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Blank correction in IDMS – possible pitfalls

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Abstract

Blank correction in isotope dilution mass spectrometry (IDMS) is investigated using the double IDMS exact matching technique. The effects of different amounts of blanks in the sample, reference and spike solutions are simulated for the determination of the mass fractions of Pb and Cu. The simulations are compared to and confirmed by respective interlaboratory CCQM key comparisons. The most correct results are obtained when the blend bx of sample and spike and blend bz of reference and spike are treated in the same way (digestion, matrix separation, choice of the same solvent, amounts of sample, reference and spike, etc.) starting from sample preparation. When applying this procedure, it is not necessary to subtract the blank subsequently. A similar "blank-matching" approach has been reported by *Pagliano, Mester,* and *Meija* previously (Anal. Chem. 2015; 87: 10724-27). In the present study it is shown that in case exact matching is applied, the subsequent blank subtraction is not only superfluous but will yield a systematically wrong result with a bias up to ten times of the uncertainty depending on the blank concentration. If the procedural blank is "small", a subsequent subtraction will yield a similar result as the procedure presented in this work. This small effect obviously has hidden a systematic bias in the past. Varying the mass fraction of the blank w_{bl} in a range 0.0001 µg/g < w_{bl} < 0.0025 µg/g in case of Pb, a subsequent blank subtraction yields a significantly biased result of w_x from -0.57 % to -14 %, exceeding the associated standard uncertainty $u(w_x)$ at $w_{bl} \approx 0.0004$ µg/g.

Introduction

Over the last decades numerous measurement strategies were established and further improved for the accurate determination of analyte amounts in more or less complex matrices using mass spectrometric techniques like inductively coupled plasma mass spectrometry (ICP-MS).[1,2] In analytical chemistry as well as in related disciplines like geochemistry, forensics, food chemistry, environmental analysis, and metrology in chemistry in general, a few measurement strategies have crystallized yielding smallest uncertainties associated with the intended quantities.[1-4] The term ”analyte amount” is just a generalized description which means in terms of metrology usually the “mass fraction” w_x of an analyte x (unit: g/g) which directly points out the gravimetric treatment of the samples and procedures during analysis. If the analyte element consists of at least two stable isotopes, isotope dilution mass spectrometry (IDMS) yields the most accurate and precise (smallest associated measurement uncertainty) results of the targeted mass fraction w_x based on internal calibration.[5] The IDMS principle has been discussed in numerous textbooks and research papers during the last decades.[6-11] Briefly, in IDMS the isotopic composition and thus molar mass of the analyte element is known. A blend bx is prepared from the sample x containing the analyte element usually with a natural isotopic composition and from a so-called spike material y. The latter containing the analyte element with one isotope enriched compared to the natural isotopic composition, preferably with an almost inverse isotopic composition. If the spike material is completely characterized and if it is a certified reference material (CRM) at its best, the knowledge of the masses of the blend components and the isotope ratios in the parent materials and the blend are needed to yield w_x with lowest associated uncertainty. This procedure is called single IDMS. In most cases the spike is insufficiently characterized with respect to its isotopic composition and especially its chemical purity. To overcome this problem, double IDMS has to be applied. In double IDMS, a third material – the reference material z (sometimes called primary standard or back-spike) with the same or similar isotopic composition as the analyte in the sample is

used to prepare a second blend bz consisting of the spike y and reference material z. In double IDMS, the purity of the spike cancels out from the model equation and the impact of the knowledge of the isotopic composition on the result and its uncertainty is drastically reduced. Double IDMS yields results with lowest associated measurement uncertainties; it is completely understood; it exhibits highest metrological quality and serves as a primary method in metrology in chemistry with results traceable to the International System of Units (SI). Practical considerations of IDMS are e.g. that due to the principle of measuring ratios of intensities, a loss of substances after blend preparation does not affect the result or its associated uncertainty. It is important that the sample, the spike, the reference material and the respective blends are treated in the same way during the whole preparation process (e.g. digestion, separation, …). This means that respective blanks will affect all materials in the same way ("blank-matching"). Several types of IDMS have been developed and applied: single IDMS, double IDMS, triple and higher order IDMS.[12,13] With each additional blend another quantity (like the usually difficult to determine ratios in the spike) can be eliminated from the model equation. However, the latter procedures suffer from laborious preparation efforts but usually yield only a small improvement in slightly reduced measurement uncertainty. When using IDMS, in most cases double IDMS is applied yielding smallest uncertainties. A special case which is in the focus of this work, is called exact-matching (double) IDMS.[14,15] In this method, the blends (bx) of the sample and spike as well as of reference and spike (bz) are almost equal (with a ratio equal to unity). Moreover, the ratio of the amount-of-substances n_x/n_z of the sample x and reference z are also equal to unity (exact-matching criterion). If the isotopic compositions of the sample and spike are equal, the molar masses in the final equation will cancel out, too.

Before presenting the blank-matching procedure we applied, its implications and consequences, the disambiguation of the term blank used here and in the context of analytical chemistry should be briefly outlined: A guide for the term "blank" used in analytical

chemistry was released from Eurachem in 2019, defining several types of a blank.[16] In that guide, terms like calibration blank, procedural blank, reagent blank, solvent blank, and sample blank are outlined. In isotope ratio IDMS literature, usually the term "procedural blank" is used. This is a combination of a first compound – the procedural blank (according to ref. [16]) – which is generated from a sample without the respective matrix of the analyte including the effect of e.g. sample tubes, bottles, vials, surfaces, and additional reagents.[17] The second compound of our investigated blank is the "solvent blank" according to ref. [16] which is self-explanatory. A third contribution is the sample blank emerging from the matrix and the sample treatment (digestion, separation). A fourth contribution results from the very measurement: carry-over effects, contamination of machine surfaces (e.g. skimmer, sampler, lenses…). It is often very difficult to distinguish between these different blank contributions. Therefore, the term "procedural blank" used here is a composition of these four individual blanks and what is determined usually in an ICP-MS lab applying IDMS. Parallel to the development of IDMS methods, the handling and quantification of a procedural blank has evolved: Historically, the procedural blank has to be determined quantitatively in a separate experiment and is subtracted from the result of the analyte (within its matrix). Thus, the blank-corrected result is an indirect result from the blank and the contaminated sample.[18] Moreover, the blank determination of analytes on an ultra-trace level is difficult and time-consuming.

Theoretical Methods

According to the basic version of the isotope dilution mass spectrometric approach – single IDMS – briefly the resulting double IDMS and its respective special variant (exact-matching double IDMS) should be outlined: Equation (1) represents the basic single IDMS equation for the determination of a mass fraction w_x of an analyte (element) in a sample x of interest:

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$$w_x = w_y \times \frac{m_{yx}}{m_x} \times \frac{M_x}{M_y} \times \frac{(R_{bx} - R_y)}{(R_x - R_{bx})} \times \frac{\sum_j R_{x,j}}{\sum_j R_{y,j}} \quad (1)$$

The requirements are the known masses of a) the sample solution m_x, and b) the spike solution m_{yx} (which is the same element as the analyte element with an artificially enriched isotope) in a blend bx consisting of the sample and the spike material. Here, the spike material must be fully characterized (isotopic composition, molar mass M_y, purity). Especially, the mass fraction w_y of the spike solution in the blend bx must be known. R_x, R_y, and R_{bx} are the isotope ratios of the sample, spike and blend; $R_{x,i}$ and $R_{y,i}$ are the isotope ratios in x and y with respect to the reference isotope. One advantage is the fact that once the spike is added to the sample and homogenization as well as isotopic equilibrium is achieved, a loss of the analyte does not change the result due to the measurement of ratios. In MC-ICP-MS, relative standard uncertainties associated with R are in the range $\leq 1 \times 10^{-5}$. However, due to the limited number of available fully characterized spike materials y, single IDMS is usually replaced by the double IDMS approach. In this case, the spike material y can be characterized using a second "reference" material z with natural isotopic composition (similar to x). A second blend bz is prepared (containing the spike y and reference material z). Another term of bz is "calibration blend". Analogue to eq. (1) follows

$$w_z = w_y \times \frac{m_{yz}}{m_z} \times \frac{M_z}{M_y} \times \frac{(R_{bz} - R_y)}{(R_z - R_{bz})} \times \frac{\sum_j R_{z,j}}{\sum_j R_{y,j}} \quad (2)$$

yielding

$$w_y = w_z \times \frac{m_z}{m_{yz}} \times \frac{M_y}{M_z} \times \frac{(R_z - R_{bz})}{(R_{bz} - R_y)} \times \frac{\sum_j R_{y,j}}{\sum_j R_{z,j}} \quad (3)$$

Inserting eq. (3) into eq. (1) gives the general double IDMS-equation (also known as "reverse IDMS"):

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$$w_x = w_z \times \frac{m_z}{m_{yz}} \times \frac{M_y}{M_z} \times \frac{(R_z - R_{bz})}{(R_{bz} - R_y)} \times \frac{\sum_j R_{y,j}}{\sum_j R_{z,j}} \times \frac{m_{yx}}{m_x} \times \frac{M_x}{M_y} \times \frac{(R_{bx} - R_y)}{(R_x - R_{bx})} \times \frac{\sum_j R_{x,j}}{\sum_j R_{y,j}} \quad (4)$$

$$w_x = w_z \times \frac{m_{yx}}{m_x} \times \frac{m_z}{m_{yz}} \times \frac{M_x}{M_z} \times \frac{(R_{bx} - R_y)}{(R_x - R_{bx})} \times \frac{(R_z - R_{bz})}{(R_{bz} - R_y)} \times \frac{\sum_j R_{x,j}}{\sum_j R_{z,j}} \quad (5)$$

Equation (5) does no more contain w_y; the masses in m_z and m_{yz} in the blend bz must be known as well as the molar masses M_x and M_z. The respective isotope ratios have to be measured. If the isotopic composition of the sample x and the reference z are equal, it follows: $M_x = M_z$ and $\Sigma R_{x,j} = \Sigma R_{z,j}$, and eq. (5) is reduced to

$$w_x = w_z \times \frac{m_{yx}}{m_x} \times \frac{m_z}{m_{yz}} \times \frac{(R_{bx} - R_y)}{(R_x - R_{bx})} \times \frac{(R_z - R_{bz})}{(R_{bz} - R_y)} \quad (6)$$

which is used e.g. in ref. [14,15].

In this case, the molar masses do not have to be known and also mass bias correction is no more necessary (calibration factors will cancel out). The exact-matching conditions are:

$R_{bx}/R_{bz} \approx 1$ and $n_{bx} \approx n_{bz}$. (7), (8)

The isotope ratios of the blends can be expressed as

$$R_{bx} = \frac{n_{bx,2}}{n_{bx,1}} = \frac{n_{x,2} + n_{y,2}}{n_{x,1} + n_{y,1}} = \frac{\frac{m_x \cdot w_x}{M_x} \cdot x_{x,2} + \frac{m_{yx} \cdot w_y}{M_y} \cdot x_{y,2}}{\frac{m_x \cdot w_x}{M_x} \cdot x_{x,1} + \frac{m_{yx} \cdot w_y}{M_y} \cdot x_{y,1}} \quad (9)$$

$$R_{bz} = \frac{n_{bz,2}}{n_{bz,1}} = \frac{n_{z,2} + n_{y,2}}{n_{z,1} + n_{y,1}} = \frac{\frac{m_z \cdot w_z}{M_z} \cdot x_{z,2} + \frac{m_{yz} \cdot w_y}{M_y} \cdot x_{y,2}}{\frac{m_z \cdot w_z}{M_z} \cdot x_{z,1} + \frac{m_{yz} \cdot w_y}{M_y} \cdot x_{y,1}} \quad (10)$$

Eqs. (9) and (10) denote the compositions of the respective isotope ratios of the blends bx and bz according to the initial preparation of the masses m_x, m_{yx}, m_z, and m_{yz} using the sample x and the spike and reference solutions y and z. In this established procedure used for the

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determination of w_x, no indication of an additional blank contribution is included a priori. Since every analytical procedure is accompanied by a blank contamination (of the analyte element), application of eqs. (5) and (6) already included a procedural blank induced when the sample, spike and blends were prepared (e.g. digested) consecutively under slightly different conditions. Thus, it seemed reasonable to subtract the amount of the procedural blank after the application of eqs. (5) or (6). However, this required the additional determination of the mass fraction of the procedural blank $w_{x,bl}$ in a separate measurement. These are at least three main challenges: First, the content of the procedural blank is usually very small and therefore difficult to measure; second, an additional blank determination is time-consuming, and third, the uncertainty associated with blank mass fraction $w_{x,bl}$ adds to the uncertainty of the final result $u(w_x)$. Nevertheless, this approach was applied by numerous studies during the last decades, emphasizing a subsequent blank subtraction.[18-20] As mentioned, in 2015 *Pagliano*, *Mester*, and *Meija* have published a sophisticated method called "blank-matching isotope dilution", showing that the efforts of a separated determination of the procedural blank and its subsequent subtraction of the initial result can be shortened and improved.[21] In their approach, a separate blank determination and elimination is not necessary, if the sample, spike and blend solutions are treated from the very beginning of the preparation in the same way; which means that in case of digestion steps, all components are treated equally at the same time under the same conditions using the same amounts. Since the procedural blank is apparent in the same amount in all these solutions, it will virtually cancel out when applying eqs. (5) and (6). Moreover, laborious separate blank measurements are no longer necessary. This technique has been applied also in our laboratory already for more than two decades. However, an additional subtraction of a procedural blank leads to an overestimation of the blank, thus yielding a systematically biased w_x. In this work, we will show the effect and the amount of the respective bias by simulations, if a subsequent (and overestimated) blank subtraction will be performed. This in turn will prove that only the blank-matching procedure

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similar to that described in ref. [21] yields the correct value, and a subsequent subtraction induces a (usually slightly but sometimes completely) wrong result. Thus, we demonstrate that blank-matching and subsequent subtraction will yield different results.

Simulation of procedural blank impact

While eq. (5) as the "full" double IDMS expression does not include any blank contributions of natural isotopic composition, its application should theoretically yield exactly the same result w_x as can be calculated from the gravimetric preparation.

In practice however, the blend bx can be prepared with an excess of acids used e.g. for digestion and other preparation steps. These additional solutions contain the blank (bl) with natural isotopic composition.

Imagine, that this additional blank contribution (bl) is included in R_{bx}^* (R_{bz}^*, R_x^*, and R_z^*), compare eqs. (9) and (10):

$$R_{bx}^* = \frac{n_{bx,2}^*}{n_{bx,1}^*} = \frac{\frac{m_x \cdot w_x}{M_x} \cdot x_{x,2} + \frac{m_{yx} \cdot w_y}{M_y} \cdot x_{y,2} + \frac{m_{bl} \cdot w_{bl}}{M_{x,IUPAC}} \cdot x_{x,2,IUPAC}}{\frac{m_x \cdot w_x}{M_x} \cdot x_{x,1} + \frac{m_{yx} \cdot w_y}{M_y} \cdot x_{y,1} + \frac{m_{bl} \cdot w_{bl}}{M_{x,IUPAC}} \cdot x_{x,1,IUPAC}} \quad (11)$$

$$R_{bz}^* = \frac{n_{bz,2}^*}{n_{bz,1}^*} = \frac{\frac{m_z \cdot w_z}{M_z} \cdot x_{z,2} + \frac{m_{yz} \cdot w_y}{M_y} \cdot x_{y,2} + \frac{m_{bl} \cdot w_{bl}}{M_{x,IUPAC}} \cdot x_{x,2,IUPAC}}{\frac{m_z \cdot w_z}{M_z} \cdot x_{z,1} + \frac{m_{yx} \cdot w_y}{M_y} \cdot x_{y,1} + \frac{m_{bl} \cdot w_{bl}}{M_{x,IUPAC}} \cdot x_{x,1,IUPAC}} \quad (12)$$

$$R_{x,2}^* = \frac{\frac{m_x \cdot w_x}{M_{x,sample}} \cdot x_{x,2} + \frac{m_{bl} \cdot w_{bl}}{M_{x,IUPAC}} \cdot x_{x,2,IUPAC}}{\frac{m_x \cdot w_x}{M_{x,sample}} \cdot x_{x,1} + \frac{m_{bl} \cdot w_{bl}}{M_{x,IUPAC}} \cdot x_{x,1,IUPAC}} \quad (13)$$

The index "IUPAC" indicates a natural blank composition. In case of an analyte element with 4 stable isotopes (Pb), the molar mass in the sample including the natural blank consists of:

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$$M_{\mathrm{x}}^{*} = \frac{R_{\mathrm{x},1}^{*}}{\sum R_{\mathrm{x},i}^{*}} \cdot M_{1,\mathrm{IUPAC}} + \frac{R_{\mathrm{x},2}^{*}}{\sum R_{\mathrm{x},i}^{*}} \cdot M_{2,\mathrm{IUPAC}} + \frac{R_{\mathrm{x},3}^{*}}{\sum R_{\mathrm{x},i}^{*}} \cdot M_{3,\mathrm{IUPAC}} + \frac{R_{\mathrm{x},4}^{*}}{\sum R_{\mathrm{x},i}^{*}} \cdot M_{4,\mathrm{IUPAC}} \quad (14)$$

$$R_{\mathrm{z},2}^{*} = \frac{\frac{m_{\mathrm{z}} \cdot w_{\mathrm{z}}}{M_{\mathrm{z}}} \cdot x_{\mathrm{z},2} + \frac{m_{\mathrm{bl}} \cdot w_{\mathrm{bl}}}{M_{\mathrm{x,IUPAC}}} \cdot x_{\mathrm{x},2,\mathrm{IUPAC}}}{\frac{m_{\mathrm{z}} \cdot w_{\mathrm{z}}}{M_{\mathrm{z}}} \cdot x_{\mathrm{z},1} + \frac{m_{\mathrm{bl}} \cdot w_{\mathrm{bl}}}{M_{\mathrm{x,IUPAC}}} \cdot x_{\mathrm{x},1,\mathrm{IUPAC}}} \quad (15)$$

In case of 4 isotopes, the molar mass in the reference including the natural blank is:

$$M_{\mathrm{z}}^{*} = \frac{R_{\mathrm{z},1}^{*}}{\sum R_{\mathrm{z},i}^{*}} \cdot M_{1,\mathrm{IUPAC}} + \frac{R_{\mathrm{z},2}^{*}}{\sum R_{\mathrm{z},i}^{*}} \cdot M_{2,\mathrm{IUPAC}} + \frac{R_{\mathrm{z},3}^{*}}{\sum R_{\mathrm{z},i}^{*}} \cdot M_{3,\mathrm{IUPAC}} + \frac{R_{\mathrm{z},4}^{*}}{\sum R_{\mathrm{z},i}^{*}} \cdot M_{4,\mathrm{IUPAC}} \quad (16)$$

Experimental

Materials and sample preparation

The chemicals used, the sample preparation procedures, and the measurement techniques were described in detail elsewhere.[22,23] Here, a brief description is given to understand the potential influences of experimental blank sources. High purity reagents and materials were used to reduce any additional contamination (blank) sources. All sample solutions were based on aqueous HNO_3 (0.15 mol/kg → $w(HNO_3)$ = 0.0094 g/g ≈ 1 %). The purification of HNO_3 in case of the Pb measurements ($w(HNO_3)$ = 0.65 g/g, EMSURE™ for analysis, Supelco) was performed in a perfluoroalkoxy alkane (PFA) sub boiling distillation system (OmniPure™, Teledyne CETAC Technologies, USA). Aqueous HNO_3 (0.15 mol/kg) solutions were used as the blank solutions and for rinsing in the mass spectrometric determinations. The purified water was generated in a water purification system (Merck KGaA) yielding a final resistivity ≥ 18 MΩ cm. The purified labware (vials, bottles) used, was mainly made of PFA. Masses used during gravimetric preparation were corrected for air buoyancy. Argon gas used for mass spectrometric measurements had a purity of 5.0 (Pb) and 4.6 (Cu).

Pb samples

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The initial Pb sample material/matrix was rice flour distributed for the CCQM-K158 interlaboratory comparison.[23] 0.8 g of rice sample material was weighed into quartz vials. 2 g of Pb spike (y) solution ($w_{Pb} \approx 22$ ng/g) and 2.5 g of 0.15 mol/kg HNO_3 (sub-boiled) were added. Prior to the microwave assisted acid digestion, 5 mL HNO_3 (65 %, sub-boiled) and 3 mL H_2O_2 (30 %, Suprapur) were additionally added. The latter is the amount of material mainly contributing to the procedural blank. The following certified reference materials (CRMs) were used: NIST SRM 981 (for mass bias correction and molar mass determination); BAM-Y004 (BAM-A-primary-Pb-1 for element content); NIST SRM 991 (spike) highly enriched in ^{206}Pb ($x(^{206}Pb) = 0.999\,79$ mol/mol). In exactly the same way the reference/spike-blends were prepared by adding 2.5 g Pb reference (z) solution ($w_{Pb} \approx 65$ ng/g) instead of the rice flour sample. During one digestion run, four sample/spike-blends were digested together with four reference/spike blends in an MLS ultraCLAVE III™ microwave oven (p(Ar) = 50 bar, ϑ = 250 °C, t = 2 hours). After digestion, the samples were evaporated on a heating block at ϑ = 140°C to dryness. The residues were redissolved in 8 mL HNO_3 (1 mol/L) and subsequently transferred to Triskem™ Pb resin columns. These are used for separating the Pb fraction (in 6 mol/L HCl) completely from the matrix. HCl was removed by evaporation to dryness on a hot plate at 140°C. Then, the residues were redissolved in 2.5 mL HNO_3 (65 %, sub-boiled) to get rid of potentially abraded column material. The dried residues were redissolved in 8 mL HNO_3 (0.15 mol/kg) to obtain measurement solutions with $w_{Pb} \approx 26$ ng/g.

Cu samples

The Cu samples were taken from ampoules distributed within the CCQM-K100 interlaboratory comparison.[22] 2.6 g Cu sample material (Cu in fuel ethanol) was blended with 3.7 g Cu spike solution (Chemotrade # 52-5 Cu-65) enriched in ^{65}Cu ($x(^{65}Cu) = 0.9970$ mol/mol) with $w_{Cu} = 0.1$ µg/g in a quartz vessel. After homogenization, the solutions were evaporated to dryness on a hotplate at ϑ = 100 °C. After the addition of 5 mL HNO_3 (65 %,

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sub-boiled), again the solutions were evaporated to dryness (ϑ = 150 °C). The measurement solutions were prepared by adding 10 mL HNO_3 (0.15 mol/kg) to the residues.

BAM-A-primary-Cu-1 (BAM) as calibration standard (z) was used as a reference material; as spike material (y) Cu (#52-5 Cu-65, Chemotrade™ Germany) was applied. The respective reference-spike blends consisted of 4.6 g reference Cu solution (w_{Cu} = 0.2 µg/g) and 3.7 g Cu spike solution (w_{Cu} = 0.1 µg/g).

Mass spectrometry

The Pb content was determined using a multicollector-inductively coupled plasma mass spectrometer (MC-ICP-MS) Neptune XT™ (Thermo Fisher Scientific GmbH, Bremen, Germany). The Ar gas load was removed with a high-throughput jet-interface OnTool Booster™ pump (Pfeiffer, Germany). To avoid any oil diffusion and contamination, the turbomolecular pumps are backed with a dry scroll pump (nXDS6i™, Edwards). The correction of Hg interferences with Pb was performed during molar mass determination. The mass bias of $^{206}Pb/^{208}Pb$ was used to calculate the $^{202}Hg/^{204}Hg$ mass bias via the exponential law, and the mass bias-corrected ^{204}Hg signal was then subtracted from the m/z = 204 signal to calculate the ^{204}Pb signal.[24]

Cu was analyzed using a high-resolution inductively coupled plasma mass spectrometer (HR-ICP-MS) Element 2™ (Thermo Fisher Scientific GmbH, Bremen, Germany).

The instrumental parameters of the mass spectrometers are listed in Table 1.

Table 1 Instrumental parameters

	Neptune XT™ MC-ICP-MS (Pb)	Element 2 HR-ICP-MS (Cu)
General parameters		
radio frequency power / W	1200	1200
cool gas (Ar) / L min^{-1}	16.0	16.0
auxiliary gas (Ar) / L min^{-1}	0.8	0.8
nebulizer gas (Ar) / L min^{-1}	1.0 ...1.2	1.1
nebulizer (sample flow rate / µL min^{-1})	PFA, self-aspirating (50)	PTFE, Meinhard (200)
sampler, orifice / mm	Nickel, 1.1	Nickel, 1.1

skimmer, orifice / mm	nickel ("H-type"), 0.8	nickel ("H-type"), 0.8
mass resolution $M/\Delta M$	400 (LR, pseudo low res. mode)	300 (LR), 10000 (HR)
Sample introduction system	ASX110FR autosampler (CETAC™)	-
	in a class-100 laminar flow hood	-
spray chamber	double pass cyclonic/Scott (quartz)	cyclonic (PEEK)
torch, injector tube, bonnet	quartz	quartz
Data acquisition		
operation mode	static	scanning (counting mode HR, analogue mode LR)
rotating amplifiers	applied	-
baseline measurement	defocusing at start (30 s)	-
integration time / s	2.1	-
number of integrations / cycle	1	-
number of cycles / block	1	-
number of blocks	20	-
Detectors	Faraday cups: L3 (^{202}Hg), L1(^{204}Pb), C (^{206}Pb), H1(^{207}Pb), H2 (^{208}Pb) with $R = 10^{11}$ Ω	single collector (SEM)

PTFE: polytetrafluoroethylene; PEEK: polyether ether ketone; SEM: secondary electron multiplier

Results and discussion

Pb and Cu measurements

As a basis for the discussion of the blank effects according to the simulations, the results of the underlying measurements are summarized in Table 2. The detailed reports are given elsewhere.[22,23] Both Pb and Cu measurements and evaluations were carried out using the exact-matching double IDMS approach. Samples and blends (bx, bz) were treated in the same way during the entire preparation steps (e.g. same digestion procedures). Due to this blank matching, it was not necessary to determine a potential blank in a separate experiment which would bias the result systematically as will be shown in the following.

Table 2 Results (PTB) of double IDMS determinations used as reference values.[22,23]

Element	Unit	Mass fraction w_x	Expanded uncertainty U	k
Pb	mg kg^{-1}	0.2189	0.0046	2.11
Cu	mg kg^{-1}	0.3589	0.0049	2.13

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The determination of the contents of Pb and Cu yielded relative expanded uncertainties of 2.1 % and 1.4 %, respectively. These results have been confirmed in the context of interlaboratory comparisons and can be used as validated anchor points in our study.

A representative uncertainty budget for w_{Pb} according to the "Guide to the Expression of Uncertainty in Measurement" (GUM) is shown in Table 3.[25] The budget was calculated using the GUM Workbench Pro™ software (version 2.4.1. 392; Metrodata GmbH, Germany).

Table 3 Uncertainty budget of $w_{Pb} = w_x$. Molar masses M were taken from ref. [26, 27].

Quantity	Value	Unit	Standard Uncertainty	Sensitivity Coefficient	Index
w_{dry}	0.98435	g/g	$3.35 \cdot 10^{-3}$	-0.22	12.1 %
f_{smp}	1.00000	1	$6.50 \cdot 10^{-3}$	0.22	44.2 %
f_{exp}	1.00000	1	$3.80 \cdot 10^{-3}$	0.22	15.1 %
w_z	0.0650504	µg/g	$97.6 \cdot 10^{-6}$	3.4	2.4 %
m_{yx}	2.066418	g	$800 \cdot 10^{-6}$	0.11	0.2 %
m_x	0.80619	g	$4.00 \cdot 10^{-3}$	-0.27	25.7 %
m_z	2.45942	g	$800 \cdot 10^{-6}$	0.089	0.1 %
m_{yz}	2.052304	g	$800 \cdot 10^{-6}$	-0.11	0.2 %
$r_{bx}(^{206}Pb/^{208}Pb)$	0.9840883	V/V	$52.2 \cdot 10^{-6}$	-0.45	0.0 %
$r_{bz}(^{206}Pb/^{208}Pb)$	0.9814721	V/V	$59.9 \cdot 10^{-6}$	0.42	0.0 %
$x_y(^{206}Pb)$	0.9997900	mol/mol	$10.0 \cdot 10^{-6}$	$75 \cdot 10^{-9}$	0.0 %
$x_y(^{208}Pb)$	$130.0 \cdot 10^{-6}$	mol/mol	$10.0 \cdot 10^{-6}$	$-580 \cdot 10^{-6}$	0.0 %
$M(^{204}Pb)$	203.97302800	g/mol	$1.50 \cdot 10^{-6}$	$-940 \cdot 10^{-9}$	0.0 %
$M(^{206}Pb)$	205.97444900	g/mol	$1.50 \cdot 10^{-6}$	$18 \cdot 10^{-6}$	0.0 %
$M(^{207}Pb)$	206.97588000	g/mol	$1.50 \cdot 10^{-6}$	$-12 \cdot 10^{-6}$	0.0 %
$M(^{208}Pb)$	207.97663600	g/mol	$1.50 \cdot 10^{-6}$	$-4.8 \cdot 10^{-6}$	0.0 %
$r_x(^{204}Pb/^{208}Pb)$	0.02530368	V/V	$4.81 \cdot 10^{-6}$	0.11	0.0 %
$r_x(^{206}Pb/^{208}Pb)$	0.493402	V/V	$113 \cdot 10^{-6}$	0.56	0.0 %
$r_x(^{207}Pb/^{208}Pb)$	0.4024912	V/V	$52.3 \cdot 10^{-6}$	0.11	0.0 %
$r_{z,IDMS}(^{206}Pb/^{208}Pb)$	0.4572387	V/V	$43.0 \cdot 10^{-6}$	0.063	0.0 %
w_x	**0.21865**	**µg/g**	**$2.14 \cdot 10^{-3}$**		

Main uncertainty contributions stem from the handling and treatment of liquids and samples during digestion and column separation by 44 % which is summarized by a factor f_{smp} (according to a type A contribution). A similar contribution is estimated by a factor f_{exp} by 15

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% which indicates uncertainty contributions due to sampling and homogeneity issues. The only quantity entering the original double IDMS equation (5) is m_x with a contribution of 26 %. The measurements of the intensity ratios (which will be transferred into isotope ratios) do not contribute to a significant amount.

For Cu, a representative uncertainty budget according to the GUM is given in Table 4, calculated using the GUM Workbench Pro™ software.[25]

Table 4 Uncertainty budget of $w_{Cu} = w_x$.

Quantity	Value	Unit	Standard Uncertainty	Sensitivity Coefficient	Index
f_{exp}	1.00000	1	$2.60 \cdot 10^{-3}$	0.36	16.8 %
w_z	0.199845	µg/g	$300 \cdot 10^{-6}$	1.8	5.6 %
m_{yx}	2.930800	g	$800 \cdot 10^{-6}$	0.12	0.2 %
m_x	2.559000	g	$800 \cdot 10^{-6}$	-0.14	0.2 %
m_z	4.216500	g	$800 \cdot 10^{-6}$	0.085	0.0 %
m_{yz}	2.939300	g	$800 \cdot 10^{-6}$	-0.12	0.2 %
$r_{bx}(^{65}Cu/^{63}Cu)$	0.91357	mol/mol	$1.92 \cdot 10^{-3}$	-0.77	42.0 %
$r_{bz}(^{65}Cu/^{63}Cu)$	0.95703	mol/mol	$1.91 \cdot 10^{-3}$	0.70	35.0 %
$x_y(^{65}Cu)$	0.994400	mol/mol	$500 \cdot 10^{-6}$	$-89 \cdot 10^{-6}$	0.0 %
$x_y(^{63}Cu)$	$5.600 \cdot 10^{-3}$	mol/mol	$500 \cdot 10^{-6}$	0.016	0.0 %
$x(^{65}Cu)$	0.308300	mol/mol	$150 \cdot 10^{-6}$	0.094	0.0 %
$x(^{63}Cu)$	0.691700	mol/mol	$150 \cdot 10^{-6}$	-0.042	0.0 %
w_x	**0.35892**	**µg/g**	**$2.28 \cdot 10^{-3}$**		

In case of the Cu exact-matching double IDMS, the main uncertainty contributions result from the intensity ratios $r_{bx}(^{65}Cu/^{63}Cu)$ (42 %) and $r_{bz}(^{65}Cu/^{63}Cu)$ (35 %) which is a direct consequence of the less precise single collector measurements. The factor f_{exp} denotes the contributions due to liquid handling and sample preparation (17 %, type A).

Pb and Cu blank simulations

In order to assess the origin and the impact of the blank, we used the experimentally determined mass fractions w_x given in Table 2 as reference values, validated during interlaboratory comparisons. These w_x were evaluated using the double IDMS equation (5) in

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case of Pb and (6) in case of Cu ($M_x = M_z$ and $\Sigma R_{x,j} = \Sigma R_{z,j}$), applying an exact-matching preparation: all samples and blends were equally treated throughout the whole preparation process. To get an idea about the blank impact, a stepwise consideration of the blank was simulated. In total, two additional (biased) results for w_x are finally simulated: $w_{x,c}$ and $w_{x,c,cl}$. Table 5 summarizes the individual properties and meaning of the symbols used. The blank contribution was considered in a respective quantity marked with an * (e.g. R_x^*). Fig 1 schematically describes the different simulated (and biased) results. The detailed calculations using Pb and Cu as representative analytes are given in the supporting information (with a stepwise contribution of quantities including the blank).

Table 5 Assignment of the individual results (mass fractions) with different ways to account for blank contributions.

result	derivation	blank	blank subtraction
w_x	eq.(5), reference value	exact-matching measurement	-
$w_{x,c}$	eq.(5) using R_{bx}^*, R_{bz}^* (eqs. (11), (12)), R_x^* (eq. (13)) and R_z^* (eq. (15))	simulation with blank impact on R_{bx}^*, R_{bz}^*, R_x^*, and R_z^* taken into account	no
$w_{x,c,cl}$	see $w_{x,c}$ and "classical" (cl) subsequent blank subtraction	see above plus blank subtraction	yes

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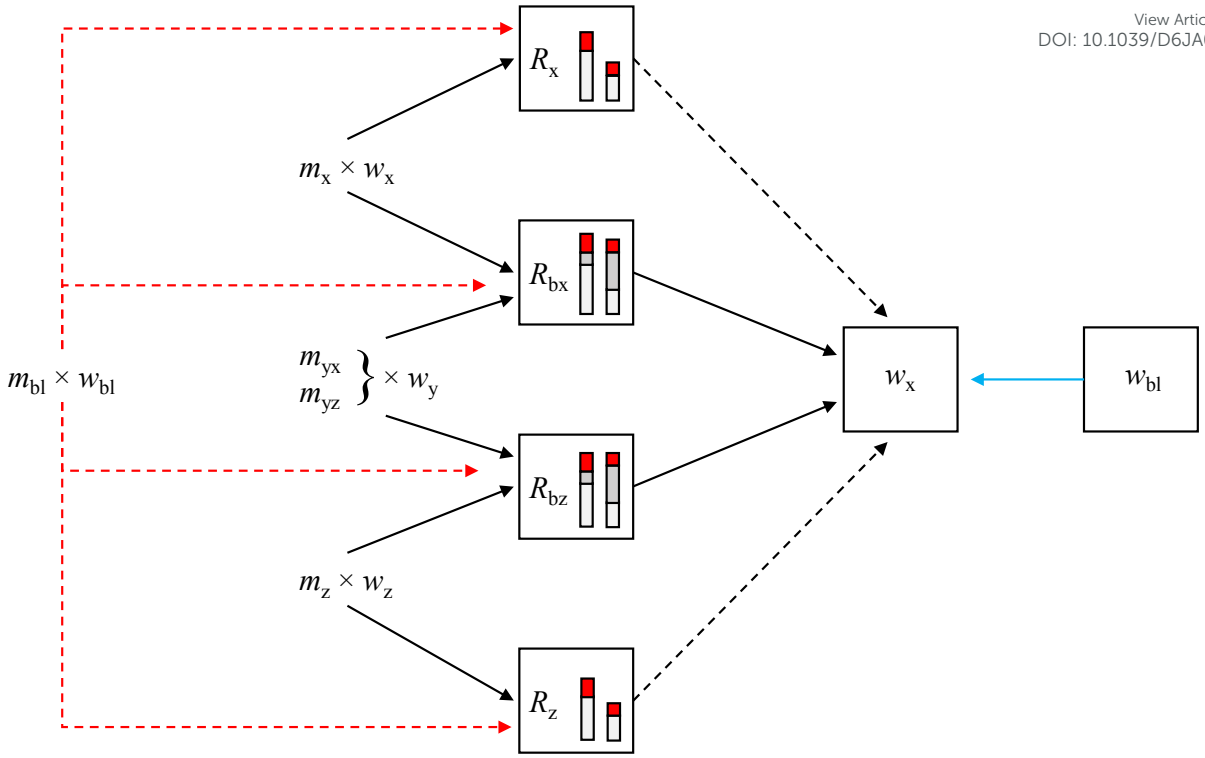

Fig. 1 Impact of the blank on the isotope ratios and the final result w_x. The blank impacts both blend ratios R_{bx} and R_{bz}. In case of a different isotopic pattern in the sample x, reference z and blank bl, e. g. Pb, the blend impacts the ratios R_x and R_z as well. w_x depends on the altered isotope ratios in a complex way (see text for details) while the direct subtraction of the blend impacts w_x straightforward.

In case of Pb, in the simulations an additional solvent contributing mainly to the blank bl with m_{sln} = 10 g (e.g. mass of added acids during digestion) was used as a constant value. If the respective mass fraction w_{Pb} of this blank is varied within 0.0001 µg/g ≤ w_{bl} ≤ 0.0025 µg/g, the deviation of $w_{x,c}$ (including all quantities influenced by a procedural blank) from the reference value w_x varies then from -0.00088 % to -0.019 % (compare supplementary information). This deviation is very small and can be neglected in practice since $U_{rel}(w_x)$ = 2.1 %. Instead, if a subsequent classical (index cl) blank subtraction is performed, $w_{x,c,cl}$ deviates

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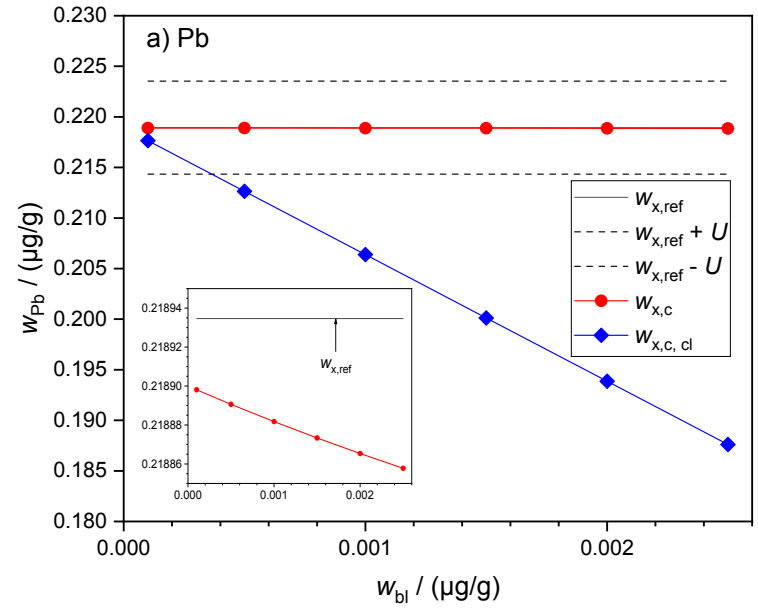
from -0.57 % to -14.30 %. Assuming a potential (realistic) procedural blank w_{bl}(Pb) in the range of 1% up to 10%, this corresponds to w_{bl}(Pb) = 2 ng/g up to 20 ng/g (similar for Cu).

Fig 2a shows the absolute variation of $w_{x,c}$(Pb) and $w_{x,c,cl}$(Pb) vs. w_{bl} in detail.



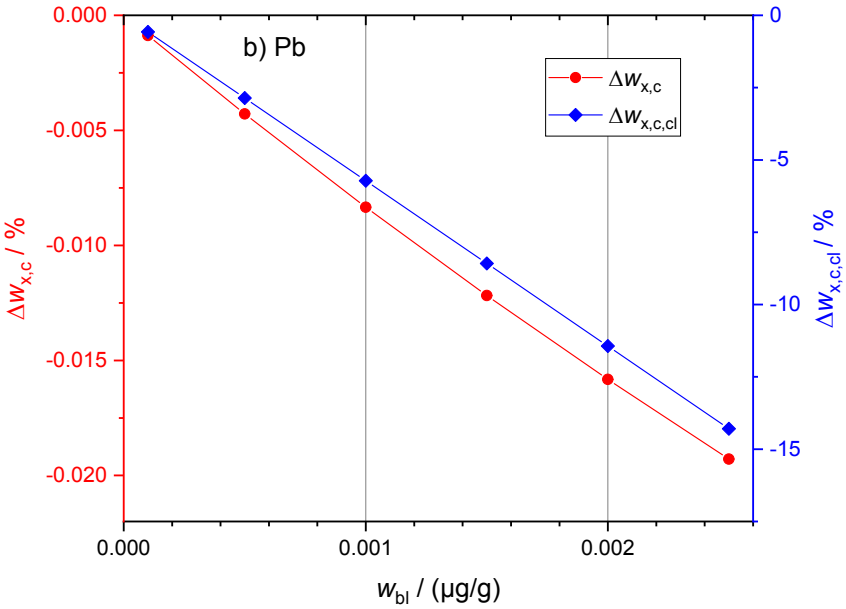


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Fig. 2 Simulation of mass fractions $w_{x,c}$ (red) and $w_{x,c,cl}$ (blue) of Pb after consideration of blank contributions. The black solid line (2a) refers to the reference value w_x (table 2). The dashed lines indicate the expanded uncertainty range associated with w_x (experimentally determined). In 2a, the absolute variation of w_{Pb} is shown. In 2b, the relative changes of w_{Pb} are displayed.

The inclusion of the relevant blank contributions is shown with the values $w_{x,c}$ (red lines). In the displayed range of w_{bl}, the impact of the blank on w_{Pb} is still covered by the expanded uncertainty $U_{rel}(w_{Pb})$= 2.1%.

But: A subsequent subtraction of the procedural blank after consideration of all input quantities (blue lines (values $w_{x,c,cl}$) in Figs. 2a, b) induces already at $w_{bl} > 0.0005$ µg/g a deviation of $w_{x,c,cl}$ from w_x of -2.9 %, which is larger than the expanded uncertainty associated with w_x, indicating a systematically biased result due to the subsequent (additional) blank subtraction. When increasing the mass fraction of the blank from w_{bl} = 0.0005 µg/g to w_{bl} = 0.001 µg/g, the result of w_{Pb} will be even stronger biased. Already this is a clear proof that a subsequent blank subtraction will yield a (strong) blank overcorrection and thus a systematically wrong result.

The simulations for the second example, Cu are shown in Figs. 3a-b. For the Cu simulations, a blank bl with m_{bl} = 8 g (e.g. mass of added acids during digestion) was used as an estimation (constant value).

In case of Cu, the calculation of w_x was performed and simplified by using eq. (6) (thus: $M_x = M_z$ and $\Sigma R_{x,j} = \Sigma R_{z,j}$; and only R_{bx}* and R_{bz}* will enter as blank contributors). This procedure was used in the experiment, therefore the respective calculation scheme of w_{Cu} will yield $w_{x,a}$ and $w_{x,a,cl}$ (compare the supporting information). For comparison with Pb, also $w_{x,c}$ and $w_{x,c,cl}$ were calculated which almost agree with the results of $w_{x,a}$ and $w_{x,a,cl}$.

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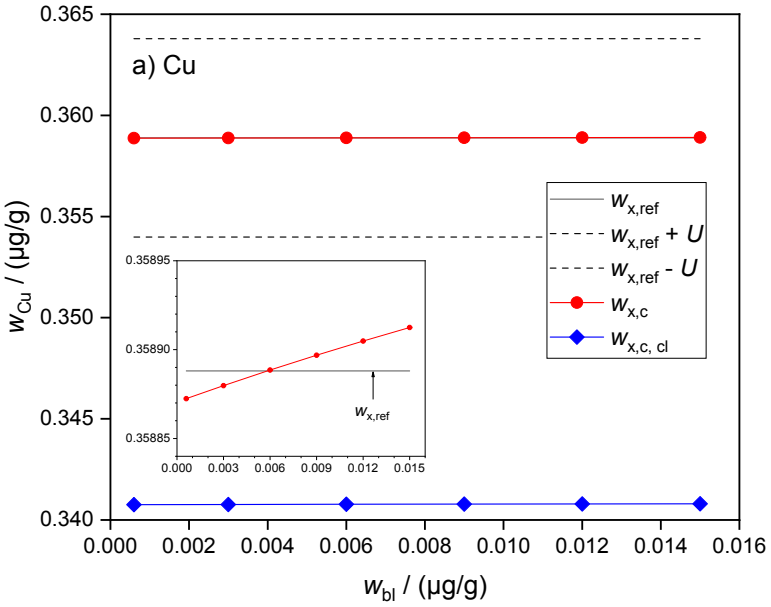
Varying the respective mass fraction w_{Cu} in the blank from 0.0006 µg/g ≤ w_{bl} ≤ 0.015 µg/g, the deviation of $w_{x,a}$ from the reference value w_x varies from 0.00052 % to 0.012 % which is that small that it can be also neglected compared to the expanded uncertainty $U_{rel}(w_x)$ = 1.4 % associated with w_x. If, on the other hand, a subsequent classical blank subtraction is done, $w_{x,a,cl}$ deviates from -5.056 % to -5.046 %. This means that a subsequent subtraction of the blank will always induce a clearly biased value (compare Figs. 3a and b for $w_{x,c}$ and $w_{x,c,cl}$).



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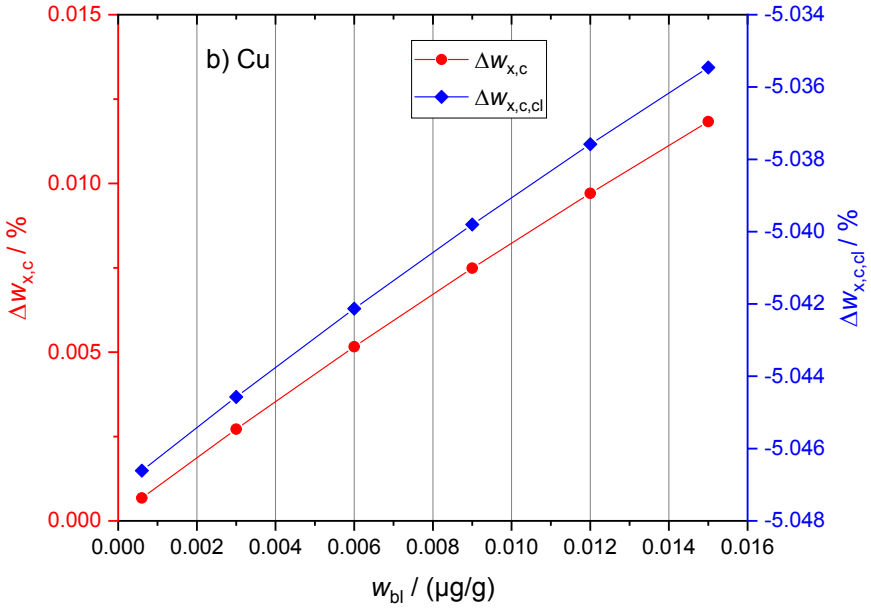

Fig. 3 Simulation of mass fractions $w_{x,c}$ (red) and $w_{x,c,cl}$ (blue) of Cu after consideration of blank contributions. The black solid line (3a) refers to the reference value w_x (table 2). The dashed lines indicate the expanded uncertainty range associated with w_x (experimentally determined). In 3a, the absolute variation of w_{Cu} is shown. In 3b, the relative changes of w_{Cu} are displayed.

In tables 6 (for Pb) and 7 (for Cu) some examples of different simulated scenarios of a perfect (A) and slightly deviating (B, C) exact-matching IDMS protocol are listed. For two options (1: all solutions were treated in the same way from the beginning, 2: bz was not digested and/or separated by using e.g. a column) the relative deviations from the reference values of some selected results are shown (details, see the tables). The calculations and assumptions can be found in the supporting information.

Table 6 Some examples of Pb mass fractions and their deviation from the correct result (w_x = 0.2189 µg/g) under different conditions (scenario A: exact matching, B: more blend bz, C:

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more blend bx) calculated ignoring the blank completely (option 1) and subtracting it (option 2). For more details on the blends etc. see the electronic supplement.

scenario		A	B	C
n_{bl}/n_x / %		5.7	5.7	5.7
option 1	n_{bl}/n_z / %	5.7	11	3.1
option 2	n_{bl}/n_z / %	0.57	1.1	0.31
n_x/n_z / (mol/mol)		1.002	1.996	0.539
R_{bx}/R_{bz} / (mol/mol)/(mol/mol)		1.001	0.994	1.002
option 1	Δw_x / %	-0.0083	-5.1	2.6
option 2	Δw_x / %	-0.60	-1.2	-0.32

Table 7 Some examples of Cu mass fractions and their deviation from the correct result (w_x = 0.3589 µg/g) under different conditions (scenario A: exact matching, B: more blend bz, C: more blend bx) calculated ignoring the blank completely (option 1) and subtracting it (option 2). For more details on the blends etc. see the electronic supplement.

scenario		A	B	C
n_{bl}/n_x / %		5.0	5.0	5.0
option 1	n_{bl}/n_z / %	5.0	10	2.5
option 2	n_{bl}/n_z / %	0.50	1.0	0.25
n_x/n_z / (mol/mol)		0.999	2.024	0.501
R_{bx}/R_{bz} / (mol/mol)/(mol/mol)		1.001	1.001	0.999
option 1	Δw_x / %	0.0052	-4.7	2.5
option 2	Δw_x / %	-0.53	-1.1	-0.27

Conclusions

In the context of the metrological analysis of contents (e.g. mass fractions) of analytes (e.g. elements) in complex matrices, the discussion on how to consider the influence of the procedural blank remains important. This work investigated blank correction effects

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quantitatively in a wider range. Two representative analytes (Pb and Cu) were chosen, which have been experimentally analyzed during interlaboratory comparisons using the exact-matching double IDMS method. The results were used as a kind of (validated) reference in this study. In simulations, blank contributions with a varying mass fraction of the respective blank were considered. In case of Pb (see Table 6), when completely ignoring the blank in the calculation, the mass fraction is biased by a negligible value < 0.05 % assuming exact matching (and blank matching) of the blends bx and bz ($0.99 \leq n_x/n_z \leq 1.01$ and $0.99 \leq R_{bx}/R_{bz} \leq 1.01$) was achieved and a blank of 5.7 % of the analyte amount is considered both in bx and bz. The bias due to the blank would therefore be well within the limits of the uncertainty associated with the mass fraction. On the other hand the result would be biased under the same conditions by nearly 6 % when the blank was subtracted. When preparing the blend bz differently in a way that it does not undergo the sample preparation steps (like digestion and separation etc.) so that the blank in blend bz is much lower than the blank in blend bx, the results are completely different. In case the blank in blend bz is only 10 % of the blank in bx with all other parameters unchanged, ignoring the blank in the calculation yields a mass fraction about 5.1 % too large, while a subtraction yields a mass fraction approximately 0.5 % too small. In case especially the exact matching condition $n_x \approx n_z$ is ignored, the subtraction yields a result 1.2 % too small, a deviation already in the same order of magnitude as the uncertainty. In case of Cu, it is no surprise that nearly the same behaviour of the deviation Δw_x of the calculated result from the correct one is observed (see Table 7). Conditions can be assumed (and experimentally adjusted) where the subtraction leads to results much closer to the correct mass fraction, but in practice it is hardly predictable if and when these conditions are achieved, while the exact matching always yields results with deviations from the correct result well within the limits of the uncertainty virtually independent from the amount of blank. Therefore, the exact matching as described by *Pagliano, Mester,* and *Meija* in ref. [21] and *Henrion* in ref. [14] is the much safer bet, because the classical blank subtraction might

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yield the correct result (under the best of conditions and sometimes purely by coincidence) but it does not have to, and it is virtually impossible to know when it does.

Conflicts of interest

The authors declare no competing interests.

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References

1. M. Sargent, H. Goenaga-Infante, K. Inagaki, L. Ma, J. Meija, A. Pramann, O. Rienitz, R. E. Sturgeon, J. Vogl, J. Wang, L. Yang, The role of ICP-MS in inorganic chemical metrology, *Metrologia*, 2019, **56**, 034005.
2. L. Yang, Accurate and precise determination of isotopic ratios by MC-ICP-MS: A review, *Mass Spectrom. Rev.*, 2009, **28**, 990-1011.
3. F. Vanhaecke, P. Degryse, Isotopic Analysis: Fundamentals and Applications Using ICP-MS. Wiley 2012.
4. J. Irrgeher, J. Vogl, J. Santner, T. Prohaska. Measurement strategies in: T. Prohaska, J. Irrgeher, A. Zitek, N. Jakubowski (eds.). New Developments in Mass Spectrometry

No. 3 Sector Field Mass Spectrometry for Elemental and Isotopic Analysis, 2015. Royal Society of Chemistry.

5. P. A. Penanes, A. R. Galán, G. Huelga-Suarez, J. A. Rodríguez-Castrillón, M. Moldovan, J. I. García Alonso, Isotopic measurements using ICP-MS: a tutorial review, *J. Anal. At. Spectrom.*, 2022, **37**, 701-26.
6. P. De Bièvre, Isotope dilution mass spectrometry: what can it contribute to accuracy in trace analysis? *Fresenius J. Anal. Chem*., 1990, **337**, 766-71.
7. K. G. Heumann, Isotope dilution mass spectrometry, *Int. J. Mass Spectrom. and Ion Processes*, 1992, **118/119**, 575-92.
8. M. Sargent, C. Harrington, R. Harte, Guidelines for achieving high accuracy in isotope dilution mass spectrometry (IDMS). Royal Society of Chemistry, LGC Limited 2002.
9. J. Vogl, Characterisation of reference materials by isotope dilution mass spectrometry, *J. Anal. At. Spectrom*., 2007, **22**, 475-92.
10. J. Meija, Z. Mester, Paradigms in isotope dilution mass spectrometry for elemental speciation analysis, *Anal. Chim. Acta*., 2008, **607**, 115-25.
11. J. I. García Alonso, P. Rodríguez-Gonzáles, Isotope dilution mass spectrometry, RSC Publishing 2013.
12. J. Vogl, Measurement uncertainty in single, double, and triple isotope dilution mass spectrometry, *Rapid Commun. Mass Spectrum*., 2012, **26**, 275-81.
13. E. Pagliano, Z. Mester, J. Meija, Reduction of measurement uncertainty by experimental design in high-order (double, triple, and quadruple) isotope dilution mass spectrometry: application to GC-MS measurement of bromide, *Anal. Bioanal. Chem*., 2013, **405**, 2879-87.
14. A. Henrion, Reduction of systematic errors in quantitative analysis by isotope dilution mass spectrometry (IDMS): an iterative method, *Fresenius J. Anal. Chem*., 1994, **350**, 675-58.

15. L. G. Mackay, C. P. Taylor, R. B. Myors, R. Hearn, B. King, High accuracy analysis by isotope dilution mass spectrometry using an iterative exact matching technique, *Accred. Qual. Assur.*, 2003, **8**, 191-94.

16. H. Cantwell (ed.), Blanks in Method validation - Supplement to Eurachem Guide The Fitness for Purpose of Analytical Methods, (1st ed. 2019).

17. A. Pramann, O. Rienitz, Blank overcorrection in ICP-MS – influence of the torch material used on the molar mass of highly enriched silicon and on the redefinition of the kilogram., *J. Anal. At. Spectrom*., 2018, **33**, 901-07.

18. A. Lamberty, J. Pauwels, How to correct for blanks in isotope dilution mass spectrometry, *Int. J. Mass Spectrom. And Ion Processes*, 1991, **104**, 45-48.

19. I. Trešl, C. R. Quétel, Low Uncertainty Reverse Isotope Dilution ICP-MS Applied to Certifying an Isotopically Enriched Cd Candidate Reference Material: A Case Study, *J. Am. Soc. Mass Spectrom*., 2005, **16**, 708-16.

20. L. Yang, R. E. Sturgeon, Blank correction considerations for isotope dilution and reverse isotope dilution calibration: Determination of methylmercury in fish tissue, *J. Anal. At. Spectrom*., 2005, **20**, 724-29.

21. E. Pagliano, Z. Mester, J. Meija, Blank Correction in Isotope Dilution, *Anal. Chem*., 2015, **87**, 10724-27.

22. T. Zhou *et al*., Final report on key comparison CCQM-K100: Analysis of copper in ethanol, *Metrologia*, 2014, **51**, Tech. Suppl. 08013, DOI 10.1088/0026-1394/51/1A/08013.

23. Y.-H.Yim *et al.*, CCQM-K158 elements and inorganic arsenic in rice flour, *Metrologia*, 2025, **62**, 08001, DOI 10.1088/0026-1394/62/1A/0800.

24. S. R. Hart, A. Zindler, Isotope fractionation laws: A test using calcium. *Int. J. Mass Spectrom. Ion Proc*., 1989, **89**, 287-301.

25. BIPM, IEC, IFCC, ILAC, ISO, IUPAC, IUPAP, and OIML. Evaluation of measurement data - Guide to the expression of uncertainty in measurement. Joint Committee for Guides in Metrology, JCGM 100:2008.

26. J. R. de Laeter, J. K. Böhlke, P. de Bièvre, H. Hidaka, H. S. Peiser, K. J. R. Rosman, P. D. P. Taylor, Atomic Weights of the Elements: Review 2000 (IUPAC Technical Report), *Pure Appl. Chem*., 2003, **75**(6), 683–800.

27. M. Wang, W. J. Huang, F. G. Kondev, G. Audi, S. Naimi, The AME 2020 atomic mass evaluation (II). Tables, Graphs and References, *Chinese Physics C*., 2021, **45**(3), 030003.

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Data availability

The data supporting this article are in the ESI.