

MATHEMATICAL ANALYSIS OF SPECIATED ISOTOPE DILUTION MASS SPECTROMETRY

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1 INTRODUCTION

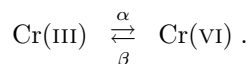
Speciated Isotope Dilution Mass Spectrometry (SIDMS) is a patented process whereby the concentrations of k species in a sample are measured in the presence of inter-species conversion. Most SIDMS applications in the literature determine the concentration of $k = 2$ species, including chromium (III) and chromium (VI) [Kingston 1998,...], inorganic and methylmercury [Monperrus 2007,...], and dibutyltin and tributyltin [Rodriguez-Gonzalez 2007].

In the case where the concentrations of k species are being measured, SIDMS adds to the sample k isotopically enriched spikes. Through knowledge of the species concentrations and isotope ratios within each spike, SIDMS enables researchers to measure the original species concentrations in the sample, as well as the proportions of any inter-species conversion that may have occurred during measurement.

We now establish the SIDMS framework in the popular context of a $k = 2$ species chromium example, where the goal is to determine the concentrations of Cr(III) and Cr(VI) in a sample. Generalizing this framework to other $k = 2$ species contexts is straightforward, as shown in Section 3.2. Define

$$\begin{aligned} x &= \text{Cr(III) concentration in sample} \\ y &= \text{Cr(VI) concentration in sample} \end{aligned}$$

and let proportions α and β describe the bidirectional inter-conversion of Cr(III) and Cr(VI) as follows:



Kingston[ref] show the ratios of the Cr(III) and Cr(VI) ion intensities obtained from the mass spectrometer can be equated to these two unknown concentrations and crossover proportions using the following four equations:

$$R_1 = \frac{(A_1x + B_1)(1 - \alpha) + (A_1y + B_2)\beta}{(A_2x + B_3)(1 - \alpha) + (A_2y + B_4)\beta} \quad (1)$$

$$R_2 = \frac{(A_3x + B_5)(1 - \alpha) + (A_3y + B_6)\beta}{(A_2x + B_3)(1 - \alpha) + (A_2y + B_4)\beta} \quad (2)$$

$$R_3 = \frac{(A_1x + B_1)\alpha + (A_1y + B_2)(1 - \beta)}{(A_2x + B_3)\alpha + (A_2y + B_4)(1 - \beta)} \quad (3)$$

$$R_4 = \frac{(A_3x + B_5)\alpha + (A_3y + B_6)(1 - \beta)}{(A_2x + B_3)\alpha + (A_2y + B_4)(1 - \beta)} . \quad (4)$$

The thirteen known quantities represented in equations (1)–(4) consist of:

- Four ion intensity ratios, corrected for dead-time and mass-bias: $\{R_1, R_2, R_3, R_4\} = \{R_{50/52}^{III}, R_{53/52}^{III}, R_{50/52}^{VI}, R_{53/52}^{VI}\}$. For example, $R_{50/52}^{III}$ denotes the ion intensity of Cr(III) isotope 50 divided by that of Cr(III) isotope 52. Such intensities are obtained from a mass spectrometer.
- The three sample weights of each chromium isotope, using naturally occurring isotope proportions and sample weight W_x : $\{A_1, A_2, A_3\} = \{^{50}A_x W_x, ^{52}A_x W_x, ^{53}A_x W_x\}$. Here $^{50}A_x$ represents the proportion of naturally occurring chromium that is isotope 50.
- The amounts of $^{50}\text{Cr(III)}$, $^{52}\text{Cr(III)}$, and $^{53}\text{Cr(III)}$ in the Cr(III) spike: $\{B_1, B_3, B_5\} = \{^{50}A_s^{III} N_s^{III}, ^{52}A_s^{III} N_s^{III}, ^{53}A_s^{III} N_s^{III}\}$, as well as the amounts of $^{50}\text{Cr(VI)}$, $^{52}\text{Cr(VI)}$, and $^{53}\text{Cr(VI)}$ in the Cr(VI) spike: $\{B_2, B_4, B_6\} = \{^{50}A_s^{VI} N_s^{VI}, ^{52}A_s^{VI} N_s^{VI}, ^{53}A_s^{VI} N_s^{VI}\}$. If W_s^{III} is the weight of the Cr(III) spike, and x_s is the concentration of Cr(III) that spike, then $N_s^{III} = W_s^{III} x_s$.

2 SOLUTION METHODS

Solving equations (1)–(4) for the four unknowns $\{x, y, \alpha, \beta\}$ can be accomplished in a variety of ways. We identify four such ways in this section, starting with those that have been used in the literature, and ending with the yet unpublished method that we recommend.

2.1 The Iterative Method

The original and thus far most widely used solution method in the literature is the iterative method. Fully documented in [ref], it begins by assigning starting values to the unknowns $\{x, \beta\}$, and then solves equations (1) and (2) for $\{y, \alpha\}$. Note that if $\{x, \beta\}$ are fixed, equations (1) and (2) are linear in

$\{y, \alpha\}$ and can be easily solved. These values $\{y, \alpha\}$ are then used to solve equations (3) and (4) for $\{x, \beta\}$, which are then used to solve equations (1) and (2) for $\{y, \alpha\}$, etc. This iterative process is repeated until the values of $\{x, y, \alpha, \beta\}$ obtained at, say, the i th iteration differ by less than some pre-specified threshold from the values at iteration $(i - 1)$.

Although the term “iterative method” is used almost exclusively to describe this solution algorithm in the field of analytical chemistry, from a mathematical standpoint this algorithm is commonly known as the *fixed point method* for, in this case, non-linear equations. Conditions that will guarantee the convergence of this method exist, but have never been identified—much less checked—in the SIDMS literature. It should be noted that these convergence criteria, which we omit here, guarantee convergence only when the initial values of $\{x, \beta\}$ are ‘close’ enough to the true values. While completely effective, this fixed point solution method can be—and in some cases, has been—appraised unfavorably on two fronts:

- Complete implementation of this method is cumbersome and, relative to other solution methods, complex.
- The starting values can impact convergence. (Empirical evidence suggests convergence can be reliably obtained by initializing all concentrations and crossover proportions at zero.)

2.2 The Matrix Method

It is possible to approach solving (1)–(4) from an isotope pattern deconvolution perspective, as introduced and detailed in Meija et al. This method treats the three ion intensities for a given species as dependent variable values, and considers as predictor variables the isotope ratios in both spikes, as well as those in nature. The coefficient estimates for these predictor variables, as obtained by multiple, zero-intercept regression, can then be used to explicitly solve for the unknown crossover proportions and concentrations. We consider this method as a member of the class of matrix methods.

An alternative linear regression based (matrix) approach can be taken wherein the following two quantities are calculated simultaneously using linear regression:

- The proportion of Cr(III) moles at the time of spiking that originated from the Cr(III) spike, and

- The proportion of Cr(III) moles at the time of spiking that originated from the Cr(VI) spike.

Upon obtaining in analogous fashion the two corresponding Cr(VI) proportions, solving for α, β, x and y can be accomplished explicitly. Comprehensive coverage of this matrix method is given in Sun 2007.

Ultimately, solving (1)–(4) using a matrix method is less computationally intensive than an iterative method, and is not dependent on the specification of initial conditions. This method does, however, require the ability to invert matrices (i.e. multiple linear regression software).

2.3 Newton’s Method

If we express—using straightforward algebra—the system of equations (1)–(4) as the following functions f_1, f_2, f_3, f_4 of $\{x, y, \alpha, \beta\}$

$$\begin{aligned} f_1 &= (A_1 - A_2R_1)x - (A_1 - A_2R_1)x\alpha + (A_1 - A_2R_1)y\beta \\ &\quad - (B_1 - B_3R_1)\alpha + (B_2 - B_4R_1)\beta + B_1 - B_3R_1 \\ f_2 &= (A_3 - A_2R_2)x - (A_3 - A_2R_2)x\alpha + (A_3 - A_2R_2)y\beta \\ &\quad - (B_5 - B_3R_2)\alpha + (B_6 - B_4R_2)\beta + B_5 - B_3R_2 \\ f_3 &= (A_1 - A_2R_3)x\alpha + (A_1 - A_2R_3)y + (-A_1 + A_2R_3)y\beta \\ &\quad + (B_1 - B_3R_3)\alpha + (-B_2 + B_4R_3)\beta + B_2 - B_4R_3 \\ f_4 &= (A_3 - A_2R_4)x\alpha + (A_3 - A_2R_4)y + (-A_3 + A_2R_4)y\beta \\ &\quad + (B_5 - B_3R_4)\alpha + (-B_6 + B_4R_4)\beta + B_6 - B_4R_4, \end{aligned}$$

then solving the system (1)–(4) is equivalent to finding the common roots of the (continuously differentiable) functions f_1 through f_4 . That is, the values $\{x, y, \alpha, \beta\}$ that solve equations (1)–(4) are also the values that satisfy

$$f_i = 0 \quad \text{for } i = 1, 2, 3, 4.$$

Newton’s method efficiently finds the roots of continuously differentiable functions by defining the Jacobian matrix J as

$$J = \begin{pmatrix} \partial f_1/\partial x & \partial f_1/\partial \beta & \partial f_1/\partial y & \partial f_1/\partial \alpha \\ \partial f_2/\partial x & \partial f_2/\partial \beta & \partial f_2/\partial y & \partial f_2/\partial \alpha \\ \partial f_3/\partial x & \partial f_3/\partial \beta & \partial f_3/\partial y & \partial f_3/\partial \alpha \\ \partial f_4/\partial x & \partial f_4/\partial \beta & \partial f_4/\partial y & \partial f_4/\partial \alpha \end{pmatrix}$$

where, for example, $\partial f_1/\partial x$ is the partial derivative of f_1 with respect to x . The inverse of this Jacobian is then used to update current values $\mathbf{u}^{(i)} = (x^{(i)}, y^{(i)}, \alpha^{(i)}, \beta^{(i)})'$ in the following iterative scheme:

$$\mathbf{u}^{(i+1)} = \mathbf{u}^{(i)} - J^{-1}(\mathbf{u}^{(i)})\mathbf{f}(\mathbf{u}^{(i)}), \quad i = 0, 1, 2, \dots$$

Here $J^{-1}(\mathbf{u}^{(i)})$ is the inverse of J evaluated at $\mathbf{u}^{(i)}$, while $\mathbf{f}(\mathbf{u}^{(i)})$ is the vector of functions $\mathbf{f} = (f_1, f_2, f_3, f_4)'$ evaluated at the same $\mathbf{u}^{(i)}$.

Convergence of this method is guaranteed provided the functions \mathbf{f} are differentiable, the inverse of J is nonsingular in a neighborhood of the true solution, and the initial values $\mathbf{u}^{(0)}$ are chosen appropriately. These conditions are analogous to those required for convergence of the fixed point method in Section 2.1. Furthermore, since both Newton's and the fixed point method are iterative in nature, their implementation is unnecessarily complicated relative to matrix methods, and, to a much greater extent, the method introduced in the following section.

2.4 The Explicit Solution

Existing techniques for solving (1)–(4) treat the system as a set of four non-linear equations in four unknowns. Here we show that the system can actually be written as two coupled linear systems, each containing two equations in two unknowns. Exact values for x , y , α and β can thus be obtained by simply inverting two different two by two matrices. This approach obviates the need to invoke non-linear tools such as iteration and approximation, makes clear the conditions for which the solutions x , y , α and β are unique, and, unlike the matrix-inversion based methods described in Section 2.2, provides these solutions using an explicit set of four transparent equations that do not require matrix inversion.

2.4.1 Explicit Solution Derivation

To decouple equations (1)–(4), clear denominators and group terms, yielding

$$x\alpha - y\beta - x + \alpha K_{11} - \beta K_{12} = K_{11} \quad (5)$$

$$x\alpha - y\beta - x + \alpha K_{21} - \beta K_{22} = K_{21} \quad (6)$$

$$x\alpha - y\beta + y + \alpha K_{31} - \beta K_{32} = -K_{32} \quad (7)$$

$$x\alpha - y\beta + y + \alpha K_{41} - \beta K_{42} = -K_{42}, \quad (8)$$

where the coefficients K_{ij} , $1 \leq i \leq 4$ and $1 \leq j \leq 2$, are assumed to exist and are given by

$$\begin{aligned} K_{11} &= \frac{B_1 - R_1 B_3}{A_1 - R_1 A_2} & K_{12} &= \frac{B_2 - R_1 B_4}{A_1 - R_1 A_2} \\ K_{21} &= \frac{B_5 - R_2 B_3}{A_3 - R_2 A_2} & K_{22} &= \frac{B_6 - R_2 B_4}{A_3 - R_2 A_2} \\ K_{31} &= \frac{B_1 - R_3 B_3}{A_1 - R_3 A_2} & K_{32} &= \frac{B_2 - R_3 B_4}{A_1 - R_3 A_2} \\ K_{41} &= \frac{B_5 - R_4 B_3}{A_3 - R_4 A_2} & K_{42} &= \frac{B_6 - R_4 B_4}{A_3 - R_4 A_2}. \end{aligned}$$

Subtracting equation (6) from equation (5), and equation (8) from equation (7) yields a matrix equation of the form

$$M_1 \vec{u}_1 = \vec{v}_1, \quad (9)$$

where

$$\begin{aligned} M_1 &= \begin{bmatrix} (K_{11} - K_{21}) & (K_{22} - K_{12}) \\ (K_{31} - K_{41}) & (K_{42} - K_{32}) \end{bmatrix}, \\ \vec{u}_1 &= \begin{bmatrix} \alpha \\ \beta \end{bmatrix}, \quad \text{and} \quad \vec{v}_1 = \begin{bmatrix} K_{11} - K_{21} \\ K_{42} - K_{32} \end{bmatrix}. \end{aligned}$$

The values of α and β that solve (9) will be unique if and only if the determinant d_1 of the matrix M_1 is non-zero. This determinant is given by

$$\begin{aligned} d_1 &= (K_{11} - K_{21})(K_{42} - K_{32}) \\ &\quad - (K_{22} - K_{12})(K_{31} - K_{41}). \end{aligned}$$

While d_1 should certainly be computed for every SIDMS application, it is of interest to note that d_1 will always be 0 when both $R_1 = R_3$ and $R_2 = R_4$. Perhaps the most common way for equality within these pairs of isotope ratios to occur is when $\alpha + \beta = 1$; casual inspection of (1)–(4) reveals $R_1 = R_3$ and $R_2 = R_4$ whenever $\alpha + \beta = 1$.

Once α and β are known, they can be substituted into the system (5)–(8). The four equations that result are linear in the unknowns x and y . Discarding equations (6) and (8)—they being redundant with equations (5) and (7), respectively—yields a matrix equation of the form

$$M_2 \vec{u}_2 = \vec{v}_2, \quad (10)$$

where

$$\begin{aligned} M_2 &= \begin{bmatrix} \alpha - 1 & -\beta \\ \alpha & 1 - \beta \end{bmatrix}, \quad \vec{u}_2 = \begin{bmatrix} x \\ y \end{bmatrix}, \\ \text{and} \quad \vec{v}_2 &= \begin{bmatrix} K_{11}(1 - \alpha) + K_{12}\beta \\ K_{32}(\beta - 1) - K_{31}\alpha \end{bmatrix}. \end{aligned}$$

Since the determinant d_2 of the matrix M_2 is just

$$d_2 = \alpha + \beta - 1,$$

the values of x and y that solve (10) will be unique as long as $\alpha + \beta \neq 1$. Although $\alpha + \beta = 1$ is the only condition for which $d_2 = 0$, it is but one of the conditions that makes $d_1 = 0$. Therefore, confirmation that $d_1 \neq 0$ is also confirmation that $d_2 \neq 0$.

2.4.2 Explicit Solution

Solving (9) for α and β , and then using these values to solve (10) for x and y gives the following explicit solution to equations (1)–(4):

$$\begin{aligned} \alpha = & (B_2R_4A_2 - B_2A_3 + R_3B_4A_3 - B_6R_3A_2 + B_6A_1 \\ & - R_4B_4A_1)(B_1A_3 - B_1R_2A_2 - R_1B_3A_3 - B_5A_1 \\ & + B_5R_1A_2 + R_2B_3A_1 - R_1B_4A_3 + B_2A_3 - B_2R_2A_2 \\ & + R_2B_4A_1 - B_6A_1 + B_6R_1A_2)/K \end{aligned} \quad (11)$$

$$\begin{aligned} \beta = & -(B_1A_3 - B_1R_2A_2 - R_1B_3A_3 - B_5A_1 + B_5R_1A_2 \\ & + R_2B_3A_1)(-R_3B_3A_3 - B_1R_4A_2 + B_1A_3 + R_4B_3A_1 \\ & + B_5R_3A_2 - B_5A_1 - B_2R_4A_2 + B_2A_3 - R_3B_4A_3 \\ & + B_6R_3A_2 - B_6A_1 + R_4B_4A_1)/K \end{aligned} \quad (12)$$

$$x = \frac{-(R_3R_2B_3 - R_3B_5 - R_1R_4B_3 + R_1B_5 - R_2B_1 + R_4B_1)}{-R_3A_3 + R_3R_2A_2 + R_1A_3 + A_1R_4 - R_1A_2R_4 - R_2A_1} \quad (13)$$

$$y = \frac{-(R_3R_2B_4 - R_3B_6 - R_1B_4R_4 + B_2R_4 - R_2B_2 + R_1B_6)}{-R_3A_3 + R_3R_2A_2 + R_1A_3 + A_1R_4 - R_1A_2R_4 - R_2A_1} \quad (14)$$

The common value of K in the denominators of (11) and (12) is given by

$$\begin{aligned} K = & d_1(A_1 - R_1A_2)(A_3 - R_2A_2) \\ & \times (A_1 - R_3A_2)(A_3 - R_4A_2). \end{aligned}$$

Since this denominator K is proportional to the determinant d_1 , we are again reminded that d_1 cannot equal 0. Note that evaluating (11)–(14) requires only manipulation of the thirteen known quantities using the four basic mathematical operations. Such evaluation requires no iteration, no initialization, no matrix inversion, and is guaranteed to provide a unique solution for α , β , x , and y if $d_1 \neq 0$.

3 IMPLEMENTATION

To demonstrate the soundness of all four solution methods, we apply them to a chromium application considered in the literature and an application involving mercury.

3.1 Chromium Example

Meija et al. consider a Cr(III) and Cr(VI) determination in yeast example with the following values of the thirteen knowns:

	R_i	A_i	B_i
$i = 1$	1.137422	0.0434518	7.208347
$i = 2$	1.090267	0.8379343	0.005456632
$i = 3$	0.9654383	0.0950139	0.1913327
$i = 4$	4.773563		0.3874209
$i = 5$			0.01409039
$i = 6$			13.22961

The four methods are in excellent agreement, as seen in the table below. This solution is unique since d_1 is nonzero.

	Iterative	Matrix	Newton's	Explicit
α	0.2233	0.2232	0.2233	0.2233
β	0.3818	0.3818	0.3818	0.3818
x	7.3657	7.3672	7.3657	7.3657
y	0.1718	0.1718	0.1718	0.1718

3.2 Mercury Fish Example

For the sake of expanding the test suite, we performed a similar comparison with a data set from our own lab. This time the element of interest was mercury. The raw data was as follows:

	R_i	A_i	B_i
$i = 1$	7.858855	0.05014945	0.1211932
$i = 2$	1.535217	0.08876482	0.001489574
$i = 3$	0.568328	0.06866937	0.0009621648
$i = 4$	1.142659		0.001369204
$i = 5$			0.006484727
$i = 6$			0.1450604

As the table below shows, the four methods are once again in excellent agreement. The solution is again unique since d_1 is nonzero. Notice that with the given data, all methods yield a negative estimate for x , a physical impossibility (since x represents a material quantity.) Since all methods yielded the same impossible value, the issue is not one of calculational technique but rather of model stability: the particular relation between the sample concentrations, the spike ratios, and measurement uncertainties. This issue is addressed in the next section.

	Iterative	Matrix	Newton's	Explicit
α	0.0047	0.0047	0.0047	0.0047
β	0.0474	0.0474	0.0474	0.0474
x	-0.0339	-0.0339	-0.0339	-0.0339
y	4.3814	4.3814	4.3814	4.3814

4 STABILITY ANALYSIS

The fact that every solution technique yielded the same negative value for x in the mercury example above suggests two important truths about speciated isotope dilution mass spectrometry: one, that the technique can yield false results, and two, that these results are due to the parameters of the experiment rather than any particular solution technique. While the question of which solution technique to use thus reduces to which one is easiest to implement, there remains a basic question of how stable the results are. While a thorough analysis of the stability of the problem is beyond the scope of this paper, this section suggests an analytic ansatz, and concludes with a numerical uncertainty analysis under an assumption of white Gaussian measurement noise.

The most straightforward way to analyze the stability of the problem is with the tools of matrix analysis, using the matrix formulation of Meija et. al. In this formulation, the estimation depends on the following measurements:

- the ion intensity readings (I_i^j , proportional to the amount of the j th isotope in the i th species.)
- the isotope proportions in the spikes (A_i^j , the percentage by mass of the j th isotope in the i th spike.)
- the amount of each spike that is added to the sample (n_i , the number of moles of the i th species in the i th spike.)

The basic relations between the measurements and the concentration estimates is then given by the following (nested) sequence of equations:

$$\begin{bmatrix} A_1^1 & A_2^1 & A_0^1 \\ A_1^2 & A_2^2 & A_0^2 \\ A_1^3 & A_2^3 & A_0^3 \end{bmatrix} \begin{bmatrix} a_i \\ b_i \\ c_i \end{bmatrix} = \begin{bmatrix} I_i^1 \\ I_i^2 \\ I_i^3 \end{bmatrix} \quad (15)$$

$$\begin{bmatrix} n_1 & n_2 \frac{a_1}{b_1} \\ n_1 & n_2 \frac{a_2}{b_2} \end{bmatrix} \begin{bmatrix} \alpha \\ \beta \end{bmatrix} = \begin{bmatrix} n_1 \\ n_2 \frac{a_2}{b_2} \end{bmatrix} \quad (16)$$

$$\begin{bmatrix} 1 - \alpha & \beta \\ \alpha & 1 - \beta \end{bmatrix} \begin{bmatrix} x \\ y \end{bmatrix} = \begin{bmatrix} \frac{c_1}{a_1}(1 - \alpha)n_1 \\ \frac{c_2}{b_2}(1 - \beta)n_2 \end{bmatrix}. \quad (17)$$

Each of these equations is of the form

$$Av = b, \quad (18)$$

where matrix A and vector b are known (or estimated) and vector v is to be solved for. Both A and b are subject to noise, so we end up solving a system of the form

$$(A + \Delta A)w = b + \Delta b, \quad (19)$$

where ΔA and Δb are (small) perturbations from the ideal values. The basic sensitivity theorem for square linear systems (Golub and Van Loan, pg. 83) says the relative error involved in solving system (19) instead of (18) is

$$\frac{\|w - v\|}{v} \leq \epsilon(A)\kappa(A),$$

where $\kappa(A)$ is the condition number of A and $\epsilon = \epsilon(A)$ bounds the error in A and b . In principle, estimates for measurement errors in the A_i^j 's and the I_i^j 's can be used in equation (15) to bound errors in the a_i , b_i , and c_i . These, together with error estimates for the n_i , can be used in equation (16) to bound errors in α and β , and finally, all these error bounds can be used in equation (17) to estimate the errors in x and y .

While this line of attack can be useful for estimating error bounds, it is limited by the fact that the quantities to be estimated show up explicitly in the matrices in (15)-(17). To circumvent this limitation, numerical methods can be used to estimate parameter uncertainty under fluctuations in the observation noise. The results of this approach are summarized in the Tables below. For the first table, we took as truth the values of α , β , x , and y that were calculated in Section 3.1. We further assumed that exactly the same spikes were used, and that the composition of these spikes were known perfectly. The intensity readings should in principle be known exactly, but we subjected each to 1% noise, and then solved backwards for α , β , x and y . Repeating this exercise 1000 times, the statistics on the range of calculated values were as follows:

	α	β	x	y
mean	.2232	.3819	7.3705	.1669
std. dev.	.0088	.0079	.1669	.1760

It is interesting to note that these results very much depend on the amount and the ratios of the two spikes. We repeated the above exercise varying the amount of each spike, but keeping both their composition and their relative proportion the same. Multiplying the total amount of each spike by 1/8, the same statistical analysis yields the following:

	α	β	x	y
mean	.2229	.3823	7.3532	.1728
std. dev.	.0190	.0312	.3936	.2208

On the other hand, if we multiply the total amount of the spikes by a factor of 8, we get the following:

	α	β	x	y
mean	.2232	.3819	7.3532	.1974
std. dev.	.0086	.0067	.8135	.9595

Note that in both cases the mean estimates are the same as before, but the variance increases, in the first case across the board, in the second in the calculated values of x and y . A similar analysis obtained by varying both the levels and the ratios of the spikes provides numeric confirmation of the idea that there is an optimal way of designing the spikes. Algorithmic exploration of this idea is a subject of continuing research.

5 DISCUSSION

The SIDMS equations (1)–(4) are an example of a system of equations that can be solved using any one of several different techniques. Since the 1996 inception of the patented SIDMS process, the iterative solution method had been used exclusively for many years. Recently, other solution methods have surfaced whose advantage over the iterative method was strictly in ease-of-implementation (one solution method being more “correct” than another was never an issue). We have presented in this document the explicit solution to the system (1)–(4), and recognize several appealing properties: it yields the same solutions as all other methods, does not require initialization, provides the entire solution in terms of four transparent equations, carries arguably the greatest ease-of-implementation advantage, and, most importantly, it incorporates Use of the explicit solution when solving (1)–(4), is formalized in the following three steps:

1. Obtain the thirteen quantities identified in Sec-

tion 1 (or for non-chromium applications, the analogous thirteen quantities).

2. Check for uniqueness: Use these thirteen quantities to calculate the determinant d_1 of the system (9). If d_1 exists and is nonzero, then the solutions for α , β , x and y are unique. Otherwise, the system (1)–(4) either has no solution, or infinitely many solutions.
3. Use these unknowns and d_1 to calculate α , β , x and y as specified in (11)–(14).

We remind readers that in cases where both $R_1 = R_3$ and $R_2 = R_4$, then d_1 and d_2 will both equal zero, and there will be no solution to (1)–(4). This will always occur when $\alpha + \beta = 1$. If by some rarity an application where both $R_1 = R_3$ and $R_2 = R_4$ is encountered, then researchers must seek alternative methods to solve for the unknown concentrations and crossover proportions. As far as applications involving more than two species is concerned, the coupled-linear systems approach used in the explicit solution method generalizes in a straightforward manner to $k > 3$ species problems, as do the fixed-point, matrix, and Newton’s solution methods. The $k > 3$ species versions of these solution methods carry similar advantages and disadvantages as their two species counterparts.

As a final note, we remind readers that the values obtained for the unknown concentrations x and y , and unknown crossover proportions α and β —whatever the solution method—are *only as good as* the required mass-spectrometer measurements $\{R_1, R_2, R_3, R_4\}$. If one of the documented solution methods for (1)–(4) is implemented properly and an incorrect concentration or crossover proportion is obtained, it is not the fault of the solution method. Solid sample extraction techniques, choice of the isotope proportions in both spikes, and the precision/accuracy of the mass-spectrometer itself offer opportunities for the measured isotope ratios to be quite non-representative. Determining appropriate, if not optimal, extraction techniques and choice of spike isotope ratios for SIDMS has been accomplished for select applications (references here), but is still a subject of research in many others.

6 References

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