to democracy.

> Ilya Zeldes, Ph.D Forensic Scientist's Services 631 North Huron Ave. Pierre, SD 57501

Author's Response

Dear Sir:

Dr. Ilya Zeldes describes one way for interested forensic scientists to assist forensic scientists in developing democracies. Another way is through the U.S. Department of Justice's International Criminal Investigative Training and Assistance Program (ICITAP), which provides internship opportunities for visiting forensic scientists from Central America, South America, and the Caribbean countries. Agencies that may wish to have a visiting scientist study in their laboratory should contact Rodger Asbury, Forensic Science Development manager, at (telephone) 202-653-9122 for details.

Barry A. J. Fisher, M.S., M.B.A. Director, Scientific Services Bureau Los Angeles County Sheriff's Department 2020 West Beverly Blvd. Los Angeles, CA 90057-2494

Correction to "Amplification of a Variable Number of Tandem Repeats (VNTR) Locus (pMCT118) by the Polymerase Chain Reaction (PCR) and Its Application to Forensic Science"

Dear Sir:

The paper by Kasai, Nakamura, and White that was published in the September 1990 issue of the *Journal of Forensic Sciences* (Vol. 35, No. 5, pp. 1196–1200) contains an error in the original designation of the genetic locus described in the article which has been brought to the authors' attention. Dr. Nakamura gave MCT118 the locus number D1S58, which was, in fact, assigned to another of his probes.

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The correct designation for MCT118 is D1S80, and it is so listed with ATCC. Because this discrepancy may cause confusion for scientists who wish to obtain the pMCT118 probe for forensic purposes, the authors are anxious that this correction be printed in the *Journal*.

Ruth Foltz Howard Hughes Medical Institute Research Laboratories University of Utah Medical Center 603 Wintrobe Bldg. Salt Lake City, UT 84132

Description of the Abrasion Furrow in Hanging

Dear Sir:

As I review yet another suicidal hanging case in which a pathologist is trying to describe the abrasion furrow as an "inverted V-shaped furrow, with inverted V in the left posterior neck," I again wonder why we don't just describe the injury as a teardrop-shaped abrasion furrow with the apex behind the left ear. Taken in its entirety, the furrow is exactly teardrop shaped and there is only one apex. This is not only more concise and accurate but possibly more understandable to those we are addressing.

> Collie M. Trant, M.D. Medical Examiner Tripler Army Medical Center Honolulu, Hawaii 96859-5000

Estimating the Second Breath Alcohol Measurement from the First: A Model Refinement

Sir:

Simple linear regression is used as a model for prediction in many areas involving bivariate data. The application of this method to duplicate breath alcohol analysis was previously discussed [1], and a linear model and prediction intervals were developed for estimation of a particular second breath alcohol measurement (BrAC2) given the first breath alcohol measurement (BrAC1). This letter is an expansion and refinement of that analysis.

Figure 1 shows the scatter plot of bivariate data (BrAC1, BrAC2), which is the same as that previously reported [1]. Only data with BrAC1 and BrAC2 ≥ 0.01 g/210 L were employed, and each value was truncated to two digits. Important parameters in simple linear regression that evaluate the model include the slope (b_1) , the intercept (b_0) , the standard error of the estimate (SEE), and the coefficient of linear correlation (r). For the data presented in Fig. 1, the parameters, along with their standard errors and confidence intervals, are shown in Table 1 [2]. It is apparent that the slope (b_1) is very close to unity, and the intercept (b_0) is very close to zero. Their 95% confidence intervals do not include unity or zero, respectively, probably because n is so large (n = 2668). The data are also well distributed throughout the range of model estimation, which is an important criterion in linear regression. Admittedly, both variables would be expected to have the same measurement error, since, in each case, the measurements were made using the same instrument and the same subject. Although some may question this application of simple linear regression, it at least does not violate the important regression principle that the dependent variable must be less precise than the independent variable [3].

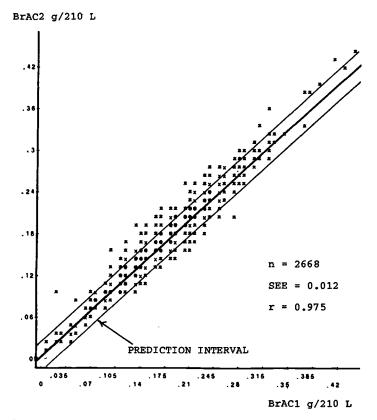


FIG. 1—Regression of the second breath alcohol measurement (BrAC2) upon the first (BrAC1).

 TABLE 1—Regression parameters, along with their standard errors and 95% confidence intervals [2].

Parameter	Value	Standard Error	95% Confidence Interval
Slope (b_1)	0.966	0.004	0.958 to 0.974
Intercept (b ₀)	0.004	0.0007	0.0025 to 0.0055
Correlation coefficient (r)	0.975	0.019	0.973 to 0.977
Standard error of the estimate			
(SEE)	0.012		
Data points (n)	2668		

Since the data set is so large (n = 2668), the prediction interval about the line will be essentially parallel, which implies that there is an equal prediction interval throughout the measurement range. This is shown in Fig. 1 and represents the 95% prediction interval for estimating the dependent variable (BrAC2) given any particular independent variable (BrAC1). Predicting a particular dependent variable will have more uncertainty associated with it than predicting the mean dependent variable for a given independent variable [4].

The equation for computing BrAC2 for a given BrAC1 is

$$BrAC2 = 0.966 BrAC1 + 0.004$$
 (Eq 1)

Given a particular BrAC1 value computed from Eq 1, the prediction interval around the result is computed from Ref 5 as

BrAC2
$$\pm t \cdot \text{SEE} \sqrt{1 + \frac{1}{n} + \frac{(\text{BrAC1} - \overline{\text{BrAC1}})^2}{(n-1)S_x^2}}$$
 (Eq 2)

Equation 2 may be better described as a prediction interval rather than a confidence interval since the predicted value is a variable rather than a population parameter [5].

As previously reported, the important part of the prediction interval calculation is the SEE. Since n is so large, the portion under the radical is insignificant and can be disregarded.

Figure 2 shows a plot of standardized residuals about the best-fit predicted line. The residuals are standardized by dividing by SEE [6]. Residuals contain information on variability not explained by the regression line [7]. The uniformity of residuals indicates the homoscedastic nature of the data, which is an important assumption in simple linear regression [3].

The application, again, of this model is seen in its ability to predict a second breath alcohol measurement (BrAC2) from the first (BrAC1). In some circumstances, BrAC2 may not be available and some estimate of its value and prediction interval needs to be assessed. It is important to remember that extrapolation beyond the limits of the data and fitted line is generally unwarranted [8]. The present data had BrAC1 limits of 0.01 to 0.44 g/210 L. Again, jurisdictions that may apply this model should have regression line estimates determined from their own data, employing their own instrumentation, operators, protocol, and environment. Models based on fewer data may also require that

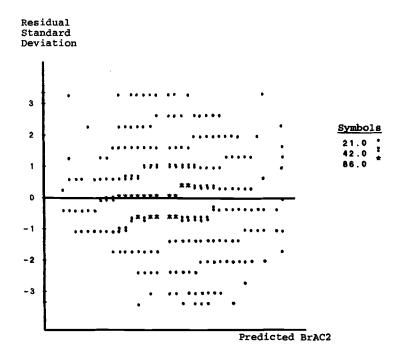


FIG. 2—Plot of standardized residuals with respect to the predicted BrAC2 from the regression line.

the value under the radical sign in Eq 2 be included in computing the prediction interval. Models can also be updated as data accumulation continues.

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