

## Articles

# Gravimetric Approach to the Standard Addition Method in Instrumental Analysis. 1.

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A mathematical formulation for a gravimetric approach to the univariate standard addition method (SAM) is presented that has general applicability for both liquids and solids. Using gravimetry rather than volumetry reduces the preparation time, increases design flexibility, and makes increased accuracy possible. SAM has most often been used with analytes in aqueous solutions that are aspirated into flames or plasmas and determined by absorption, emission, or mass spectrometric techniques. The formulation presented here shows that the method can also be applied to complex matrixes, such as distillate and residual fuel oils, using techniques such as X-ray fluorescence (XRF) or combustion combined with atomic fluorescence or absorption. These techniques, which can be subject to matrix-induced interferences, could realize the same benefits that have been demonstrated for dilute aqueous solutions.

The frequently used standard addition method (SAM) was first described for the flame photometric analysis of Sr in seawater by Chow and Thompson<sup>1</sup> more than 50 years ago. They stated, “The ‘internal standards’ technique was developed to eliminate the interferences caused by the fluctuations of the physical and chemical properties of the solution.” SAM is now a well-known and established means of eliminating multiplicative biases in chemical determinations. In SAM one adds varying amounts of the analyte ( $x_0 < x_1 < x_2 \dots < x_{n-1} < x_n$ ) to a series of unknown solutions of constant volume and then dilutes the solutions to the same volume so as to yield a series of solutions with identical matrix concentrations but with increasing concentrations of the analyte. The additions are usually added in equally spaced increments with  $x_0$  equal to zero, but they need not be. One then measures the responses ( $R_0, R_1, R_2, \dots, R_n$ ) of the solutions. From regression of the responses versus the additions, the concentration of the analyte in the unknown is given by the abscissa intercept.

Improvements in both inductively coupled plasma mass spectrometry (ICPMS) and optical emission spectrometry (ICP-OES) instrumentation and software<sup>2</sup> now make possible relative precisions of  $\leq 0.1\%$ , but these techniques are still subject to matrix interferences, and therefore SAM is frequently and increasingly used in inorganic analysis. While many textbooks on analytical chemistry cover SAM, most give only a rudimentary description of the method and an incomplete uncertainty analysis. An excellent and easily readable introduction to SAM is the often-cited paper of Bader<sup>3</sup> who gives the mathematical formulation for nine different cases, the first five of which are for an instrument with linear response. Bader’s uncertainty analysis omits covariance and does not consider optimization of experimental design; both of these topics and bias will be the subject of a future paper.<sup>4</sup> A more comprehensive and general treatment is that of Saxberg and Kowalski.<sup>5</sup>

Previous theoretical and experimental treatments of SAM assume the use of volumetric dilutions. With the advent of isotope dilution analysis after World War II, dilutions on strictly a mass basis became commonplace in the nuclear and geochemical communities. The invention of single-pan mechanical analytical balances in the early 1960s and the more recent digital analytical balances have now made mass determinations (“weighings”) both rapid and accurate. A modern five-place digital single pan balance is about 100 times more accurate than volumetric determinations based on tolerances from NIST (formerly known as Bureau of Standards) specifications.<sup>6</sup> Top-loading balances now have 1 mg accuracy if properly shielded from vibrations and air currents. Gravimetric dilution is now commonly used in laboratories where analyses of the highest precision and accuracy are required.

Christopher et al.<sup>7</sup> recently published a new variant of the SAM procedure based on gravimetry of an internal standard rather than volumetry alone and demonstrated its advantages in the determination of trace elements in biological samples by collision-cell

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(1) Chow, T. J.; Thompson, T. G. *Anal. Chem.* **1951**, *27*, 18–21.

(2) Salit, M. L.; Turk, G. C. *Anal. Chem.* **1998**, *70*, 3184–3190.

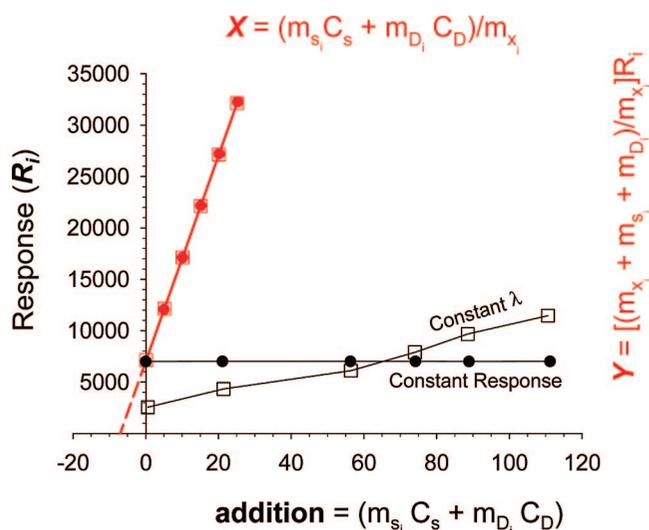
(3) Bader, M. J. *Chem. Educ.* **1980**, *57*, 703–706.

(4) Kelly, W. R.; Guthrie, W. F. In preparation.

(5) Saxberg, B. E. H.; Kowalski, B. R. *Anal. Chem.* **1979**, *51*, 1031–1038.

(6) Hamilton, L. F.; Simpson, S. G. *Quantitative Analysis*, 12th ed.; MacMillan: New York, 1964; p 122, see Table VI.

(7) Christopher, S. J.; Day, R. D.; Bryan, C. E.; Turk, G. C. *J. Anal. At. Spectrom.* **2005**, *20*, 1035–1043.



**Figure 1.** Plot of the data in Table 1 showing two extreme designs of standard addition experiments involving the mixing of three complex matrix solutions: case B<sub>1</sub>, constant response, and case B<sub>2</sub>, constant  $\lambda$ . The mean count rate in both cases was made to be identical. The data for both cases transformed for gravimetric analysis are shown in red.

ICPMS. They added a nonanalyte element internal standard before chemical treatment which served as both a chemical yield and instrumental drift monitor.

Barker et al.<sup>8</sup> have recently demonstrated the use of these procedures in the determination of sulfur in diesel and biodiesel fuels by XRF and demonstrate the unique advantages of this approach in paper II. Both of these treatments are an extension of Bader's case 5 (variable total volume with continuous variation of standard) and demonstrate and suggest new and improved applications of the technique.

The treatment presented here is a general formulation based on gravimetry that essentially covers all five cases considered by Bader for linear instruments. In this paper, the notation and initial formulation will follow that of Bader<sup>3</sup> as shown in the Glossary. The discussion of uncertainties and optimal design associated with gravimetric SAM will be presented in a future companion paper.<sup>4</sup>

**Case A, Aqueous Solutions.** The treatment that follows assumes linear response of an instrument over the domain of interest where the instrument response is proportional to the concentration or is proportional to the absolute amount of the analyte, E, of interest:

$$\begin{aligned} r_i &= k[\text{moles}_{E_i}/\text{mass}_i] = kC_{E_i} \\ r_i &= k\text{moles}_{E_i} \end{aligned} \quad (1)$$

The gross response,  $r_i$ , of an analyte from a series ( $i = 0, 1, 2, 3, \dots, n$ ) of binary mixtures of solutions, the unknown,  $C_x$ , of volume  $M_i V_x$  and a higher concentration standard,  $C_s$ , of volume  $N_i V_s$  is given by the following

$$r_i = k \left[ \frac{M_i V_x C_x}{M_i V_x + N_i V_s} + \frac{N_i V_s C_s}{N_i V_x + N_i V_s} \right] + kB + \sum_j k\beta_j \quad (2)$$

The first term of eq 2 is identical to Bader's eq 23 except in this general treatment the volume of  $C_x$  is not held constant, hence

inclusion of the parameter  $M_i$  in both the numerator and denominator of the first term. The value in the brackets is the concentration of the mixtures, the second term is the response from the blank atoms or molecules that are identical to the analyte of interest, and the third term represents interferences, response from species that mimic the analyte of interest either in mass or emission or absorption of radiation.

In trace analysis the last two terms of eq 2 govern the method detection limit and are frequently the dominant sources of uncertainty. It is usually possible to design experimental conditions such that the last term in eq 2 is negligible by choosing the optimum emission line or a mass that is interference free. For an ideal instrument, this last term would be zero for all experimental conditions. Conversion of the volumes to masses gives the following

$$r_i = k \left[ \frac{m_x C_x}{m_x + m_s} + \frac{m_s C_s}{m_x + m_s} \right] + kB + \sum_j k\beta_j \quad (3)$$

where the  $m_x$  and  $m_s$  are the masses of the unknown and standard. For instruments that require aspiration of the sample into a flame or plasma, it is important that the physical and chemical characteristics of the different samples remain essentially identical which in turn requires  $m_x$  to be much greater than  $m_s$  or vice versa. Alternately, a diluent,  $C_D$ , of mass  $m_{D_i}$  may be added to each sample. The diluent solution is typically high-purity water or dilute acid, and it is usually assumed that the diluent does not change the relative concentration of the analyte between spike and unknown. If the diluent contains a significant and known concentration of the analyte, then the formulation can be changed to correct for this as is shown in the next section in eq 10. For the present discussion it is assumed that the product,  $m_{D_i} C_D$ , is negligible. The net response,  $R_i$ , for each mixture is given by the following

$$R_i = r_i - \left( kB + \sum_j k\beta_j \right) = k \left[ \frac{m_x C_x}{m_x + m_s + m_{D_i}} + \frac{m_s C_s}{m_x + m_s + m_{D_i}} \right] \quad (4)$$

where the net response values are assumed to be statistically independent. This requires the uncertainties of the two terms in parentheses to be negligible compared to those for the values of  $r_i$ . It is usual for the interference term to be extremely small by proper design. If the blank term is not small, then paired blanks and samples must be determined to maintain independence.

Equation 4 can be rearranged into a linear form,  $y = mx + b$ ,

$$\left( \frac{m_x + m_s + m_{D_i}}{m_x} \right) R_i = k \left( \frac{m_s C_s}{m_x} \right) + kC_x \quad (5)$$

The masses are subject to the following condition if the intent is to hold the physical and chemical characteristics of each sample constant, which is the normal motivation for employing the technique:

$$\frac{m_s + m_{D_i}}{m_x} = \lambda \quad (6)$$

(8) Barker, L. R.; Kelly, W. R.; Guthrie, W. F. *Energy Fuels*. In press.

**Table 1. Hypothetical Data To Illustrate the Two Extreme Cases of Standard Additions**

$m_{x_i}^a$	$m_{s_i}^a$	$m_{D_i}^a$	addition <sup>b</sup>	$C_i^c$	$\lambda^d$	$R_i^e$	$X^f$	$Y^g$
Case B <sub>1</sub> , Constant Response, $R_i$								
4.327 71	0	0	0	7.0000	0	7000	0	7 000
4.174 50	0.522 74	2.48960	21.086	7.0000	0.7216	7000	5.0512	12 051
5.571 70	1.39 540	6.64570	56.288	7.0000	1.4432	7000	10.1025	17 102
4.894 68	1.838 77	8.75730	74.173	7.0000	2.1648	7000	15.1537	22 154
4.400 52	2.204 17	10.4976	88.912	7.0000	2.8864	7000	20.2049	27 205
4.402 72	2.756 59	13.1285	111.20	7.0000	3.6080	7000	25.2562	32 256
Case B <sub>2</sub> , Constant $\lambda$								
4.32771	0	7.807 18	0.5543	2.5421	1.804	2542	0.1281	7128.1
4.17450	0.522 74	7.008 07	21.407	4.3253	1.804	4325	5.1281	12128
5.57170	1.395 40	8.655 95	56.431	6.1085	1.804	6108	10.1281	17128
4.89468	1.838 77	6.991 23	74.047	7.8916	1.804	7892	15.1281	22128
4.40052	2.204 17	5.734 37	88.574	9.6748	1.804	9675	20.1281	27128
4.40272	2.756 59	5.185 92	110.63	11.458	1.804	11458	25.1281	32128

<sup>a</sup>  $m_{x_i}$  are the masses of the unknown that were chosen randomly.  $m_{s_i}$  and  $m_{D_i}$  are the masses of known sample and the diluent, respectively. <sup>b</sup> The addition column gives the amount of analyte added from the masses,  $m_{s_i}$  and  $m_{D_i}$ . <sup>c</sup> This is the concentration in the final solution mix. <sup>d</sup>  $\lambda$  is defined by eq 6 in the text. <sup>e</sup> The response  $R_i$  is equal to  $kC_i$ ;  $k$  was set equal to 1000. <sup>f</sup> The  $X$  and  $Y$  values are calculated from eq 10 and are shown along the axes in Figure 1. The ratio of  $b$  over  $m$  from the regression of  $X$  and  $Y$  determines the concentration.

where  $\lambda$  is a constant. There is no restriction on the magnitude of the masses of standard and unknown because the analyst fixes the parameter,  $\lambda$ . After the initial mixes of sample and standard are combined, then the amount of diluent to add to each sample is computed from eq 7:

$$m_{D_i} = \lambda m_{x_i} - m_{s_i} \quad (7)$$

If a three-place balance with 1 mg accuracy or better is used, then eq 7 will yield a very precise value for amount of diluent to be added, but the accuracy needed for the actual addition will be dependent on the sensitivity ( $k$ ) of the system to small changes in the matrix concentration.

If the plot of the array of points (see Figure 1, red line) given by the values on the left-hand side (lhs) of eq 5 versus the values of the factor in parentheses on the right-hand side (rhs) yields a straight line, then a linear regression model gives the slope  $m$  and intercept  $b$  which in turn are equal, on average, to the following quantities:

$$\begin{aligned} m &= k \\ b &= kC_x \end{aligned} \quad (8)$$

The unknown concentration,  $C_x$ , can then be estimated by the intercept divided by the slope:

$$C_x = \frac{b}{m} \quad (9)$$

The masses of the standard and unknown solutions need not be exactly equal to the calculated optimum mixtures. The use of mass rather than volume makes experimental design easier, faster, completely flexible, and more accurate.

**Case B, Complex Nonaqueous Matrix.** SAM has traditionally been applied to highly dilute aqueous solution samples. The matrix may be complex, but the addition solution and the diluent are highly dilute acid solutions which are completely matrix free. However, the procedure and formulation presented here is well-suited for complex matrixes in which the addition and diluent are not dilute aqueous solutions. For example, sulfur in diesel fuel

can be determined by XRF using this technique. Normally, in XRF the response of the unknown is compared to the response defined by a calibration curve. However, sulfur can be determined in diesel fuel without resorting to a calibration curve by adding several portions of the unknown to a CRM of a similar matrix having a higher level of sulfur than the unknown. If necessary, some or all of the samples can be diluted such that the gross responses of the mixtures fall within the linear range of the response curve. If the diluent contains a non-negligible amount of the analyte, then eq 4 will contain an extra term in the rhs bracket and eq 5 will equal the following:

$$\left( \frac{m_{x_i} + m_{s_i} + m_{D_i}}{m_{x_i}} \right) R_i = k \left( \frac{m_{s_i} C_x + m_{D_i} C_D}{m_{x_i}} \right) + kC_x \quad (10)$$

The solution to eq 10 is identical in form to eq 5. In this case, a near-zero sulfur diesel fuel, such as RM 8771 [(0.071 ± 0.014) μg/g], might be used as the diluent to bring the mixtures into the linear range subject to the condition below:

$$r_n > k \left[ \frac{m_{x_i} C_x + m_{s_i} C_s + m_{D_i} C_D}{m_{x_i} + m_{s_i} + m_{D_i}} \right] + kB + \sum_j k_j s_j \quad (11)$$

where  $r_n$  is below the upper limit to the linear range of the response. However, it may be possible by careful design to perform an accurate determination on a nonlinear portion of the response curve as discussed below.

To illustrate this technique, two extreme cases are considered: case B<sub>1</sub>, constant response, in which the count rates for all solutions are identical and case B<sub>2</sub>, constant  $\lambda$ , in which all solutions have identical matrix concentrations. The mass of unknown was chosen randomly using a uniform distribution with a range from 4 to 6 to illustrate that the volume or masses of the unknown need not be constant. In both cases, the addition of the known or spike sample,  $m_{s_i}$ , was identical. The hypothetical data for the two cases are listed in Table 1 and plotted in Figure 1.

**Case B<sub>1</sub>, Constant Response ( $R_i$ ).** If it were desired to keep a constant count rate, then one would add sufficient amount of the diluent such that all the solutions gave the same response as

illustrated in the top half of Table 1 (case B<sub>1</sub>). Unlike traditional SAM where equal increments of  $m_{s_i}$  are added to constant volume of the unknown, it is the value of the abscissa that must be in equal increments as shown in Table 1 and Figure 1. This design might be used for a high concentration sample that is well beyond the linear range of the detector or to minimize dead time corrections at high count rates. The mass balance equation below can be solved for the necessary values of  $m_{D_i}$ . One may wish the count rate to be as low as possible which would be equal to that of the unspiked sample:

$$k \left[ \frac{m_{x_i} C_x + m_{s_i} C_s + m_{D_i} C_D}{m_{x_i} + m_{s_i} + m_{D_i}} \right] = k C_x \quad (12)$$

Solving eq 12 for  $m_{D_i}$  yields the following:

$$m_{D_i} = \frac{m_{s_i} (C_s - C_x)}{C_x - C_D} \quad (13)$$

Equation 13 is a bit unwieldy because an approximate value for  $C_x$  is required for its solution. This value is easily approximated by comparing the response of a solution of known concentration to the unknown solution. In the example shown in Table 1 and Figure 1, the values for  $k$  and for  $kC_x$  are 1000 and 7000, respectively.

**Case B<sub>2</sub>, Constant  $\lambda$ .** If it were desired to keep the matrix constant among all the mixes, then  $m_{D_i}$  can be adjusted according to eq 6 such that all solutions have the same matrix concentration. This is the typical standard addition procedure, and one would use this to remove multiplicative interferences. Once the series of  $m_{x_i}$  solutions has been prepared, then it is necessary to choose the masses,  $m_{s_i}$  and  $m_{D_i}$ , such that all final mixtures have the same  $\lambda$  value. If the design chosen has equally spaced points, then it is the  $X_i$  values that must be equally spaced (see Figure 1) and not the values of  $m_{s_i}$ . Once the values of  $m_{x_i}$ ,  $\lambda$ , and  $X_i$  have been fixed, then the masses of  $m_{s_i}$  and  $m_{D_i}$  are found from the roots of the following two equations:

$$m_{s_i} + m_{D_i} = m_{x_i} \lambda \quad (14)$$

$$C_s m_{s_i} + C_D m_{D_i} = m_{x_i} X_i \quad (15)$$

The needed roots are conveniently calculated from the determinants:

$$m_{s_i} = \frac{\begin{vmatrix} m_{x_i} \lambda & 1 \\ m_{x_i} X_i & C_D \end{vmatrix}}{\begin{vmatrix} 1 & 1 \\ C_s & C_D \end{vmatrix}} \quad (16)$$

$$m_{D_i} = \frac{\begin{vmatrix} 1 & m_{x_i} \lambda \\ C_s & m_{x_i} X_i \end{vmatrix}}{\begin{vmatrix} 1 & 1 \\ C_s & C_D \end{vmatrix}} \quad (17)$$

## CONCLUSIONS

A general solution to the standard additions problem based on gravimetry is described by the formulation in eq 5 with the restrictions of eqs 6 and 11 when applicable. This formulation can be used for solutions that are aspirated into atomic absorption and atomic emission instruments including the now widely used ICP-OES and ICPMS instruments. This mathematical formulation subsumes the first five cases in the paper of Bader<sup>3</sup> and has wide applicability.

SAM can be applied to X-ray fluorescence analysis for the determination of analytes in liquids of a complex matrix. For example, this approach can be used for fossil fuel samples subject to the condition  $C_s \gg C_x \gg C_D$  where all three samples are of the same matrix. In this case an oil containing a higher concentration of the analyte ( $C_s$ ) would be added to the unknown sample ( $C_x$ ) of much lower concentration and diluted with  $C_D$  into the linear range of the instrument. An application to the determination of sulfur in diesel and biodiesel fuels has been presented in paper II.<sup>8</sup>

In addition, conversion from volume to mass makes SAM also applicable for solid samples. For example, for the determination of S and Hg in coal or coke samples by combustion techniques, the total sample is consumed; therefore, powdered samples could be mixed by mass and determined in the same way as liquid samples.

The approach presented here and the discussion of optimal design in the companion paper<sup>4</sup> should result in wider use of standard additions with increased accuracy of the results.

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## GLOSSARY

$B$	blank (atoms or molecules of analyte)
$b$	y-intercept of straight line regression
$C_E$	concentration of an analyte, E
$C_s$	concentration of E in the standard
$C_x$	concentration of E in the unknown
$C_D$	concentration of E in the diluent
$C_t$	true concentration of unknown solution
$i$	number of particular mixture
$k$	instrument sensitivity (response units per mole or per unit of concentration)
$k_j$	instrument sensitivity for species $s_j$
$M$	units of fixed volume of unknown
$m$	slope of straight line
$m_s$	mass of known solution
$m_x$	mass of unknown solution
$m_D$	mass of diluent
$N$	units of fixed volume of standard
$R$	net instrument response for analyte, E
$r$	gross instrument response for analyte
$V_x$	fixed unit volume of unknown
$V_s$	fixed unit volume of known

X value of the transformed abscissa in Table 1 and Figure  
1  
Y value of the transformed ordinate in Table 1 and Figure  
1

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