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Prototype of a computerized system to automatically supply the parameters needed to compute 95% confidence intervals for chemical (and other) measurements (in both biased and unbiased measurement form)

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Abstract. A prototype of a computerized system has been developed to automatically acquire, statistically test and supply the parameters needed (standard deviation and percent recovery--obtained by running control samples) to compute 95% confidence intervals for chemical (and other) measurements contained in an organizations's main database (or locally) and ultimately to unbias those measurements and their confidence intervals. All sources of stochastic variation within the analytical methods are characterized, manipulated and corrected so as to provide parameters that are truly representative of the stochastic processes that occur in each individual analytical method as it is being done in a particular laboratory. This is done by running chemical, biological, microbiological or radiological control samples on specially designed computer spreadsheet forms over several analytical runs that automatically test the data statistically as it is being accumulated. These forms and their control samples are often suitable to be continued to be run for quality assurance purposes after their respective parameters have been obtained. The entire computerized system could be adapted and operated from a particular internet website making it available to fee-paying subscribers all over the world.
Key Words: prototype, computerized system, chemical, biological, microbiological, radiological analysis, unbiased measurements, systematic error, confidence interval, quality control, internet.

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Introduction. A prototype of a computerized system to automatically supply the parameters needed (standard deviation and percent recovery--obtained by running control samples) to compute 95% confidence intervals for chemical (and other) measurements contained in an organizations's main database was developed and tested in its entirety in 2005. The parameters are normally uploaded automatically from a DPSP (Derived Parameter Supplying Program) and entered directly into the main database by its DBMS (Database Management System). It is demonstrated that these parameters are characterized only by the particular measurement levels of the analytical chemistry methods being used to obtain them rather than by the measurements themselves. The standard deviations are used by the DBMS to compute 95% confidence intervals for the particular measurements and the percent recoveries are used to ultimately unbias the particular measurements and their associated 95% confidence intervals. The computer spreadsheet forms that are used to acquire the proper parameters (by running control samples) and supply them to the DPSP are called PAF's (Parameter Acquisition Forms) or

PAF-forms. The DBMS normally computes the 95% confidence intervals from the uploaded parameters or else it does so when the required parameters become available for uploading. Any unbiased measurements and unbiased 95% confidence intervals further computed by the DBMS are to be contained in hidden columns and only made available to top management officials. The DPSP, which is specific to the particular analytical chemistry method as it is being done in a particular laboratory, has its own database and can also do the computing of the 95% confidence intervals, and the unbiasing, but for reasons which are well known, it is highly inadvisable for the laboratory staff to do the unbiasing themselves. The system applies only to normally distributed measurements but it can be shown that most chemical measurements are normally distributed, especially if more than one stage of analytical processing is involved, due to the fact that the Central Limit Theorem (Annis, URL). As for non-normally distributed data, such as Binomial-distributed or Poisson-distributed biological, microbiological or radiological data, the measurements can usually be transformed into normally distributed measurements by utilizing the appropriate transformation and retransformation formulae. In this case, it will be the end points for the respective retransformed 95% confidence intervals themselves that are uploaded and entered into the organization's main database rather than the parameters used to obtain them and the respective measurements usually need no unbiasing. The present paper deals only with data that is generated linearly by the chemical instrumentation being used. The system can also be used with titrimetric, gravimetric and other simple methods, where no calibration graph is being utilized. Statistical testing and control charting are done automatically on the PAF's, so their control samples can double as quality control samples and be continued to be run for quality assurance purposes. The entire computerized system could be adapted and operated from a particular internet website making it available to fee-paying subscribers all over the world. The subscriber's database (if it is not too large) could be kept on the website or the required parameters and/or 95% confidence intervals could be downloaded into the subscriber's existing internal database.

Abbreviations and Definitions

DBMS: Database Management System.
This is a computer program such as R:Base or Dbase that is used to manage, query, and maintain a huge database.

DPSP: Derived Parameter Supplying Program.
The functionality of the computerized system relies upon the proper parameters (standard deviations and percent recoveries, determined over several analytical runs at usually three measurement levels: low, medium and high) being supplied to a particular computer program which is specifically dedicated to each individual analytical method in use in the particular laboratory. This particular computer program is called a DPSP (Derived Parameter Supplying Program) and routinely supplies the derived parameters (standard deviation and percent recovery for each measurement) to the main database DBMS.

PAF: Parameter Acquisition Form.
The computer spreadsheet forms that are used to acquire and supply the proper parameters (standard deviations and percent recoveries, determined over several analytical runs by running control samples at distinct measurement levels) to the DPSP are called PAF's (Parameter Acquisition Forms) or PAF-forms which may also be used to transform non-normally distributed data to normally distributed data. These computer spreadsheet forms track and record the measurements obtained by running control samples at distinct measurement levels. Sometimes the control samples are specialized and sometimes they are merely regular sample duplicates. A brief description of each of these PAF's is given in the Description of Parameter Acquisition Forms Section.

SRM: Standard Reference Material.
A material sample, solid or liquid, in which the concentration of one or more analytes that has been determined usually by several laboratories and/or analytical methods.

PPM: Parts Per Million.
This is the dimensional unit (Parts Per Million) of an actual concentration of an ingredient in a solid material or liquid medium or of the extracted ingredient in solution or of a chemical element or compound, ion or molecule in solution or the measurement of any of these. PPM may alternatively be expressed as µg/ml (micrograms per milliliter) for liquid medium or µg/g (micrograms per gram) for solid material.

WRME: Within Run Measurement Error.
This is random error emanating from all stages of the analytical chemistry processing in total, including the instrument reading step.

BRSE: Between Run Systematic Error.
This includes all systematic error between analytical runs but excludes the WRME of the premeasurements. It includes all the BRSME that is generally present during all analytical runs plus any other sources such as an electrical supply brown-up or brown-down occurring between reading the regular samples and reading the calibration standards on the chemical instrumentation.

BRSME: Between Run Systematic Measurement Error.
This is restricted to only the systematic error being generated between analytical runs by the WRME of all the submeasurements being utilized during each of the analytical runs which is occurring because of using the traditional calculation procedure described below to calculate the overall measurements at M-level.

BLSE: Between Laboratory Systematic Error.
This is the total of all forms of systematic error occurring between laboratories but excluding any BRSE.

CBLSE: Cumulative Between Laboratory Systematic Error.
This is the total of all forms of systematic error occurring between laboratories and between analytical runs (BLSE and BRSE) including all BLSME and BRSME and excludes the WRME of the premeasurements.

BLSME: Between Laboratory Systematic Measurement Error.
This is restricted to only the systematic error produced by the sum total of all laboratory biases.

CBLSME: Cumulative Between Laboratory Systematic Measurement Error.
This is restricted to the total of all BLSME and BRSME and excludes the WRME of the premeasurements.

Important Note: As can be inferred from the above definitions, there is an ascending and descending "ladder" of the above types of variation and systematic error. It can be shown that all forms of "systematic error" of the random and/or bias types, cannot exist "above the level" where unbiasing of the measurements is properly done. This is one good reason why, that at some point, as early as is practicable, unbiasing should be done. Not many people working in the field of chemistry understand this principle. It is not practicable nor advisable to unbias the analytical run even though it is possible. And the laboratory staff should not be the ones who do the unbiasing for a host of good reasons. The next "rung up the ladder" is to unbias the laboratory, that is, over several analytical runs. If this were done by the laboratory staff, then it would be impossible to compare measurements from the same analytical chemistry method between laboratories since all would be getting the same measurements for the same material sample no

matter what their percent recovery ratings were for the method. That is why, with the exception of research scientists, the unbiasing should be done by the DBMS in the main database of large corporations or government departments as is recommended in this paper.

WAV: Within Analysis Variation (or Within Analytical Run Variation or Between Replicate Subsample Variation).
This abbreviation is used to prefix a variance or standard deviation for a premeasurement or submeasurement random variable to indicate that it has been determined (statistically sampled) "within" a run (or runs). It does not have to be done during a single analytical run, although it can be, but it is usually done over several analytical runs. It is also used to indicate this kind of statistical sampling. This will be explained more fully in the Theory Section.

BAV: Between Analyses Variation (or Between Analytical Run Variation or Within Laboratory Variation).
This abbreviation is used to prefix a variance or standard deviation for a premeasurement or submeasurement random variable to indicate that it has been determined (statistically sampled) "between analytical runs." This has to be done between analytical runs, although it is not necessary to run a control sample in every run. It is also used to indicate this kind of statistical sampling. This will be explained more fully in the Theory Section.

BLV: Between Laboratory Variation (or Within Organization Variation).
This is the total of all of all forms of systematic error (laboratory biases and random error) occurring between laboratories. This would normally be determined (statistically sampled) by an inter-laboratory collaborative study. Unbiased measurements are unacceptable for this kind of study. This kind of statistical sampling is not taken up in this paper.

RBV: Reagent Blank Variation.
This variation normally occurs as BRSME (RBV), since the normal practice is to average the readings for all multiple reagent blanks before subtracting that average reading from the readings for all other samples and subsample replicates or to subtract the reading for a single reagent blank from the readings for all other samples and subsample replicates. However, under certain statistical sampling procedures, this variation can be forced out within the run as WRME (RBV).

IBV: Instrument Baseline Variation.
This is refers to variation (baseline noise and/or baseline drift) being produced by the instrument while nothing (no sample extract or calibration standard) is being input into it or else while a "zero concentration" sample extract or standard's blank is being input into it. Usually, there is no difference in the variation under the two conditions but the latter is more of a "scientific" concept.

IRV: Instrument Response Variation.
This is instrument response variation (relative to some concentration constant such as an instrument calibration standard)--can be random or proportional (see SRLV and PRLV). The term, when used in reference to a particular instrument measurement level, is sometimes called the "sensitivity" of the instrument.

PRLV: Population Regression Line Variation due to proportional IRV.
Proportional changes in the slope of the population regression line (calibration line) will likely occur between analytical runs (and sometimes during the analytical run if the instrument is at high expansion levels). This is due to differences in instrument alignment (between runs) or to gradual non-random changes in the instrument electrical output level (during the run). This is normal between analytical runs and is taken into

account by the very calibration graph itself. If the proportional IRV gradually changes during the analytical run, then the calibration standards should be re-read from time to time during the instrument reading step and the calculated average slope for each serial pair of the calibration standard runs should be used to determine the concentration of the block of regular samples and subsample replicates that were run (bracketed) between them.

SRLV: Sample Regression Line Variation which due to random IRV.
This is variation in the slope of the sample regression line (calibration line) due only to the "scatter" in the calibration points obtained for each calibration standard (which is a concentration constant) as they are (theoretically) being read over and over again as if to prepare a succession of calibration lines, assuming no proportional changes in the slope of the population regression line (calibration line) during that time period. Usually, only one such calibration line (calibration graph) is prepared for the analytical run but the slope of it is theoretically only one random outcome from many possibilities (unless the standard deviation of the random IRV is near zero). This variation normally occurs as BRSME (SRLV), since the normal practice is either to average the slopes for two different runs on the calibration standards before dividing the readings for all bracketed samples and subsample replicates by that averaged slope or to divide the readings for all samples and subsample replicates by the slope of the calibration line obtained from a single run of the calibration standards. See the definition of "traditional calculation procedure." However, under certain statistical sampling procedures, this variation can be forced out within the run as WRME (SRLV). For calibration lines, the mathematical model is $y = mx + 0$ (here, "m" is the slope variable and "b" is a constant y-intercept set to "zero"). The SRLV is variation in the slope of this sample regression line usually manifesting as BRSME (SRLV), as explained above. But for the standard additions determination line, the mathematical model is $y = mx + b$ (here, "m" is the slope variable and "b" is the y-intercept variable). This SRLV is also variation in the slope of the sample regression line (determination line). If the standard additions technique that is being used is "through the method," this variation would likely be manifested as BRSME (SRLV) but if the standard additions technique that is being used is "at the instrument," the variation would likely be manifested as WRME (SRLV).

VSAM: Variation of Concentration in the Matierial Sample.
This is variation of the (actual or measured) concentration of the ingredient itself in the solid, semi-solid, or semi-liquid material itself or in liquid suspension (for example, blood). For laboratory-prepared sample homogenates, the VSAM (and the standard deviation of it) will usually be near zero with respect to two or more grams of extracted subsample.

AU: Absorbance Units.

XAU: Expanded Absorbance Units.

AREA: This is the "Area Units" under "peaks" or "equilibrium plateaus" on a chart recorder or similar device.

Q-level; Q1-level; Q2-level:
Not to be confused with low, medium and high measurement levels, these are particular measurement stages in the analytical process. Let "Q-level" be the intermediate analytical measurement stage (instrument reading stage) of the concentrations of the ingredient (analyte) in the regular or control sample extracts being processed by a particular analytical chemistry method whether or not the instrument readings have been converted to concentrations in PPM. Let "Q1-level" be the readings on the instrument (in AU, XAU, or AREA) where the instrument either does not have a direct concentration read-out device or, if it does have one, it is not being used. If it is using a direct concentration readout device, then the measured concentrations of analyte (in PPM) of

the regular or control sample extracts being processed are considered to be at "Q2-level." If it does not have a direct concentration readout device, then a calibration graph must be prepared, based on the instrument readings (in AU, XAU, or AREA at "Q1-level") obtained for the instrument calibration standards, and used to convert the instrument readings (in AU, XAU, or AREA at "Q1-level") for the regular or control sample extracts being processed to their respective measured concentrations of analyte (in PPM) which are at that point considered to be at "Q2-level." "Q2-level" is also the final measurement stage of recovery constant (RC) and recovery sample (RS) control samples, their concentrations being calculated and expressed in terms of PPM or percent recovery, respectively.

M-level:
Not to be confused with low, medium and high measurement levels, this is the final measurement stage in the analytical process. Let "M-level" be the overall analytical measurement stage (reporting level) of measurements (in PPM) produced by a particular analytical chemistry method as it is applied to the determination of the overall concentrations of a particular ingredient (analyte) in various kinds of solid or liquid material samples. "M-level" is the level of overall measurements produced (final measurement output, including the averaging of replicate subsamples) in accordance with the procedures and calculations formula specified in the analytical chemistry method.

Premeasurement; Premeasurement random variable:
The premeasurement is the instrument reading at Q1-level or the concentration determined at Q2-level of the regular or control sample extracts for each sample or subsample replicate having passed through all stages of the chemical processing but before subtracting any reagent blank reading or dividing by the slope of the calibration line. See the definition of "traditional calculation procedure." Even though each stage of chemical processing inherits random variation from each previous stage, to which the Central Limit Theorem applies (Annis, URL), the premeasurement is considered to be a primary and non-composite random variable. However, the mean, variance and standard deviation of the premeasurement can be evaluated and expressed at any of the Q1-, Q2-, or M-levels. The premeasurement, in the case of standard additions "through the method," is actually the y-intercept of the sample regression line (determination line) and this is not taken up in this paper.

Submeasurement; Submeasurement random variable:
There are three possible submeasurements in analytical chemistry processing: 1) the reagent blank, 2) the slope of the calibration line, and 3) the y-intercept, if any, of the calibration line. Only the linear case of calibration lines going through the origin are being considered at this time for the purposes of the current edition of this computerized system prototype.

The first possible submeasurement is (1) the reagent blank. It is a primary and non-composite random variable in its own right and similar to that of the premeasurement, having passed through all stages of the chemical processing, but without any sample substrate present alongside the accurately dispensed portions of prepared chemical reagents. There can be more than one regent blank being run at a time or, in some cases, none. According to the traditional calculation procedure (see the definition of "traditional calculation procedure") the instrument reading for the reagent blank or the average instrument reading, if more than one reagent blank is being run, is subtracted from each of the premeasurements for all the other samples or subsample replicates being run either before or after dividing all readings by the slope or average slope of the calibration line. Like the premeasurement, the mean, variance and standard deviation of this submeasurement can be evaluated and expressed at any of the Q1-, Q2- or M-levels.

The second possible submeasurement is (2) the slope of the linear calibration line. This, too, can be a primary and non-composite random variable in its own right, but not

the same as that of the premeasurement. It is a primary random variable when the "calibration points" for each of the calibration standards (S_1, S_2, S_3) do not fall exactly on, or very near, a regressed linear calibration line going through the origin of the calibration graph. The matter of the error propagation for this will be taken up later in the Theory Section of this paper. The mean and standard deviation of this submeasurement are normally evaluated and expressed in terms of "instrument response," for example, [(AU, XAU, or AREA) per PPM (of the instrument calibration standards)] and the variance likewise, but in the "same units, squared."

The third possible submeasurement is (3) the y-intercept of the linear calibration line (not applicable to this computerized system). The mathematical model of such a calibration line would be y = mx + b (here, "m" is the slope variable and "b" is the variable y-intercept). But let it be clearly understood that except under some very unusual circumstance there should never be any y-intercept other than "zero" allowed in a calibration line, even when the calibration line is non-linear. This is because virtually all modern day analytical chemistry instruments are engineered, designed and manufactured to give a reading of "zero" to say three significant figures, "0.00," over and over again for any "zero-level" instrument calibration standard (S_0) that is input into it at "any reasonable" expansion or attenuation levels. Another way of saying this is that both the "x" and "y" variables in the calibration graph jointly converge to a mathematical limit of "zero." This is true, without exception, in so far as it can be ascertained, for all chemical instrumentation, even when the calibration line is non-linear. As it sometimes happens, reagents have to added to all the standards (S_0, S_1, S_2, S_3, in total, usually) and this usually produces a "standard's blank" which is equivalent to the calibration standard (S_0). Then again, because these reagents are added as concentration constants, the mathematical model for the calibration line will still be y = mx + 0 (here, "m" is the slope variable and "b" is a constant y-intercept set to "zero") since the routine established practice is to subtract the reading for S_0, it being a constant, from each of the remaining calibration standards (S_1, S_2, S_3), even if they, themselves, are random variables. It should be noted here that, in this case, for purposes of statistical regression, "n," the statistical sample size for the number of calibration points being plotted and regressed is equal to 3, not 4. Thus, for the remainder of this paper, the matter of having a y-intercept in a calibration line will not be considered. But it should be mentioned that a y-intercept as a random variable can be dealt with statistically. The problem that arises, which it is believed can be solved, is that under the condition of having a variable y-intercept, the slope and the y-intercept random variables are highly inversely correlated. In fact, for a normal distribution, the correlation coefficient for the estimates of "m" and "b" is known and can be demonstrated to be -0.886 (Watkins, URL). This has significant implications for error propagation. As it is, for this paper and for this computerized system, since no variable y-intercept is being allowed for normal routine analytical chemistry processing, and since standard additions "through the method" is not being dealt with by this computerized system (the standard additions "through the method" technique provides the required standard deviations and the percent recovery is 100%), all the premeasurements and submeasurements that are possible are statistically independent. Moreover, if a variable y-intercept were included in the computerized system that is being developed, there would be myriads of chemical analysts thinking that now they should allow for a variable y-intercept in their calibration graphs when they should not.

"c" factor:

Insofar as the "calculations formula" of a particular analytical chemistry formula is concerned, it is almost invariably made up of "statistical constants," including the required standard nominal sample weight or volume in the denominator thereof, so that the entire formula is reducible to a single "c" factor where the traditional calculation procedure (defined below) is being used. What is meant by "standard" here is that analytical chemistry methods generally call for a specific "nominal" sample weight or volume to be measured out for each sample or subsample replicate to be run. [For a definition of "nominal," by way of example, see the first paragraph on page 135. In the

example given there, the calculations formula would be a "good statistical approximation" to a "statistical constant."] If more than one such nominal sample weight or volume is optionally specified in the analytical chemistry method, then one of them must be chosen to be "standard" for the particular laboratory that the analytical method is being used in for purposes of this computerized system. Any weighing error or volumetric error in any of the variables in the calculations formula, of which are in the range of one or two parts per thousand anyway, are inherited by the statistically sampled (at the back-end of the analytical method) and calculated overall standard deviations. The "c" factor can be standard or non-standard. It is non-standard when, for example, a superimposed dilution or concentration is made or when a non-standard sample weight or volume is used. In all cases, for the purposes of this computerized system, the overall "c" factor must be reducible to a single statistical constant or a good statistical approximation to it.

Traditional calculation procedure:
As previously alluded to, there is a traditional calculation procedure for routine chemical analysis that is used by virtually everyone. First of all, the submeasurement instrument reading for the reagent blank (or average reagent blank), if any is being run, is subtracted from the premeasurement instrument readings for all the other samples and subsample replicates so as to "correct" them. These "corrected results" in terms of AU, XAU or AREA at Q1-level are then manually "brought through" the "y-axis" of the prepared calibration graph and the corresponding concentrations in PPM at Q2-level for each sample or subsample extract in solution are read from the prepared calibration graph's "x-axis" or else the aforementioned "corrected results" are converted to their corresponding concentrations in PPM at Q2-level by dividing them by the slope (or average slope) of the calibration line. The traditional calculation procedure will involve using one reagent blank (or the average of two or more reagent blanks), if any is being run, and one slope (or the average of two slopes); whatever combination is required and specified as standard processing conditions in the analytical chemistry method. The calibration line is sometimes thought of as having an "inverse slope" but this is confusing terminology and is not mathematically commonplace and so it is not used in this paper. These concentrations (actually, the measurements of them) in PPM at Q2-level for each of the sample or subsample extracts in solution for each of the material samples or subsample replicates that are being run, are then entered into the numerator of the "calculations formula," for the particular analytical chemistry method that is being used for the analysis, where they are converted to the measured overall µg-amounts of ingredient (analyte) that have been determined for the actual sample weights or volumes (which were used for each of the material sample or subsample replicates) that have been entered into the denominator of the "calculations formula." Thus, the corresponding concentrations in PPM at Q2-level of the ingredient (analyte) in the material samples or subsample replicates (actually, the measurements of those concentrations) are determined in PPM at M-level. It is clear that this overall measurement at M-level will always be a kind of "proportional parts per overall number of parts" kind of ratio, for example, parts per million (PPM) which is being used for all of the examples in this paper and alternatively can be expressed as µg/ml (micrograms per milliliter) for liquid medium or µg/g (micrograms per gram) for solid materials. It should be noted here that the submeasurements of the reagent blank (or average reagent blank) and the slope (or average slope), even when they are both random variables, are being used as "statistical constants" in the traditional calculation procedure just described. This "one to many" statistical sampling is what causes the variation in the submeasurement random variables to manifest as between-run systematic error (BRSME). By way of comparison, this phenomenon does not occur in the example given below of a non-traditional calculation procedure where the statistical sampling is "one on one."

Non-traditional calculation procedure:
An example of a non-traditional calculation procedure might be where a T-distribution confidence interval is required by a top manager. In this case, the processing flasks for the subsample replicates are labelled by, for example, the subscripting letters: (a, b, c,

d) and likewise for the reagent blanks. Each subsample replicate must have a corresponding reagent blank. Likewise each subsample replicate must have a corresponding slope when doing the calculations and this is obtained by doing as many runs, as needed, in this case four, on the instrument calibration standards. These slopes are likewise labelled by the subscripting letters: (a, b, c, d). Then the submeasurement instrument reading at Q1-level for the reagent blank "a" is subtracted from the premeasurement instrument reading at Q1-level for subsample replicate "a" and the result is divided by the slope subscripted as "a" and so on throughout b, c, and d and brought through the calculations formula for the particular analytical chemistry method being used, in order to obtain the corresponding concentrations for them (actually, the measurements of those concentrations) at M-level, for each of the four material subsample replicates. A T-distribution confidence interval is then calculated from the mean and standard deviation of these overall measurements at M-level for the sample. It should be noted that, in a procedure such as this one, for the mean and standard deviation to be acceptable, equal subsample weights or volumes from a well homogenized solid or liquid material sample homogenate must be used for each of the four subsample replicates.

Theory Section

Some Basic Premises:

1) Quantitative chemical analysis is done according to high technological standards. The analytical methods are documented and often published. The analytical chemistry methods are given different identification numbers and are always followed to the letter for every analytical run. Chemists and Chemical Technicians know how to carry out their trade. They know how to do exact weighings on five decimal place high precision balances. They know how to quantitatively transfer substances in solution from one flask to another without losing any. They know how to prepare solutions to exact volumes and exact concentrations. They know the theory of matter, basic chemistry and physics. There is absolutely no reason whatsoever for one chemical analyst to get a different percent recovery or standard deviation for the same material sample under identical conditions. Great care is taken by laboratory staff to ensure that specific analytical methods can be repeated over and over again in an identical manner. However, notwithstanding all of this, there will be random variation occurring in the various stages of the chemical processing and in some of those stages, small losses will also occur which leads to one obtaining something less than 100% recovery. But the better methods have the bigger number of stages in them to take care of all potential interferences. This leads to a slightly less than desirable percent recovery at times but this can be offset by allowing the chemical measurements to be unbiased by the DBMS in the main database. This latter facility would be transparent to all laboratory staff by the proposed computerized system. This has all been said to justify the making of the first premise: The within-run variances of the premeasurements and submeasurements of a particular analytical method in a particular laboratory can be considered to be more or less constant over the several ongoing analytical runs that are routinely being made in the laboratory even though different laboratory analysts are performing the analyses.

2) The second premise that needs to be made is that: All random variation that is present in analytical chemistry measurements comes from the various stages of the chemical processing that occurs when performing the analyses. The specific analytical chemistry method as it is being done in a particular laboratory is a specific stochastic process generator. Therefore only the particular stochastic characteristics of the particular chemistry method need be determined in order to obtain the standard deviations for all the measurements to be generated by the analytical method. This obviates the need to be continually determining confidence intervals from chemical measurement data.

3) A third premise that can be made is that: While obtaining the particular stochastic characteristics of a particular analytical method in a particular laboratory at a specific measurement level, the percent recovery can also often be concurrently determined from the same control sample data for that measurement level.

4) A fourth premise: The nature of the stochastic variation that occurs in each of the various stages of the chemical processing is well known and understood by professional chemists. If a modification to the method ever needs to be done, the determined stochastic characteristics can often be modified by careful thought, chemical process stage testing, such as of a new model of chemical instrumentation, and a minimum of re-running of control samples.

5) A fifth premise is that: Stochastic variation is inherited from one stage of the chemical processing to another in the analytical method in such stochastic manner so as to be effects-additive. Even the tolerances of standard laboratory labware such as volumetric flasks and pipettes are inherited in this stochastic manner for both regular samples and calibration standards. This means that the particular stochastic characteristics of a particular analytical chemistry method in a particular laboratory can be determined by running the appropriate control samples at specific measurement levels. As to be explained more fully later on, all of this control sampling can be routinely done at a leisurely pace over several analytical runs if only the collection of control sample data can be given its justifiable priority and initiated promptly by management officials. Often, standard deviations can be obtained from database records of regular sample duplicates.

6) A sixth premise is that: It can be shown that systematic error in chemical measurements cannot properly exist beyond the level at which the measurements are properly unbiased. The levels of concern are: (1) within analytical runs, (2) between analytical runs in the same laboratory, and (3) between laboratory biases. For reasons which are quite self-evident in light of the revelations having been made in this paper, the best level to unbias at is (2), the laboratory level. In other words, the measurements from the individual analytical methods in each particular laboratory would be unbiased in such manner as this computerized system is capable of doing, as has been explained, and if possible, this would be done by the DBMS in the main database, using the proper parameters that are supplied to it, but it can also be done within the laboratory, if necessary.

7) In paragraph (6), it was noted that the unbiasing of the chemical measurements is best done within the main database, but that it could be done within the laboratory, if necessary. A particular example where this might find application could be that of a typical government research scientist. It is well known that research scientists almost invariably adopt the strategy of choosing the particular analytical methods they need in the beginning of their career and then to keep them for the duration of their research tenure. This is done to overcome the problem of bias between analytical methods, but as is evident from this paper, there could be systematic error between analytical runs. In addition, they are often driven to produce reams of analytical data in order to obtain sufficiently high statistical sample sizes for statistical testing purposes and for comparison to the data of other scientists. Often, it is desired to obtain a high degrees of freedom T-distribution confidence interval for publication. It can be shown that a T-distribution confidence interval is valid for significance testing but is useless and deceiving as a descriptive statistic. The proposed computerized system solves all these problems by determining the high degrees of freedom standard deviations needed to obtain the proper confidence intervals from the very beginning of the research project , from the analytical method itself, rather than from the reams of data produced by it for each new data set, and the research scientists can now compare unbiased data and confidence intervals with each other, resulting in huge savings in time and money. This is the

seventh premise, the research scientist functioning as the administrator of the computerized system.

Programming the DPSP:

Variances are never entered as predefined program variables into the DPSP, only their standard deviation counterparts (this helps to control the number of decimal places needed). With the exception of the standard deviation of the slope, which is entered in terms of (AU, XAU, or AREA) per PPM at Q1-level, all standard deviations must be entered into the DPSP in terms of PPM at Q2-level. This subsection and the next one deals with how to estimate the sample standard deviations of the premeasurement and submeasurement random variables that are inherent in almost every analytical chemistry method that is out there. First of all, it should be documented that the author is recommending that a minimum of 15 degrees of freedom be established as a minimum industry standard for these standard deviations before they can be thought of as being a substitute for their population parameter counterparts for routine applications and reports. It can be shown that a 95% confidence coefficient for the sample standard deviation at 15 degrees of freedom will be about 55% too high 2.5% of the time and about 26% too low 2.5% of the time. What this translates into is that a 95% confidence interval for the mean of measurements calculated as plus or minus 2.0 sample standard deviations at 15 degrees of freedom will produce an actual confidence coefficient between 95% and 97.4% about 68% of the time and between 85.4% to 95% about 32% of the time. But this should be acceptable for routine applications and reports. It can be shown, using the theory of multiple tests, that a 95% minimum confidence coefficient confidence interval (MCCCI) for the population mean of measurements should be calculated as plus or minus 3.08 sample standard deviations at 15 degrees of freedom. This includes unbiasing of the sample standard deviation (Dixon & Massey 1957, p. 76). Such a confidence interval will be at 95% confidence coefficient, or above, all of the time and would therefore be more suitable for legal purposes such as court proceedings. Some chemical analysts may want to make do with some lessor number of degrees of freedom, say a minimum of ten, where, as in gas chromatography, it can take up to an hour to get a single reading on the gas chromatograph. In this case, it would be presumed, that an exception could be made. But the reliability of the 95% confidence intervals calculated as plus or minus 2.0 sample standard deviations at 10 degrees of freedom will be much less. However, the multiplier for the sample standard deviation could be increased as an expedient measure.

Note that these standard deviations with this many degrees of freedom do not need to be determined in a single analytical run. They can be obtained at a leisurely pace by running the appropriate control samples as time and circumstances permit and the results entered into the appropriate PAF's. After a period of some weeks, months, or even in some cases, a couple of years, the estimates for these standard deviations, at the minimum standard of 15 degrees of freedom per measurement level, will be achieved. But the sooner one starts collecting the data, the better. Any authoritative reference on industrial quality control will specify that such control sampling must take place for some required period of time before legitimate quality control charting can begin. It is the same principle. In the meantime, before the required minimum standard is achieved, the regular measurements that are routinely being generated in the laboratory can be entered into the DPSP for the particular analytical chemistry method and from there eventually will be entered into the main database. From time to time, the DBMS of the main database will check the DPSP for each particular analytical chemistry method in each particular laboratory to see if the required minimum standard, standard deviations and percent recoveries, have been entered into the temporary database of the DPSP alongside the identification numbers for the respective samples. When this happens, the required standard deviations and percent recoveries for the particular samples will be uploaded and entered into the main database. Of course, all of this, or any part of it, can be done manually with now commonplace computer spreadsheet technology. The minimum standard for the percent recovery is four recovery constants

(RC) or four recovery samples (RS) per measurement level (one RC or one RS per measurement level per run) to be obtained over four analytical runs for each of the required measurement levels. If a recovery sample or recovery constant cannot be run, the developer of the analytical method will supply the estimate. The percent recovery is entered into the DPSP as a percentage (this is the most straightforward and intuitive way) for uploading into the main database where it is then converted by the DBMS to its decimal equivalent.

It should be noted that the primary standards for very new and exotic chemicals are often far from being ideally pure. If a recovery sample is run using a primary standard chemical of, say, 80% theoretical purity, and the same primary standard chemical is used to make up the calibration standards, and if, in both cases, the actual purity is not being taken into account to determine the theoretical weights of primary standard chemical required to make up the recovery sample and standards, then the percent recovery obtained is only for the chemical processing stages of the analytical method and not the whole method. The recovery run could turn out to be 100% in this hypothetical case (it is as though the primary standard chemical is being considered to be 100%). If, indeed, this were the case, then the measurements being produced by this method would be, consistently, 20% too high throughout whole measurement spectrum (method bias). It is common practice in many laboratories to do a recovery run in just this way. That is why it is absolutely stipulated for the purposes of this system that the actual lot analysis or purity of the primary standard chemical to three significant figures always be taken into account in determining the theoretical weights used for the recovery sample run. Then the actual percent recovery for this hypothetical method will turn out to be 120%, when the actual lot analysis or purity of the primary standard chemical is taken into account in determining the theoretical weights used to make up the recovery sample but not the instrument calibration standards. This common practice with the instrument calibration standards does not matter to this computerized system. But when the system is implemented, a decision must be made, whether or not to continue not taking into account the actual lot analysis or purity of the primary standard chemical in determining the theoretical weights used to make up the instrument calibration standards for all future analytical runs of the analytical chemistry method in the particular laboratory.

Generally speaking, though not always, the required minimum standard, standard deviations and percent recoveries, need to be determined at three different specific measurement levels, low, medium and high, before being entered into the DPSP for each particular analytical chemistry method being used in the laboratory. The DPSP has been programmed to adjust, usually by some form of interpolation or extrapolation to be explained later, the required minimum standard, standard deviations and percent recoveries, determined at low, medium and high measurement levels, that have been entered into it as predefined program variables, so that they can be applied to the routine overall measurements at M-level of the material samples at their various measurement levels. The DPSP has been programmed to further adjust the required minimum standard, standard deviations for application to the routine overall measurements at M-level of the material samples being analyzed according to the following data that is to be input into the data entry screen of the DPSP by the chemical analyst doing the particular analytical run:

1) The deviation of the material sample weight or volume of the sample or subsample replicates being analyzed from the standard nominal value required by the analytical chemistry method in the particular laboratory. A simple ratio, called an "f" factor, is calculated by the chemical analyst and entered into the data entry screen of the DPSP.

The "f" factor is calculated as:

$$f = \frac{\text{nominal standard sample weight or volume}}{\text{(actual or nominal) non-standard sample weight or volume}}$$

2) The number of material sample subsample replicates being processed in the particular analytical run that is being entered into the data entry screen of the DPSP.

3) The number of reagent blanks being processed in the particular analytical run that is being entered into the data entry screen of the DPSP. This includes the number "zero" if there are no reagent blanks being processed. Alternatively, a different version of the program will not have a data entry column for this or it will be hidden.

4) The number of runs being made on the instrument calibration standards for the particular block of samples and/or subsample replicates that is going to be applied to them (by averaging the slopes, if necessary) that is being entered into the data entry screen of the DPSP. The possibilities are: one slope or two slopes (being averaged), if calibration standards are being run. More than one run is sometimes made on the instrument calibration standards if there are any sensitivity changes occurring in the instrument during the course of reading all the sample or subsample extracts on the instrument.

5) Any front-end or back-end dilutions or concentrations that are required for any individual samples or subsample replicates that are over and above all of those that are specified in the documented analytical chemistry method (that is, superimposed) for all samples or subsample replicates that are being entered into the data entry screen of the DPSP.

6) The number of replicate instrument readings, that are being made on each individual sample extract and/or on each replicate subsample extract.

The computer data entry screen contains the following columns:

Column 1: The current date.

Column 2: The lab-method identifier. This identifies the particular analytical chemistry method being done in the particular analytical laboratory.

Column 3: The unique sample identifier.

Column 4: The single or average (if more than one subsample replicate was done) original measurement for the sample.

Column 5: The number of subsample replicates done on the sample, for the analytical run.

Column 6: The front-end overall superimposed (that is, over and above any dilutions/ concentrations specifically indicated to be done in the analytical method during the regular chemical processing) dilution/concentration factor for the sample.

Column 7: The back-end overall superimposed (that is, over and above any dilutions/ concentrations specifically indicated to be done in the analytical method during the regular chemical processing) dilution/concentration factor for the sample.

Column 8: The "f" factor for the sample, as explained above.

Column 9: The number of reagent blanks that were run for the block of samples or subsample replicates in the analytical run. This value can be "zero," if no reagent blanks have been included in the current analytical run.

Column 10: The number of calibration slopes (zero, one or two) that were run for the block of samples or subsample replicates in the analytical run. This value can be "zero," if no calibration standards are being used in the particular analytical chemistry method. Note that in a titrimetric analytical method, the titer (Day & Underwood 1967) is equivalent to the value of the slope but it usually has no significant variance, so a "zero" should be entered into column (10) or else the standard deviation of the titer would have to be determined and entered into the DPSP and a "1" entered into column (10).

Column 11: The number of replicate standard instrument readings that were made on each sample or subsample replicate being run. Note that all replicate instrument readings must consist of one or more (all to be averaged along with the original reading) standard readings which may already consist of one or more (regressed or averaged) standard sub-readings such as occurs, respectively, with (1) standards additions "at the instrument" or (2) as an expedient (when the sub-readings are averaged) to help normalize the output of the instrument while reducing the variation thereof. In case (2), it will be seen that there are two possibilities for what is called a "reading." To illustrate, three injections will be used per sample or subsample replicate: (a) call each injection a "reading," or (b) call each average of three injections (sub-readings) a "reading." Obviously, (2) (a) will be the most flexible choice, since then any number of readings can be done on individual samples or on each subsample replicate, to be subsequently entered into column (11), over and above what is required to help normalize the output of the instrument. For this choice, the number of replicate instrument readings (to be averaged) that are to be made on the sample or on each subsample replicate will have been pre-entered into column (11), having been pre-set to the positive whole number required as part of standard conditions (in this example, "three"), this being done for the convenience of the chemical analyst in reducing data entry time and to help reduce data entry errors, it being possible to change this value on demand. If, as in case (1) or (2) (b), multiple (regressed or averaged, respectively) instrument sub-readings are a part of standard processing conditions (that is, they are to be done on each regular or control sample extract, each replicate subsample extract, and each calibration standard), then these same multiple sub-readings must be done when determining the various standard deviations on all of the various PAF-forms, including the standard deviation of the instrument as it is being determined on the STAN-DUP, CAL-DUP or CAL-DATA forms. In cases (2) (a) and (2) (b), though, the standard deviation of the instrument could alternatively be determined as the parent random variable of the instrument (that is, considering each individual non-composite reading to be a single outcome from the instrument) and then the variance thereof (obtained from multiple consecutive individual non-composite instrument readings using a single sample extract or standard solution) can be adjusted so as to comply with the number of multiple sub-readings which are standard. In case (2) (b), this will be the number of standard multiple (to be averaged) instrument sub-readings per reading. In case (2) (a), it will be one single injection per reading. Only the respective standard deviation determined from that variance so adjusted can be entered as an alternative predefined program variable into the DPSP once it is converted to PPM at M-level by multiplying by the standard "c" factor for the specific analytical chemistry method. On the other hand, the standard deviation of "y" given "x" (also the standard deviation of the instrument response variable) determined from each run on the calibration standards, would normally be calculated from the standard number of instrument sub-readings already having been made on each calibration standard so that it would not normally need to be adjusted before entering it as a predefined program variable into the DPSP, it having been converted to PPM at M-level by multiplying by the standard "c" factor for the specific analytical chemistry method.

All of the above adjustments to the required minimum standard, standard deviations and percent recoveries, for the particular DPSP that are to accompany the overall measurements at M-level as they are being generated by the particular analytical chemistry method as it is being done in a particular laboratory and entered into the main

database, are pretty straightforward to program into the DPSP although a lot of definitions had to be formulated in order to control the data entry process on behalf of chemical analysts performing the analyses. Insofar as the "calculations formula" of the particular analytical chemistry formula is concerned, it is almost invariably made up of "statistical constants," including the required standard nominal sample weight or volume in the denominator thereof, so that the entire formula is almost invariably reducible to a single standard "c" factor. What is meant by "standard" here is that analytical chemistry methods generally call for a specific "nominal" sample weight or volume to be measured out for each sample or subsample replicate to be run. For example, this could be 10.0 grams of material sample homogenate. By "nominal" is meant that the chemical analyst could, for example, weigh out 9.88, 9.93, 10.03 and 10.11 grams for a group of four subsample replicates. In this case, the "f" factor, as explained above, would be equal to 1.00. The "f" factor column is therefore pre-loaded with "1.00's" for every row for the convenience of the chemical analyst in reducing data entry time and to help reduce data entry errors. But if only approximately 3.00 grams were available for analysis, most likely the actual sample weight, say 3.08 grams, would be used to calculate the "f" factor. But if approximately 3.00 grams of an SRM material were to be run as a control sample for every analytical run, on an ongoing basis, then even though actual weights would be used for each run, the number 3.00 would be used to calculate the "f" factor since 3.00 grams would be the "target weight" for each actual weighed-out portion of SRM material. This example is given here but there were other such definitions that had to be formulated.

There are some more statements that are required about how to program the DPSP to do the interpolation and extrapolation required in order to adjust, the required minimum standard, standard deviations and percent recoveries, determined at low, medium and high measurement levels that have been entered into the DPSP as predefined program variables, so that they can be applied, after being adjusted within the DPSP, to the routine overall measurements at M-level of all the material samples being done by the analytical method, at their various measurement levels. Originally, it was decided to include also the number of degrees of freedom as a separate adjusted parameter (for the adjusted standard deviations) to be included along with the adjusted standard deviations and percent recoveries which were to eventually be entered into the main database alongside the material sample and its measurement. But the approach taken in this paper is to establish a defined "minimum standard" for the number of degrees of freedom for the standard deviation, and statistical sample size for the percent recovery, eliminating the need for this option. But, of course, it can be done if desired. It should be noted here also that, although the interpolation and extrapolation techniques that are to be described here are in terms the required minimum standard, standard deviations and percent recoveries, determined at low, medium and high measurement levels, there are many cases where only two or even one measurement level would suffice. For example, a particular analytical chemistry method may only be in need of standard deviations and percent recoveries, for a particular restricted range of measurement levels, the ones being used, for example, to test for compliance of a certain food product to government imposed standards and regulations. But, for the purpose of explaining of the techniques, it will be assumed that there are three.

The main strategy used to describe the interpolation and extrapolation techniques will be to construct in one's imagination, a graph of the three plotted points using standard deviations or percent recoveries on the y-axis and measurement level on the x-axis. Taking the standard deviations first, linear interpolation would most likely be used, exclusively, to determine the adjusted standard deviations between points 1 (low measurement level), 2 (medium measurement level) and 3 (high measurement level). Subsequent adjustments will be made further on in the DPSP to the adjusted standard deviation determined here. Each of the three original plotted points must be for the standard deviation of a single analytical determination at M-level. Originally, it was thought that an "internal computer table" of values of the standard deviations and percent recoveries would be needed, but it was found that simple mathematical formulas would suffice. Between point 1 and the origin (0,0) of the imagined graph, linear

interpolation or a line constructed from a plot of the standard deviation according to the holding of the coefficient of relative variance (crv) of point 1 constant throughout the interval could be used, depending on what points 1, 2, and 3 are seen to doing. Such a plot makes a very nice curved line passing through the origin in somewhat of a logarithmic fashion. The system administrator, laboratory supervisor or analytical chemistry method developer would be the one making the choices. For points above point 3, linear extrapolation could be used, or extrapolation by means of holding the coefficient of relative standard deviation (crsd) of point 3 constant could be used, or extrapolation by means of holding the "crv" of point 3 constant, as previously explained, could be used. Again, it depends on what the points 1, 2 and 3 are seen to be doing. For the percent recoveries, the task is even easier. Only linear interpolation need be used from the origin through to point 3 and beyond that the value at point 3 is extrapolated as a maximum. Note that although simple formulas are to be used in this manner, the concept of an "internal computer table" will be used throughout the rest of this paper so as to facilitate the understanding of the computer algorithm to be described below. Therefore, the term "computer table," when it appears in this paper, will also refer to the "computer table subroutine" just described in terms of simple formulas.

Note: Unlimited extrapolation for the standard deviation is allowed to be made for all measurement levels above the highest measurement level (point 3) where the standard deviations were determined and for the percent recovery, the value at this point is extrapolated as a maximum for all measurement levels above it. This is allowed for the purposes of the algorithm that is going to be used to determine the adjusted standard deviations and percent recoveries. For example, the extrapolation may exceed the highest measurement level (point 3) by a factor of ten times, if there is a back-end overall superimposed dilution/concentration factor equal to ten. This may not seem very reasonable but the limiting factor for the percent recovery and standard deviation is usually not the chemical processing stages themselves (overall measurement spectrum) but the limited measurement spectrum of the instrument.

It is necessary, at this point, to fully describe how a "computer algorithm" will be used to adjust the required minimum standard, standard deviations and percent recoveries, determined at low, medium and high measurement levels that have been entered into the DPSP as predefined program variables, so that they can be applied, after adjustment, to the routine overall measurements at M-level of all the material samples being done by the analytical method, at their various measurement levels. To understand this is to understand how the system works. First of all, it needs to be pointed out that along with each of the predefined program variables for the standard deviations and percent recoveries, determined at low, medium and high measurement levels, there are other predefined program variables entered in the DPSP that record the number of reagent blanks and slopes that were being run when the various PAF-forms were being used to determine the minimum standard, standard deviations and percent recoveries for the measurement levels. The standard deviation of the chemical instrumentation being used and the standard deviation of the slopes, both of which were determined under standard processing conditions, are also to be entered into the DPSP. These are obtainable from any of the STAN-DUP, CAL-DUP or CAL-DATA forms. It is the responsibility of the system administrator, laboratory supervisor or analytical method developer, to enter all of these predefined program variables into the DPSP. Then, for the purpose of describing the algorithm below, it will be assumed that the chemical analyst will have also entered into the data entry screen of the DPSP, the required variables concerning each material sample or group of subsample replicates that have been run. The algorithm will be described below in stepwise fashion with annotation.

Data Processing Algorithm:

Note: There are three possible "steps" that can be superimposed onto the standard chemical processing stages of the analytical chemistry method and each has its

equivalent "factor" to be used in calculating the overall measurement. For example, there can be a front-end overall superimposed dilution/concentration giving rise to a front-end overall superimposed dilution/ concentration factor and there can be a back-end overall superimposed dilution/concentration giving rise to a back-end overall superimposed dilution/concentration factor. In other words, a superimposed dilution/concentration factor is the reciprocal of the degree of superimposed dilution/concentration that was used for the sample. A non-standard sample weight or volume may also be used. An "f" factor has been created for the chemical analyst to enter into the data entry screen so that the standard deviations may be adjusted according to the ratio of the standard to non-standard sample weight or volume. It can be shown that the non-standard sample weight or volume and the front-end overall superimposed dilution/concentration both affect the input to the standard chemical processing stages while the back-end overall superimposed dilution/ concentration only affects the output. It can be further be shown that for purposes of determining a mock measurement for entering the computer table at the correct µg-amount of analyte flowing through the various standard chemical processing stages, that the "f" factor and/or the front-end overall superimposed dilution/concentration factor should be removed from the original overall single or average measurement for the sample that has been entered into column (4). This is done by dividing by the respective "factors." The "f" factor is an implicit multiplicand in the calculations formula because the actual non-standard sample weight or volume will have been used in the denominator of the calculations formula instead of the actual standard sample weight of volume. The back-end overall superimposed dilution/concentration factor is not taken out in this manner because then the mock measurement would no longer be representative of the correct µg-amount of analyte flowing through the various standard chemical processing stages of the analytical chemistry method. While the standard deviation of the various standard chemical processing stages of the analytical method are unaffected by this choice (the back-end dilution/concentration, a divisor, and the back-end dilution/concentration factor, a reciprocal multiplicand, cancel each other off), the standard deviation of the instrument can be magnified (or diminished) because it is only being multiplied by the back-end overall superimposed dilution/concentration factor and nothing is cancelling it off. A back-end superimposed dilution is usually not made unless the concentration of the sample extract is very high and above the range of the calibration standards. To compensate for this possibility, the DPSP does unlimited extrapolation above the highest measurement level at which the standard deviations for the DPSP were determined so that the standard deviation of the sample will continue to vary as it has been doing over the standard measurement levels. Since the system administrator, laboratory supervisor or analytical method developer will have entered the standard deviation of the instrument and the standard deviation of the slopes into the DPSP as predefined program variables and the chemical analyst will have entered the number of replicate (and averaged) instrument readings that were made on each sample or subsample replicate along with the back-end overall superimposed dilution/concentration factor, the algorithm given below will be adjusted to deal with these possibilities.

1) Divide the single or average measurement for the sample that has been entered into column (4) by the "f" factor entered in column (8). Call this result "mock measurement-1" and store it in computer memory. The "f" factor would have been used implicitly as a multiplier in the traditional calculation procedure when an (actual or nominal) non-standard sample weight or volume was used in determining the single or average measurement for the sample that was entered into column (4). Thus, by this action, it is removed.

2) Divide the mock measurement-1 determined in step (1) by the front-end overall superimposed dilution/concentration factor from column (6). Call this result "mock measurement-2" and store it in computer memory. The front-end overall superimposed dilution/concentration factor would have been used as a multiplier in the traditional calculation procedure for determining the single or average measurement for the sample

that was entered into column (4). Thus, by this action, it is removed. This mock measurement-2, is the most representative measurement for entering the computer table in order to determine the eventual standard deviation and the percent recovery for the single or average measurement that was entered into column (4).

Note: If there have been no superimposed dilutions/concentrations, then "1.00" will have been automatically entered into both column (6) for the front-end overall superimposed dilution/ concentration factor and column (7) for the back-end overall superimposed dilution/ concentration factor. This is also true for the "f" factor entered in column (8), if there have been no non-standard sample weights or volumes used. The number, "n," of subsample replicates being done on the sample (and averaged) for the current analytical run in column (5) and the number of replicate (and averaged) instrument readings that were made on the sample or on each subsample replicate in column (11) will also have been pre-set to the positive whole number required as part of standard conditions for the convenience of the chemical analyst in reducing data entry time and to help reduce data entry errors.

Note: There may have been more than one back-end superimposed dilution/concentration. Thus, the word "overall" is used to reflect this.

Note: All subsample replicates must have the same degree of front-end and/or back-end overall superimposed dilutions/concentrations and their associated reagent blank or "reagent blanks" (to be averaged) must also (each of them) have the same degree of back-end overall superimposed dilutions/concentrations. In addition, all subsample replicates must also have the same number of replicate instrument readings. Note that each replicate instrument reading may consist of more than one standard sub-reading such as occurs with standards additions "at the instrument"or as an expedient (when the sub-readings are averaged) to help normalize the output of the instrument while reducing the variation thereof. Refer to column (11) in the data entry section for an explanation of the number of replicate instrument readings that have been made on each sample or subsample replicate being run.

Note: For the rest of the algorithm, the word "sample" will refer to each material sample or group of subsample replicates that have been run for which a single or average measurement is to be calculated and entered into the main database. Also, the "columns" refer to the various data entry columns described above. The algorithm will be described as though a particular material sample or group of subsample replicates from a single sample homogenate has being processed for which the single or average measurement for the sample has been entered into column (4).

Note: At each step described in this algorithm, the intermediate calculated results are stored in a computer memory input and output grid for further computer data processing and error checking. The details of where and how they are stored are not given.

3) Using the above described procedure for interpolation and extrapolation in the computer table subroutine, the DPSP determines the standard deviation and percent recovery for the exact measurement level given for mock measurement-2. This will be the true percent recovery for the original single or average measurement for the sample that has been entered into column (4). It is stored in the computer memory grid for output later on. Further data processing is done on the standard deviation. Call this standard deviation "mock standard deviation-1."

Note: All the standard deviations entered as predefined programmed variables in the DPSP are either BAV-standard deviations, corrected BAV-standard deviations or corrected WAV-standard deviations so that they only apply to single determinations at M-level. These standard deviations have been determined under the standard or "corrected to standard" processing conditions specified in the particular analytical chemistry method to

which the particular DPSP program applies. The number of reagent blanks and/or slopes that were used to determine the standard deviations under these standard processing conditions have also been recorded in the DPSP as predefined program variables as well as the standard deviations for the parent random variables of the reagent blanks and the slopes. If they are BAV-standard deviations such as are determined on the RS-form, they will contain the correct proportion of all forms of between-run systematic error (BRSE), including any between-run systematic measurement error, BRSME (RBV and/or SRLV), being generated by the WRME (RBV and/or SRLV) of the reagent blank(s) or slopes(s) that are being run under standard conditions using the traditional calculation procedure. If they are WAV-standard deviations, such as are obtained on the SAM-DUP form, they will have been corrected by having had added to them the appropriate terms for the WRME (RBV and/or SRLV) variation of the reagent blank(s) and/or slopes(s) that were being run to determine the standard deviations of the reagent blank(s) and/or slopes(s) under standard conditions.

4) The mock standard deviation-1 determined in step (3) is squared giving mock variance-1.

5) If the number of reagent blanks that were being run when the standard deviations for the regular samples were being determined under standard processing conditions is not "zero," the standard deviation for the parent random variable of the reagent blanks determined under standard processing conditions is squared, giving the respective variance. This variance for the parent random variable of the reagent blanks is then divided by the number of reagent blanks that were used to determine the standard deviation of the reagent blanks on the RB-DUP form under standard processing conditions and the result is subtracted from mock variance-1 giving mock variance-2. If the number of reagent blanks that were being run when the standard deviations for the regular samples were being determined under standard processing conditions is "zero," then the value in mock variance-1 is assigned to the memory location for mock variance-2.

Note: Not every analytical method runs a reagent blank or count blank as part of standard conditions. In this case, a "zero" would automatically be entered into column (9) and the column hidden on the data entry screen. The standard deviation for the reagent blanks (or count blanks) would automatically be set to "zero" as a predefined program variable in the DPSP.

6) If the number of calibration slopes (zero, one or two) that were being run when the standard deviations for the regular samples were being determined under standard processing conditions is not "zero," the standard deviation for the parent random variable of the slopes determined under standard processing conditions is squared, giving the respective variance. The variance for the parent random variable of the slopes is then divided by the number of slopes (one or two) that were used to determine the standard deviation of the slopes on the STAN-DUP, CAL-DUP or CAL-DATA forms under standard processing conditions. This result is then multiplied by the square of mock measurement-2. This, in turn, is divided by the square of the mean or grand mean of the slopes as determined under standard processing conditions. Finally, this last result is subtracted from mock variance-2 giving mock variance-3. If the number of slopes that were being run when the standard deviations for the regular samples were being determined under standard processing conditions is "zero," then the value in mock variance-2 is assigned to the memory location for mock variance-3.

Note: Not every analytical method runs instrument calibration standards as a part of standard conditions. In this case, a "zero" would automatically be entered into column (10) and the column hidden on the data entry screen. The standard deviation for the slopes would then also be automatically set to "zero" as a predefined program variable in the DPSP as a precaution. Another special case is with standard additions "at the

instrument." In this case, the calibration standards (including a "zero" standard) are added on top of each sample or subsample replicate injection or else mixed with each sample or subsample extract before injection. Therefore, a run on the calibration standards is being done for each sample or subsample extract as a part of obtaining an overall individual instrument reading (one sub-reading from each injection) for each extract. In this case, the number of calibration slopes would also be automatically set to "zero" in column (10) and the column hidden on the data entry screen, since the variation in the individual "standard additions" slopes for each overall reading per determination will be included (as inherited variation), in the standard deviation of the instrument as determined for, and/or corrected to, a single instrument reading (composed of more than one sub-reading). The "standard additions" technique is too complex to be described here but note that this computerized system is not applicable to doing standard additions "through the method," in which case, the overall standard deviation at M-level for each determination is obtainable from the technique itself and the overall recovery is normally 100%.

Note: Mock variance-3 is an unmixed variance, not containing any BRSME (RBV and/or SRLV) that would have been generated by the WRME (RBV and/or SRLV) of the reagent blank(s) and/or slopes(s) that were being run under standard processing conditions, nor likewise any variation from the WRME (RBV and/or SRLV) itself, when the standard deviations were being determined. As a result, this variance can now be manipulated by standard statistical procedures. If it were BAV-standard deviations that had been entered as predefined program variables into the DPSP, there could be some other form of BRSE contained in this variance, but in theory, there shouldn't be any, and if there is, it has a right to be included as long as it is random. Any form of non-random BRSE should have been screened out on the respective PAF-forms. The basic idea is to remove, in steps (5) and (6), all variation due to the reagent blank(s) and/or slopes(s) that were being run under standard processing conditions using the traditional calculation procedure when the standard deviations for the measurement levels were being determined for the DPSP. In steps (13) and (15), the variance for the parent random variable of the reagent blanks divided by the number of reagent blanks that are entered into column (9) for the current analytical run and the variance term for the number of calibration slopes {one or two, as entered into column (10)} for the current analytical run, will be put back into the overall variance for the sample in their stead.

7) The standard deviation of the instrument at M-level, such as determined on the STAN-DUP, CAL-DUP or CAL-DATA forms under standard processing conditions, must be for only a single standard instrument reading per sample or per subsample replicate with no back-end overall superimposed dilution/concentration factor employed. This standard deviation of the instrument, having been entered into the DPSP as a predefined program variable, is squared giving the respective variance of the instrument. This variance is then subtracted from mock variance-3 giving mock variance-4. Note that under standard processing conditions, each standard individual instrument reading may consist of more then one standard sub-reading such as occurs with standard additions "at the instrument" or as an expedient (when the sub-readings are averaged) to help normalize the output of the instrument while reducing the variation thereof.

Note: The assumption of a constant standard deviation of the instrument throughout the linear range of the instrument measurement levels at Q1-level is being made here and elsewhere throughout this paper. If this is not the case for a particular instrument, then consideration should be given to using the maximum standard deviation of the instrument within the linear range. If still more accuracy is desired, then the standard deviation of the instrument would have to be determined at low, medium, and high, instrument measurement levels and these values, once converted to M-level, would have to be collated with the respective and corresponding low, medium, and high, overall measurement levels of the analytical method as they already exist in the internal computer table. In the latter event, it needs to be mentioned that there are some

different formulas that can be used to calculate the slope depending on how the standard deviation of the instrument is varying with respect to instrument measurement level.

8) The back-end overall superimposed dilution/concentration factor from column (7) is squared.

Note: Both the front-end overall superimposed dilution/concentration factor and the back-end overall superimposed dilution/concentration factor must be very clearly defined to the user, especially what is meant by "superimposed." A message concerning this must always be output to the user on the data entry screen. An example to explain this point is given here concerning the back-end overall superimposed dilution/concentration factor. Suppose an analytical chemistry method requires under standard processing conditions, a concentration of 10 ml to 5 ml at the back-end of the analytical method. Then, a concentration factor of 0.5 will appear in the numerator of the calculations formula, as part of standard conditions. Suppose that the chemical analyst decides to concentrate further, in the above mentioned step, down to 1 ml. This is an overall concentration of 10 ml to 1 ml and the overall concentration factor is 0.1. But only the 5 ml to 1 ml is "superimposed." Consequently, the chemical analyst should enter 0.2 into column (7) of the data entry screen as the back-end overall superimposed dilution/concentration factor. To check, 0.2 which is entered into column (7) times 0.5 which is in the numerator of the calculations formula, is equal to 0.1 which is the correct overall concentration factor.

9) Multiply the variance of the instrument as determined in step (7) by the result from step (8) and divide this result by the number of replicate instrument readings that were made on the sample, or on each subsample replicate, that is entered into column (11) of the data entry screen.

Note: Each standard individual instrument reading may consist of more than one standard sub-reading such as occurs with standard additions "at the instrument" or as an expedient (when the sub-readings are averaged) to help normalize the output of the instrument while reducing the variation thereof. Only replicate instrument readings are being dealt with here, not sub-readings. Refer to column (11) in the data entry section for an explanation of the number of replicate instrument readings that have been made on each sample or subsample replicate being run. Also see the first note for step (6).

10) The result from step (9) is added to mock variance-4 from step (7), giving mock variance-5.

Note: Thus, the variance of the instrument is either put back into the overall variance for the sample the way it was or, as modified by steps (8), (9) and (10).

11) Mock variance-5 is then divided by "n," the number of subsample replicates done on the sample, for the current analytical run, as entered into column (5), provided "n" is a positive whole number greater than or equal to "1," giving mock variance-6.

12) If the number of reagent blanks entered into column (9) that were being run for the block of samples or subsample replicates in the current analytical run is not "zero," the variance for the parent random variable of the reagent blanks from step (5), is divided by the number of reagent blanks that are entered into column (9). Call this result the "blank variance correction term" (BVCT). If the value entered into column (9) is "zero," then the value of "zero" is assigned to the BVCT.

Note: The same note as for step (5) applies to this step.

13) The BVCT, determined in step (12), is added to mock variance-6 giving mock variance-7.

14) If the number of calibration slopes (zero, one or two) entered into column (10) that were run for the block of samples or subsample replicates in the current analytical run is not "zero," the variance for the parent random variable of the slopes from step (6), is divided by the number of slopes (one or two) that are entered into column (10). This result is then multiplied by the square of mock measurement-2. This, in turn, is divided by the square of the mean or grand mean of the slopes as determined under standard processing conditions. Call this result the "slope variance correction term" (SVCT). If the value entered into column (10) is "zero," then the value of "zero" is assigned to the SVCT.

Note: The same notes as for step (6) apply to this step.

Note: In a titrimetric analytical method, the titer (Day & Underwood 1967) is equivalent to the value of the slope but it usually has no significant variance, so a "zero" should be entered into column (10) or else the standard deviation of the titer would have to be determined and entered into the DPSP and a "1" entered into column (10).

15) The SVCT, determined in step (14), is added to mock variance-7 giving mock variance-8.

16) Mock variance-8 is then converted to a standard deviation by taking the square root of it.

17) The result from step (16) is then multiplied by the "f" factor entered in column (8) and this result is further multiplied by the front-end overall superimposed dilution/concentration factor from column (6). This last result will then be the computed standard deviation at M-level for the original single or average (if more than one subsample replicate was done) measurement for the sample that was entered into column (4).

Note: It would be prudent to remember at this point, the two basic assumptions that underlie this algorithm in its present form, which are that (1) any unbiasing that needs to be done will be done by the DBMS in the main database with the parameters that are supplied to it, and that (2) the percent recoveries that have been entered into the DPSP, being averages based on a minimum of four (and where possible, sixteen) recovery samples that have been run, one per run, over the required number of analytical runs, means that the random variation in these average percent recoveries can usually be ignored. If, in defiance of the first assumption, the unbiasing is to be optionally done within the DPSP, then the algorithm would have to be modified at this point to allow for it. But these two basic assumptions will be maintained for the purpose of the algorithm as it is being presented here, on the basis that a bias-error tolerance of approximately plus or minus 1.00% would likely be acceptable to the user. However, in defiance of the second assumption, it might be desirable to have the DBMS further adjust the unbiased standard deviation that was computed by it from the (possibly biased) standard deviation that was obtained from step (17) so that a further corrected version could be applied to determine the unbiased 95% confidence interval for the unbiased single or average measurement in such manner that would take into account the random variation in the average percent recovery. This would require that an additional parameter, the standard deviation of the average percent recovery, also called the standard error of the percent recovery, be entered as a predefined program variable in the DPSP and stored in the temporary database in the DPSP to be uploaded along with the other two parameters that were determined by the algorithm for the particular sample. This would only be done in the event that the standard error of the percent recovery is unusually high and/or the degree of bias-error tolerance in the unbiased measurement is unacceptable. [The standard error of the percent recovery, as obtainable from either the RC-form or the RS-form, is not independent from the standard deviation of the measurement as

calculated on these same forms, but, nevertheless, it should be suitable for the purpose of correcting the overall standard deviation of the single or average measurement. The standard error of the percent recovery will be independent if the data set obtained by running the recovery samples over several analytical runs is used to calculate the standard error independently from all other calculations.] This further adjustment of the unbiased standard deviation for the unbiased single or average measurement of the sample would then be done by the DBMS according to the final term that is given below in the general equation for the overall variance of a single or average determination (including the dividing by the square of the percent recovery in decimal form).

To summarize, adhering to the above two assumptions, the DBMS will calculate the (possibly biased) 95% confidence interval for the (possibly biased) single or average measurement for the sample as plus or minus two of the standard deviations that were determined in step (17). This (possibly biased) 95% confidence interval and (possibly biased) measurement data are to be maintained (not deleted) in separate columns in the main database (necessary for a variety of reasons) despite the unbiasing operation which is to be done next. The DBMS will then unbias the (possibly biased) single or average measurement for the sample and the (possibly biased) standard deviation that was obtained from step (17) by dividing both of them by the uploaded percent recovery for the measurement level in decimal form (this uploaded percent recovery value can be equal to 100% depending on the analytical method). The resulting unbiased single or average measurement and unbiased standard deviation are then stored in separate and hidden password-protected columns. The DBMS will then calculate the unbiased 95% confidence interval for the unbiased single or average measurement as plus or minus two of the unbiased standard deviations. The resulting unbiased 95% confidence interval will then be stored in a separate and hidden password-protected column in the main database. This unbiasing operation assumes, as already stated, that the uploaded percent recovery is regarded as being a statistical constant. If, in defiance of the second assumption above, the standard error of the percent recovery has also been uploaded, then the DBMS will further adjust the unbiased standard deviation so that a corrected version of it can be applied to determine a corrected version of the unbiased 95% confidence interval. The unbiased standard deviation will then be corrected according to the final term that is given below in the general equation for the overall variance of a single or average determination (including the dividing by the square of the percent recovery in decimal form) so as to take into account the random variation in the standard error of the percent recovery. The resulting corrected unbiased standard deviation will then be stored in a separate and hidden password-protected column. The DBMS will then alternatively calculate the corrected unbiased 95% confidence interval for the unbiased single or average measurement that was calculated above as plus or minus two of the corrected unbiased standard deviations. The resulting corrected unbiased 95% confidence interval will then be stored in a separate and hidden password-protected column in the main database. As previously stated, all of the above unbiasing operations can be done within the DPSP if required.

18) The percent recovery value from step (3) and the computed standard deviation at M-level from step (17) are then output in the output screen to the user along with the original single or average (if more than one subsample replicate was done) measurement at M-level that was entered into column (4) and these values are stored (along with the sample identifier and other relevant data) in a temporary database in the DPSP for uploading into the main database when accessed by the DBMS--unless step (19) applies.

19) If the data processing that has just been done to determine the standard deviation and percent recovery for the original single or average (if more than one subsample replicate was done) measurement that was entered into column (4) applies to transformed biological, microbiological or radiological data, then a 95% confidence interval is calculated for the single or average measurement by the DPSP. The end points for this 95% confidence interval are then retransformed and output in the output screen to the user along with the original single or average (if more than one subsample

replicate was done) measurement that was entered into column (4) and these values are stored (along with the sample identifier and other relevant data) in a temporary database in the DPSP for uploading into the main database when accessed by the DBMS. The percent recovery determined by the DPSP would normally always be set to 100% in this case or else this parameter is omitted altogether. The transformational and retransformational formulas would normally be entered into the DPSP by the user.

The following are examples of experiments, thinking in terms of an internal computer table:

Explanation of Computer Table Experiment 1:

1) Suppose the DPSP is using an internal computer table instead of simple formulas.

2) Suppose for purposes of checking the algorithm that the coefficient of relative standard deviation (crsd) is constant throughout the measurement spectrum.

3) Create two computer tables, one for 10g sample and one for 5g sample.

10g "c" factor = 0.1					5g "c" factor = 0.2				
M-level Meas. PPM	M-level S.D. PPM	Q2-level µg-output	Q2-level S.D. µg	Q2-level %Rec	M-level Meas. PPM	M-level S.D. PPM	Q2-level µg-output	Q2-level S.D. µg	Q2-level %Rec
100	5.0	1000	50	99	100	5.0	500	25	98
50	2.5	500	25	98	50	2.5	250	12.5	97
25	1.25	250	12.5	97	25	1.25	125	6.3	96

4) The same µg-output at the back-end of the anal. chem. method should give the same S.D. at Q2-level. The output and S.D. at Q2-level is given in "µg" instead of PPM for simplification. Therefore the "c" factors are purely hypothetical but they are in the correct proportion for 5g and 10g in the denominator of the calculations formula.

5) There is only one computer table available and it is for 10g of sample but there is only 5g of sample available to be run.

6) The overall measurement at M-level is 100 PPM for 5g of sample.

7) The "f" factor for 5g of sample, when 10g of sample is standard, is 2.0.

8) If the overall measurement at M-level (100 PPM) is divided by the "f" factor, a mock measurement of 50 PPM is obtained.

9) The table for 10g is accessed at 50 PPM, and a S.D. of 2.5 PPM is obtained. This is the correct S.D. at M-level for 500 µg of output at Q2-level in the 10g table. The percent recovery of 98% is also obtained at this time. If any adjustments need to be made to the S.D., they are done here at 2.5 PPM. It is assumed that none are needed.

10) The standard deviation (2.5 PPM) obtained in step (9) is multiplied by the "f" factor giving a value of 5.0 PPM.

11) By inspection of the hypothetical 5g table, this is the correct S.D. for the 5g sample at M-level for 500 µg of output at Q2-level in the 5g table.

12) By inspection of the hypothetical 5g table, the percent recovery is also correct since, although the measurement is divided by the "f" factor before accessing the computer table in step (9), the percent recovery obtained is not multiplied by the "f" factor.

Explanation of Computer Table Experiment 2:

1) Suppose the DPSP is using an internal computer table instead of simple formulas.

2) Suppose for purposes of checking the algorithm that the standard deviation (S.D.) is constant at Q2-level throughout the measurement spectrum.

3) Create two computer tables, one for 10g sample and one for 5g sample.

10g
"c" factor = 0.1

M-level Meas. PPM	M-level S.D. PPM	Q2-level µg-output	Q2-level S.D. µg	Q2-level %Rec
100	2.5	1000	25	99
50	2.5	500	25	98
25	2.5	250	25	97

5g
"c" factor = 0.2

M-level Meas. PPM	M-level S.D. PPM	Q2-level µg-output	Q2-level S.D. µg	Q2-level %Rec
100	5.0	500	25	98
50	5.0	250	25	97
25	5.0	125	25	96

4) The same µg-output at the back-end of the anal. chem. method should give the same S.D. at Q2-level. The output and S.D. at Q2-level is given in "µg" instead of PPM for simplification. Therefore the "c" factors are purely hypothetical but they are in the correct proportion for 5g and 10g in the denominator of the calculations formula.

5) There is only one computer table available and it is for 10g of sample but there is only 5g of sample available to be run.

6) The overall measurement at M-level is 100 PPM for 5g of sample.

7) The "f" factor for 5g of sample, when 10g of sample is standard, is 2.0.

8) If the overall measurement at M-level (100 PPM) is divided by the "f" factor, a mock measurement of 50 PPM is obtained.

9) The table for 10g is accessed at 50 PPM, and a S.D. of 2.5 PPM is obtained. This is the correct S.D. at M-level for 500 µg of output at Q2-level in the 10g table. The percent recovery of 98% is also obtained at this time. If any adjustments need to be made to the S.D., they are done here at 2.5 PPM. It is assumed that none are needed.

10) The standard deviation (2.5 PPM) obtained in step (9) is multiplied by the "f" factor giving a value of 5.0 PPM.

11) By inspection of the hypothetical 5g table, this is the correct S.D. for the 5g sample at M-level for 500 µg of output at Q2-level in the 5g table.

12) By inspection of the hypothetical 5g table, the percent recovery is also correct since, although the measurement is divided by the "f" factor before accessing the computer table in step (9), the percent recovery obtained is not multiplied by the "f" factor.

Conclusion of experiments 1 and 2:

The correct standard deviation and percent recovery are obtained in both experiments. If any adjustments had been made, they would have been made in approximately the correct proportions for the final overall standard deviations. The only error remaining will be due to the uncertainty in the standard deviations themselves in the computer table. These two experiments only deal with the "f" factor but, for example, the "f" factor could have been replaced with the "f" factor times the front-end overall superimposed dilution/concentration factor.

Some Statistical Formulas:

1) Sample variance of "x"

$$S^2_X = \frac{\Sigma_i (x_i - \bar{x})^2}{k - 1} \qquad \text{(Formula-1)}$$

"k" is the number of analytical runs.
This sample variance has "k - 1" degrees of freedom.

2) (S_X), the sample standard deviation, is equal to the square root of (S^2_X), above.
This sample standard deviation has "k - 1" degrees of freedom.

3) Sample variance of "x"

$$S^2_X = \frac{\Sigma_i (d_i^2)}{2k} \qquad \text{(Formula-2)}$$

"d" is equal to ($x_1 - x_2$), the signed difference between the duplicate measurements.
"k" is the number of sample duplicates.
This sample variance has "k" degrees of freedom.

4) (S_X), the sample standard deviation, is equal to the square root of (S^2_X), above.
This sample standard deviation has "k" degrees of freedom.

5) Sample pseudo-variance of "|d|"

$$S^2|d| = \frac{\Sigma_i (|d_i|^2)}{k} \qquad \text{(Formula-3)}$$

"|d|" is equal to $|x_1 - x_2|$, the absolute value of the difference between the duplicate measurements (also called the range of duplicates).
"k" is the number of sample duplicates.
This sample pseudo-variance has "k" degrees of freedom.

6) $(S|d|)$, the sample pseudo-standard deviation is equal to the square root of $(S^2|d|)$.
This sample pseudo-standard deviation has "k" degrees of freedom.

Notes regarding the statistical formulas and statistical sampling:

(1) Both Formula-1 and Formula-2 can be utilized under either BAV or WAV statistical sampling conditions depending on the application.

(2) Formula-2 is easy to derive. Just let "d/2" = $(x_i - \bar{x})$ in Formula-1 but with (n - 1) in the denominator instead of (k - 1). The sign of "d/2," of course, doesn't matter due to squaring. This yields the intermediate formula "$(d^2)/2$" divided by (n - 1) which is the formula for determining the sample variance of "x" from two outcomes from a non-composite primary random variable "X" in terms of the "difference" between the two outcomes. "n" is always equal to "2," so the denominator is usually omitted, but it will be needed here. Plug this intermediate formula into the general formula for the pooled variance (Dixon & Massey 1957, p. 109) using (n - 1) as the degrees of freedom in the denominators of the variances to be pooled, substituting "$(d^2)/2$" divided by (n - 1) for each of the "k" variances in the numerator of the general pooled variance formula. In the denominator of the general pooled variance formula, we have "k" times (n - 1) which is equal to "k." By using a summation identity, "2/4 = 1/2" is factored entirely out of the numerator of the general pooled variance formula and placed to the left of the summation sign. This is then taken this out of the numerator of the general pooled variance formula altogether by putting a "2" in the denominator. This yields Formula-2 which is sometimes called the "pooled variance formula for duplicates." It is an unbiased estimator of the population variance of "X" since it has been the unbiased form of the general pooled variance formula that has been used to derive it. But it must be remembered that the sample variance is not for "d" but for "x" and the number of degrees of freedom for it is not "2k" but "k." Because of its ease of programming into the computer spreadsheets, Formula-2 is used to determine the WAV-variances and the WAV-standard deviations in all of the "duplicates" PAF-forms.

(3) Another strategy, used by Pearson and Hartley, to determine the probabilities for the range at "n = 2," from the standard normal probability table is a little more difficult to describe without a diagram but it can be shown that these probabilities can be obtained from the right-hand side of the standard normal probability table (Pearson & Hartley 1942). Basically, by taking the absolute values of the distribution of $(x_1 - x_2)$ which is composed of equal frequencies of both positive and negative values, we get the distribution of $|x_1 - x_2|$ which is composed of only positive values. The frequencies of the positive values are doubled but this doesn't adversely affect the probabilities. The variance of $(x_1 - x_2)$ is double the variance of "x" so the variance of "x," as defined in Formula-2, is multiplied by "2," cancelling off the "2" in the denominator. This is the real variance of $(x_1 - x_2)$ but not of $|x_1 - x_2|$ so it is called a pseudo-variance for the distribution of $|x_1 - x_2|$ and the square root of it is called a pseudo-standard deviation for the distribution of $|x_1 - x_2|$. Thus, the standard normal probability table can still be used

to determine the probabilities for the distribution of $|x_1 - x_2|$. For example, 95% of outcomes from the distribution of $(x_1 - x_2)$ will be between -2 and +2 standard deviations for $(x_1 - x_2)$ and 95% of outcomes from the distribution of $|x_1 - x_2|$ will be between "zero" and +2 pseudo-standard deviations for $|x_1 - x_2|$. The pseudo-variance of $|x_1 - x_2|$ is shown above as Formula-3. The respective pseudo-standard deviation of $|x_1 - x_2|$ is used to determine the control limits for the range charts in all of the "duplicates" PAF-forms.

(4) Another strategy adapted by the author is called "chain-link-sampling." To explain this, imagine three identical series of outcomes, labelled S1, S2 and S3, directly on top of one another, from the same non-composite primary random variable "X," the population mean of which can be premised to be absolutely constant. The members of each series, S1, S2 and S3, are labelled by subscripting "x" as a, b, c, d, e, f, g, and so on, say for about 500 outcomes. Then referring to each of the outcomes by their subscripts, S1 and S2 will first be sampled according to the traditional sampling method: S1: a_b, c_d, e_f, and so on; S2: b_c, d_e, f_g, and so on. Then the samples for S1 could be used to calculate a sample mean from the sets of pairs, averaging each pair and then averaging the individual averages and likewise for S2. Then the two overall means could be averaged giving a grand mean. Then, applying "chain-link-sampling" to S3, the sampling would be: S3: a_b, b_c, c_d, d_e, e_f, f_g, and so on. The overall mean calculated from the sets of pairs from S3, averaging each pair and then averaging the individual averages, will obviously be equal to the grand mean calculated from S1 and S2. This is not "overlapped sampling." There is no overlapping of any of the means in each of the pairs from S3. Nor is it related in any way to any form of "re-sampling."

The same principle can be applied to sampling for the variance and standard deviation using Formula-2. In this case, the "difference between duplicates" is obtained from each pair and applied to Formula-2 to calculate a variance. Then the variances obtained from S1 and S2 could be pooled. It can be shown that the variances from S1 and S2 are not entirely independent. In fact, in the extreme hypothetical case, they are inversely correlated. But this is an advantage. If the variance from S1 is too small than the variance from S2 will be too big. But when the two variances are pooled, a better estimate is obtained with double the degrees of freedom. Of course, with random sampling, the two variances will be similar anyway. Research, using the random generation capability of the computer spreadsheet to generate random normal variates, confirms these statements. Then it can be shown that the variance obtained by applying the "difference between duplicates" obtained from S3 to Formula-2 will give the exact same variance as the former pooled variance from S1 and S2. The same justification applies to both the WAV-variances and the WAV-standard deviations determined on the "duplicates" PAF-forms. This is not "overlapped sampling" nor any form of "re-sampling." There is no overlapping of any of the deviations inherent in each of the differences obtained from each of the pairs from S3. Note that ANOVA cannot be done using the "chain-link-sampled" pairs from S3.

(5) "Chain-link-sampling" is considered to be absolutely essential for this computerized system. The time and cost of obtaining the required number of degrees of freedom for the standard deviations from some of the "duplicates" PAF-forms is quite high having to use stratified sampling according to measurement level and having to obtain the various duplicates at "random" measurement levels, since the concentrations of analyte in the regular material samples are unknown before analysis. "Chain-link-sampling" cuts this time and cost in half. In practice, any number of subsample replicates can be run on any material sample homogenate by labelling their respective flasks as: a, b, c, d, e, f, g, and so on. A rule is made to subtract "b" from "a", "c" from "b", "d" from "c", "e" from "d", "f" from "e", "g" from "f", and so on. Six pairs of "differences between duplicates" are obtained if "chain-link-sampling" is used, whereas a maximum of only three is available by using the regular sampling. Over and above this stated advantage, additional PAF-forms would otherwise have to be created for triplicates, quadruplicates, quintuplicates, and so on when running this many subsample replicates. This would be an enormous task in itself and would make the computerized system so much more

confusing and awkward and irksome to use. "Chain-link-sampling" can only be used with the SAM-DUP, RB-DUP, RS-DUP, COUNT-DUP (on transformed data), CAL-DUP and STAN-DUP forms. One big precaution: ANOVA cannot be done using "chain-link-sampled" duplicates.

General Equation for the Overall Variance of a Single or Average Determination:

The general equation for the overall variance of a single or average unbiased measurement of the concentration of a single ingredient in a single sample homogenate in PPM² at M-level (each term is to be referenced in serial order from top to bottom) is given by:

$(FE)^2 * (f)^2 * 1/E(u\text{-}bar)^2 [c^2/E(m)^2 \{ Var$ (total of all chemical processing stages)
+ Var (of any "included in measurement" VSAM in the material sample homogenate)
+ (Var (IRV + IBV) of a single instrument reading $* (BE)^2) /Nr \} /Nd$

$+ c^2/E(m)^2 \{ Var (rb) /Nrb \}$

$+ 1/E(m)^2 \{ (Var (m) /Nm) * E(BMAC)^2 \}]$

$+ 1/E(u\text{-}bar)^2 \{ Var (u\text{-}bar) * E(UMAC)^2 \}$

For the single or average measurement obtained for a particular material sample at a particular measurement level in a single analytical run of a particular analytical chemistry method (equal sample weights or volumes), the measurement being calculated in PPM at M-level as:

(FE * f * c)/u-bar { X or X-bar } = (FE * f * c)/u-bar { see term*--next line below }
{ BE/(m or m-bar) * [(Y or Y-bar) - (rb or rb-bar)] }*

(X or X-bar) is the concentration obtained from the calibration graph in PPM (µg/ml) at Q2-level. (Y or Y-bar) is the instrument reading in AU, XAU, or AREA for the sample at Q1-level.

"Var" is the variance operator.
"E" is the expectation operator.
"u-bar" is the average percent recovery (decimal equivalent) at the particular measurement level.
"c" is the "c" factor for the standard calculations formula (must be a statistical constant).
"f" is the "f" factor for the standard/non-standard--sample weight or volume ratio.
"m and m-bar" are the single/average slope of the calibration line (regression line).
"rb and rb-bar" are the single/average reading of one or more reagent blanks.
"Nrb" is the number of (averaged) reagent blanks being run.
"Nm" is the number of (averaged) slopes (one or two) for a block of samples in the run.
"Nr" is the number of (averaged) instrument readings on the sample extract for each single or replicate determination.
"Nd" is the number of (averaged) replicate determinations done on the particular sample homogenate.

"FE" is the front-end overall superimposed dilution/concentration factor.
"BE" is the back-end overall superimposed dilution/concentration factor.

"VSAM" is the measured (as opposed to actual) residual variation of the concentration of the ingredient (analyte) in the single material sample homogenate.

"BMAC" is the possibly biased measurement at M-level in PPM (µg/g or µg/ml) of the actual concentration of the ingredient (analyte) in the single material sample homogenate as determined by the particular analytical chemistry method.

"UMAC" is the unbiased (having been unbiased--the verb) measurement at M-level (µg/g or µg/ml) of the actual concentration of the ingredient (analyte) in the single material sample homogenate and closest practicable approximation to the actual concentration.

Description of Parameter Acquisition Forms

Important Note: If multiple (averaged) instrument sub-readings are a part of standard processing conditions (that is, they are done on each regular or control sample extract, each replicate subsample extract, and each calibration standard), then these same multiple sub-readings must be done when determining the various standard deviations on all of the various PAF-forms, including the standard deviation of the instrument as it is being determined on the STAN-DUP, CAL-DUP or CAL-DATA forms. In the latter case though, the standard deviation of the instrument could alternatively be determined as the parent random variable of the instrument (that is, considering each individual non-composite reading to be a single outcome from the instrument) and then the variance thereof (obtained from multiple consecutive individual non-composite instrument readings using a single sample extract or standard solution) can be adjusted so as to comply with the number of multiple sub-readings which are standard. Only the respective standard deviation determined from that variance so adjusted can be entered as an alternative predefined program variable into the DPSP once it is converted to PPM at M-level by multiplying by the standard "c" factor for the specific analytical chemistry method. On the other hand, the standard deviation of "y" given "x" (also the standard deviation of the instrument response variable) determined from each run on the calibration standards, would normally be calculated from the standard number of instrument sub-readings already having been made on each calibration standard so that it would not normally need to be adjusted before entering it as a predefined program variable into the DPSP, it having been converted to PPM at M-level by multiplying by the standard "c" factor for the specific analytical chemistry method.

RC-form: Recovery Constant Form. Note: A separate form is required for each measurement level. This PAF-form makes use of a control sample called a recovery constant (RC) which is a recovery sample prepared from accurately weighed-out, and reproducibly equal, mg-amounts of primary standard chemical, from analytical run to analytical run, so that the exact same concentration of primary standard chemical is applied to each analytical run. The actual lot analysis or purity of the primary standard chemical to three significant figures must be taken into account when determining the concentration of the RC. Only one such control sample is allowed per analytical run and the measurement thereof must be obtained under the standard processing conditions specified in the analytical chemistry method and calculated in terms of PPM at Q2-level according to the traditional calculation procedure. For example, it must be decided before beginning to run this control sample what constitutes standard conditions, whether one or two runs are to be done on the reagent blanks and likewise for the calibration slopes, even though temporarily, a different number of reagent blanks and slopes might be being run. A standard deviation and average percent recovery for the desired measurement level are then obtained over several analytical runs, usually, sixteen, in order to obtain fifteen degrees of freedom for the standard deviation and an average percent recovery at statistical sample size "n" = 16. Formula-1 is used to calculate a BAV-standard deviation in PPM at Q2-level (BAV-Sampling) and then is converted to PPM at M-level by multiplying by the standard "c" factor. The percent recovery need only be determined at Q2-level (in the same way as on the RS-form). Note that this BAV-standard deviation will contain the correct proportion of WRME (from all chemical processing stages), all forms of between-run systematic error (BRSE), including any between-run systematic measurement error, BRSME (RBV and/or SRLV),

being generated by the WRME (RBV and/or SRLV) of the reagent blank(s) or slopes(s) that are being run under standard conditions, and any IRV or IBV. This kind of sampling does not capture VSAM (since there is no material sample substrate present to contain any), but in most cases this shouldn't matter since regular samples for routine chemical analysis are usually well homogenized (this may not be true of some SRM samples and some particular kinds of regular samples). Because the standard deviation and the percent recovery are re-calculated with each new analytical run, the RC-form and the RC control sample may be continued to be run as a regular quality control sample. An X-chart in terms of PPM, outlier test and pop-up histogram are available on the form.

RS-form: Recovery Sample Form. Note: A separate form is required for each measurement level. This PAF-form makes use of a control sample called a recovery sample (RS) which is a recovery sample prepared from nominally equal mg-amounts of primary standard chemical for each analytical run. The actual lot analysis or purity of the primary standard chemical to three significant figures must be taken into account when determining the concentration of the RS. As for every recovery sample, including the RC and the RS, a targeted theoretical concentration level must be taken into account when determining the mg-amount of primary standard chemical to be weighed out for the analytical run. But the mg-amount of primary standard chemical that is actually weighed out must be as close as possible to that required to target the theoretical concentration level for the form. The measurement obtained for the single recovery sample in PPM at Q2-level is then divided by the theoretical concentration level calculated for it at that point for the particular analytical run and multiplied by 100 to obtain the percent recovery. [Note: The targeted theoretical concentration level for the form must always be held constant but not necessarily that for the analytical run. The targeted theoretical concentration level for the form is used to convert the standard deviation in terms of percent recovery back to PPM.] Only one such control sample is allowed per analytical run and the measurement thereof must be obtained under the standard processing conditions specified in the analytical chemistry method and calculated at Q2-level according to the traditional calculation procedure. Otherwise, all the comments made above for the RC-form apply to the RS-form with the following exceptions: Formula-1 is used to calculate a BAV-standard deviation at Q2-level (BAV-Sampling) first in terms of percent recovery and then is converted to PPM at Q2-level by multiplying by the targeted concentration level for the form and dividing by 100. From there, it is further converted to PPM at M-level by multiplying by the standard "c" factor. Note that this converted BAV-standard deviation will contain the correct proportion of WRME (from all chemical processing stages), all forms of between-run systematic error (BRSE), including any between-run systematic measurement error, BRSME (RBV and/or SRLV), being generated by the WRME (RBV and/or SRLV) of the reagent blank(s) or slopes(s) that are being run under standard conditions, and any IRV or IBV but does not capture VSAM. Because the standard deviation and the percent recovery are re-calculated with each new analytical run, the RS-form and the RS control sample may be continued to be run as a regular quality control sample. It must be made clear in the documented analytical chemistry method that the mg-amount of primary standard chemical that is to be actually weighed out for the single recovery sample must be as close as possible to that required to target the theoretical concentration for the form. An X-chart in terms of percent recovery, outlier test and pop-up histogram are available on the form.

Note concerning the RC and RS control samples: A regular sample has a material sample substrate to go with it from the very beginning of the analytical procedure but this is usually separated away from the analyte portion in the first few stages of the chemical processing. This is especially true in inorganic chemistry where dry-ashing or wet digestion of the regular samples with powerful concentrated acids completely destroy all organic residues. That is why an RC control sample or RS control sample can often be used as a premeasurement-equivalent substitute for a material-based control sample for the purpose of determining a standard deviation at a particular measurement level for an analytical chemistry method. Where possible, an RC or RS control sample should be run

as a preferred choice because they both capture all forms of between-run systematic error (BRSE), including any between-run systematic measurement error, BRSME (RBV and/or SRLV) being generated by the WRME (RBV and/or SRLV), so that they are the true statistical estimators of the true population standard deviations for the measurement levels of the particular analytical chemistry method, containing all the relevant sources of stochastic variation that accrue from doing the particular analysis, over and over again, in the same laboratory.

Note: Formula-1, Formula-2 and Formula-3 are defined near the end of the Theory Section. The definitions of these formulas are given in their variance forms, it being obvious that their square roots will give their corresponding standard deviations. Thus, these formulas are referenced in this paper in such manner so as to include both possibilities. Also see the general equation for the overall variance of a single or average determination at the end of the Theory Section.

SAM-DUP form: PAF-form for sample duplicates, the measurements of which are obtained from the regular chemical analysis of routine samples under the standard processing conditions specified in the analytical chemistry method and calculated in terms of PPM at M-level according to the traditional calculation procedure. The traditional calculation procedure will involve using one reagent blank (or the average of two or more reagent blanks), if any is being run, and one slope (or the average of two slopes); whatever combination is required and specified as standard processing conditions in the analytical chemistry method. Only nominally equal sample weights or volumes are required for the sample duplicates but note that only standard sample weights or volumes are allowed for this form. The sample duplicates are labelled A and B and according to the unique sample identifier required for each sample. Chain-link-sampling (as explained near the end of the Theory Section) can be used to acquire the duplicates (at M-level) for this form. There can be more than one set of duplicates entered into the form per analytical run. To rule out any form of non-random systematic error occurring between the two measurements, it is recommended that the sample duplicates be run serially adjacent to each other.

Utilizing the difference between the measurements obtained for A and B over several analytical runs (WAV-Sampling), Formula-2 is used to calculate a WAV-standard deviation in PPM at M-level. It will contain the correct proportion of VSAM, WRME (from all chemical processing stages), IRV and IBV. It does not capture any form of between-run systematic error (BRSE) or any of the between-run systematic measurement error, BRSME (RBV and/or SRLV), being generated by the WRME (RBV and/or SRLV) of the reagent blank(s) and/or slopes(s) that are being run under standard conditions. At some point, the measurements for the sample duplicates obtained over several analytical runs must be stratified to, as narrowly defined as possible, low, medium and high, measurement levels so that the WAV-standard deviations determined for these strata can be entered, after any needed correction, into the DPSP as predefined program variables. The system administrator, laboratory supervisor or analytical chemistry method developer would be the one making the choices concerning the strata. This WAV-standard deviation would need correction by having added to it the appropriate terms for the variation being generated by the WRME (RBV and/or SRLV) of the reagent blank(s) and/or slopes(s) that are being run under standard conditions, before it can be used as a predefined program variable in the DPSP. A range-chart, outlier test and pop-up histogram are available on the form. This form, along with the RB-DUP form if one or more reagent blanks are being run, and the CAL-DUP form, are the main PAF-forms used for determining the standard deviations of the analytical chemistry methods, when an RC or RS control sample cannot be run (see note concerning the RC and RS control samples).

RB-DUP form: PAF-form for duplicate reagent blanks, the measurements of which are obtained during the regular chemical analysis of routine samples under the standard processing conditions specified in the analytical chemistry method. The reagent blanks

are labelled RB-A and RB-B. The individual measurements for the duplicate reagent blanks are obtained at Q1-level and converted to Q2-level, in terms of PPM, by dividing each by the slope of a single calibration line (or the average of two calibration lines) according to the traditional calculation procedure, but note that they are not being averaged either before or after bringing them through the calibration graph. Here, they are being treated more like sample duplicates or duplicate recovery constants. Stratification, such as is required on the SAM-DUP form, is not required on this form since the reagent blanks are being run at a low and narrow measurement range. Chain-link-sampling (as explained near the end of the Theory Section) can be used to acquire the duplicates (at Q2-level) for this form. There can be more than one set of duplicates entered into the form per analytical run. To rule out any form of non-random systematic error occurring between the two measurements, it is recommended that the duplicate reagent blanks be run serially adjacent to each other.

Utilizing the difference between the measurements obtained for RB-A and RB-B over several analytical runs (WAV-Sampling), Formula-2 is used to calculate a WAV-standard deviation in PPM at Q2-level. This WAV-standard deviation will contain the correct proportion of WRME (from all chemical processing stages), IRV and IBV, and there is no VSAM to be captured. It does not capture any form of between-run systematic error (BRSE) or any of the between-run systematic measurement error, BRSME (SRLV), being generated by the WRME (SRLV) of the slopes(s) that are being run under standard conditions. This WAV-standard deviation of the submeasurement random variable of the reagent blank in terms of PPM at Q2-level is then converted to PPM at M-level by multiplying by the standard "c" factor for the specific analytical chemistry method. A range-chart, outlier test and pop-up histogram are available on the form.

COUNT-DUP form: PAF-form that uses Formula-2 to calculate a WAV-standard deviation in terms of transformed data for regular count sample duplicates or duplicate count blanks. This is a specialised form tailored to the needs of biologists, microbiologists or radiologists who are working with Binomial-distributed or Poisson-distributed data. It requires transformation of such data to normally distributed data before any calculations are done on the form. Otherwise, it is similar to the SAM-DUP form if used for regular samples or the RB-DUP form if used for count blanks. Unlike the previous forms, the standard deviations so calculated are further utilized to compute the actual 95% confidence intervals for the measurement level assigned to the form, first in terms of transformed data, then the end points of the computed interval are retransformed and entered into the DPSP for eventual uploading into the main database by the DBMS. Chain-link-sampling (as explained near the end of the Theory Section) can be used to acquire the duplicates (in terms of transformed data) for this form. There can be more than one set of duplicates entered into the form per analytical run. To rule out any form of non-random discrepancy occurring between the two measurements, it is recommended that the count sample duplicates or duplicate count blanks be run in such manner so as to make cross-contamination from any of the regular or control samples being run (including the duplicate control sample) virtually impossible. The user is responsible to enter into the form, the transformational and retransformational formulae. A range-chart, outlier test and pop-up histogram are available on the form in terms of the transformed data.

RS-DUP form: PAF-form for running duplicate recovery samples (RS's). Note: A separate form is required for each measurement level. The duplicate recovery samples (RS's) are prepared from nominally equal mg-amounts of primary standard chemical for each analytical run. The actual lot analysis or purity of the primary standard chemical to three significant figures must be taken into account when determining the concentration of the RS. As for every recovery sample, including the RC and the RS, a targeted theoretical concentration level must be taken into account when determining the mg-amount of primary standard chemical to be weighed out for the analytical run. But the mg-amounts of primary standard chemical that are to be actually weighed out for each of the duplicate RS's must be as close as possible to that required to target the theoretical

concentration level for the form. The measurement obtained for each of the recovery samples in PPM at Q2-level is then divided by the respective theoretical concentration levels calculated for each of them for the particular analytical run and multiplied by 100 to obtain the percent recoveries. [Note: The targeted theoretical concentration level for the form must always be held constant but not necessarily that for the analytical run. The targeted theoretical concentration level for the form is used to convert the standard deviation in terms of percent recovery back to PPM.] The traditional calculation procedure will involve using one reagent blank (or the average of two or more reagent blanks), if any is being required to be run, and one slope (or the average of two slopes); whatever combination is required and specified as standard processing conditions in the analytical chemistry method. The recovery samples are labelled RS-A and RS-B. Stratification, such as is required on the SAM-DUP form, is not required on this form since the RS samples must be run at a specifically targeted measurement level. Chain-link-sampling (as explained near the end of the Theory Section) can be used to acquire the duplicates (at Q2-level) for this form. There can be more than one set of duplicates entered into the form (per measurement level) per analytical run. To rule out any form of non-random systematic error occurring between the two measurements, it is recommended that the duplicate recovery samples (RS's) be run serially adjacent to each other. It must be made clear in the documented analytical chemistry method that the mg-amounts of primary standard chemical that are to be actually weighed out for each of the duplicate recovery samples (RS's) must be as close as possible to that required to target the theoretical concentration for the form.

Utilizing the difference between the percent recoveries obtained for RS-A and RS-B over several analytical runs using the traditional calculation procedure (WAV-Sampling), Formula-2 is used to calculate a WAV-standard deviation in terms of percent recovery at Q2-level. This WAV-standard deviation will contain the correct proportion of WRME (from all chemical processing stages), IRV and IBV, and there is no VSAM to be captured. It does not capture any form of between-run systematic error (BRSE) or any of the between-run systematic measurement error, BRSME (RBV and/or SRLV), being generated by the WRME (RBV and/or SRLV) of the reagent blank(s) and/or slopes(s) that are being run under standard conditions. This WAV-standard deviation so determined at Q2-level in terms of percent recovery is then converted to PPM at Q2-level by multiplying by the targeted concentration level for the form and dividing by 100. From there, it is further converted to PPM at M-level by multiplying by the standard "c" factor for the specific analytical chemistry method and applied to the variation inherent in the premeasurement-equivalent of a single determination on a regular sample. This WAV-standard deviation would need correction by having added to it the appropriate terms for the variation being generated by the WRME (RBV and/or SRLV) of the reagent blank(s) and/or slopes(s) that are being run under standard conditions, before it can be used as a predefined program variable in the DPSP. The average percent recovery at Q2-level is determined over several analytical runs by averaging the average percent recoveries for each of the analytical runs. A range-chart in terms of percent recovery, outlier test and pop-up histogram are available on the form.

See note concerning the RC-form and RS-form. The same comments apply here.

RC-DUP-SPECIAL form: Special purpose PAF-form for running duplicate recovery constants, labelled RC-A and RC-B. Note: A separate form is required for each measurement level and only one pair of duplicate recovery constants is allowed to be run on each form per analytical run. This is due to the kind of ANOVA testing being done on the form and for other reasons. The concentrations of these recovery constants must be exactly the same for each analytical run and also must be exactly the same between analytical runs. The actual lot analysis or purity of the primary standard chemical to three significant figures must be taken into account when determining the concentration of the duplicate RC's and the measurements of them must be obtained under the standard processing conditions specified in the analytical chemistry method and calculated in terms of PPM at Q2-level according to both the traditional calculation procedure and a

non-traditional calculation procedure and (unlike most of the other PAF-forms) both of these pairs of calculated measurements must be entered into their respective columns on the spreadsheet form. In order to be able to utilize both of these calculation procedures, two (or more) reagent blanks must be run and two (or more) runs on the calibration standards must be made in order to obtain two calibration slopes. The traditional calculation procedure will involve using one reagent blank (or the average of two or more reagent blanks), if any is required by the method at all, and one slope (or the average of two slopes); whatever combination is normally required and specified as standard processing conditions in the analytical chemistry method. For the non-traditional calculation procedure, the recovery constants will have been labelled RC-A and RC-B, so likewise, two of the reagent blanks must be labelled RB-A and RB-B, and the calibration slopes must be labelled SL-A and SL-B. Then, RB-A is to be subtracted from RC-A, and the result is to be divided by SL-A. Likewise, RB-B is to be subtracted from RC-B, and the result is to be divided by SL-B. Both BAV-sampling and WAV-sampling are used on this form. The average percent recovery is determined individually, over several analytical runs, in terms of percent recovery at Q2-level, for both the RC-A and RC-B series, using the traditional calculation procedure and then the two averages are averaged. The statistical sample size for the percent recovery is double what it would be if just one recovery sample were been run. Stratification, such as is required on the SAM-DUP form, is not required on this form since the RC samples are being run at a specifically targeted measurement level. [Note: Any form of "chain-link-sampling," as explained in the Theory Section, is not allowed to be used to obtain the duplicates for this form.] To rule out any form of non-random systematic error occurring between the two measurements, it is recommended that the duplicate recovery constants be run serially adjacent to each other.

For the sake of simplicity, only the instruction to calculate the measurements for both pairs of duplicate recovery constants at Q2-level before entering them into the form, has been given. But it is also possible to enter the duplicate reagent blanks as on the RB-DUP form and the duplicate slopes as on the CAL-DUP form and their respective standard deviations can then be determined on this same form. The standard "c" factor for the specific analytical chemistry method will have already been entered into the form as a predefined program variable, for this to be accomplished. This form should be programmed to be able to do both, giving the user the choice. But if the user has been using the RB-DUP and CAL-DUP forms already, he should continue to enter the duplicate reagent blank and duplicate slope data into those respective forms so as to continue the process of calculating their respective standard deviations on the same forms. The same reagent blank and slope data must not be entered into both the RC-DUP-SPECIAL form and the other forms (RB-DUP and/or CAL-DUP forms). The variances (and standard deviations) from both forms would then be partly duplicated (overlapped) and not be independent. But if this is not done, then the respective variances from each form could be pooled and then converted to a standard deviation by taking the square root.

(1) Utilizing the measurements obtained for RC-A over several analytical runs using the traditional calculation procedure (BAV-Sampling), Formula-1 is used to calculate a BAV-standard deviation in PPM at Q2-level. This BAV-standard deviation for RC-A will contain the correct proportion of WRME (from all chemical processing stages), IRV and IBV, and between analytical runs, all forms of between-run systematic error (BRSE), including any between-run systematic measurement error, BRSME (RBV and/or SRLV), that is being generated by the WRME (RBV and/or SRLV) of the reagent blank(s) and/or slopes(s) that are being run under standard conditions, and there is no VSAM to be captured. The same thing can be said about the BAV-standard deviation calculated in terms of PPM at Q2-level from the measurements for RC-B over several analytical runs. These two standard deviations (converted to variances) should not be pooled using the general equation for the pooled variance, since the two variance estimates are not entirely independent. However, if only one reagent blank and/or only one slope is being run under standard conditions, a pooled variance may be obtained from paragraph (4). If two or more reagent blanks are being run and/or two or more slopes are being obtained

and neither of these two submeasurement random variables are highly variable, it might be permissible to pool the variances but it cannot be recommended here. The BAV-standard deviations for each of the two premeasurement-equivalent random variables at Q2-level are then converted to PPM at M-level by multiplying by the standard "c" factor for the specific analytical chemistry method. Either of these two BAV-standard deviations for the RC-A series or the RC-B series, having been converted to M-level, can be used as a predefined program variable in the DPSP if their respective data sets do not contain outliers.

(2) Utilizing the measurement means calculated for RC-A and RC-B at Q2-level over several analytical runs using the traditional calculation procedure (BAV-Sampling), Formula-1 is used to calculate a BAV-variance in PPM² at Q2-level. This BAV-variance of the measurement means will contain a one-half portion of WRME (from all chemical processing stages), IRV and IBV, and a full portion of all forms of BRSE, including any between-run systematic measurement error, BRSME (RBV and/or SRLV), that is being generated by the WRME (RBV and/or SRLV) of the reagent blank(s) and/or slopes(s) that are being run under standard conditions, and there is no VSAM to be captured. This BAV-variance so determined at Q2-level is then multiplied by 2, in order to have it apply to the variation inherent in the premeasurement-equivalent of a single determination on a regular sample. The resulting BAV-variance will contain the correct proportion of WRME (from all chemical processing stages), IRV and IBV, but will have a double portion of all forms of BRSE, including any between-run systematic measurement error, BRSME (RBV and/or SRLV), that is being generated by the WRME (RBV and/or SRLV) of the reagent blank(s) and/or slopes(s) that are being run under standard conditions, and there is no VSAM to be captured. This BAV-variance is then converted to a BAV-standard deviation in PPM at Q2-level by taking the square root. It is further converted to PPM at M-level by multiplying by the standard "c" factor. This overall BAV-standard deviation is not recommended to be used as a predefined program variable in the DPSP, even if its respective data set does not contain outliers and the ANOVA testing does not result in any outcome of significance, since it could have an extra portion of all forms of BRSE, including any between-run systematic measurement error, BRSME (RBV and/or SRLV), that might go undetected.

(3) Utilizing the difference between the measurements obtained for RC-A and RC-B over several analytical runs using the traditional calculation procedure (WAV-Sampling), Formula-2 is used to calculate a WAV-standard deviation in PPM at Q2-level. This WAV-standard deviation will contain the correct proportion of WRME (from all chemical processing stages), IRV and IBV, and there is no VSAM to be captured. It does not capture any form of between-run systematic error (BRSE) or any of the between-run systematic measurement error, BRSME (RBV and/or SRLV), being generated by the WRME (RBV and/or SRLV) of the reagent blank(s) and/or slopes(s) that are being run under standard conditions. The exception would be non-random systematic error occurring between the two measurements but this is considered to be ruled out here. The two control samples should be run serially adjacent to each other to reduce the probability of this occurring. This WAV-standard deviation so determined at Q2-level is then multiplied by the standard "c" factor for the specific analytical chemistry method to convert it to PPM at M-level and applied to the variation inherent in the premeasurement-equivalent of a single determination on a regular sample. This WAV-standard deviation would need correction by having added to it the appropriate term for the variation being generated by the WRME (RBV and/or SRLV) of the reagent blank(s) and/or slopes(s) that are being run under standard conditions, before it can be used as a predefined program variable in the DPSP and its respective data set must not contain outliers.

(4) Utilizing the measurements obtained for RC-A over several analytical runs using the non-traditional calculation procedure (BAV-Sampling), Formula-1 is used to calculate a BAV-standard deviation in PPM at Q2-level. This BAV-standard deviation for RC-A will contain a full portion of WRME (from all chemical processing stages), IRV, IBV, and forms

of BRSE other than BRSME (RBV and/or SRLV), and a full portion of WRME (RBV and/or SRLV) for only one reagent blank and/or only one slope being run under otherwise standard conditions, and there is no VSAM to be captured. In this case, no BRSME (RBV and/or SRLV), is being generated by the WRME (RBV and/or SRLV) for the control samples. The same thing can be said about the BAV-standard deviation calculated in terms of PPM at Q2-level from the measurements for RC-B over several analytical runs. These two standard deviations can then be pooled (as their respective variances which are independent) by using the general equation for the pooled variance. The resulting standard deviation will have twice as many degrees of freedom as either one alone and contains the same sources of variation. The BAV-standard deviation of this premeasurement-equivalent random variable at Q2-level is then converted to PPM at M-level by multiplying by the standard "c" factor for the specific analytical chemistry method. These BAV-standard deviations have a restricted use as predefined program variables in the DPSP. Although they are obtained from basically the same kind of statistical sampling used in paragraph (1) for each individual control sample series, the two control samples series have different reagent blanks and slopes (which is why their variances are independent). Consequently, no BRSME (RBV and/or SRLV) is being generated by the WRME (RBV and/or SRLV) and the kind of WRME (RBV and/or SRLV) that is present is only equivalent to one reagent blank and/or one slope being run under otherwise standard conditions. Therefore, they can only be applied (pooled or unpooled) to the traditional calculation procedure under the restricted condition that only one reagent blank and/or only one slope are being run under standard conditions. They may also be used for some forms of significance testing if their respective data sets do not contain outliers.

Basically, the statistical sampling, called "one on one," meaning one premeasurement to one of the submeasurements, will be the same here as in paragraph (1) only if only one reagent blank and/or only one slope are being run. Also, in paragraph (1), if more than one reagent blank and/or more than one slope are being run, the statistical sampling is still "one on one," that is, one premeasurement to one of the average submeasurements. In the case of the non-traditional calculation procedure that is being used in paragraph (4), that will not be the case, as neither of the two submeasurements are being averaged at Q1-level or Q2-level before being applied to the premeasurement-equivalent. Therefore, the kind of WRME (RBV and/or SRLV) that is present is only equivalent to one reagent blank and/or one slope being run under otherwise standard conditions.

(5) Utilizing the measurement means calculated for RC-A and RC-B at Q2-level over several analytical runs using the non-traditional calculation procedure (BAV-Sampling), Formula-1 is used to calculate a BAV-variance in PPM^2 at Q2-level. This BAV-variance of the measurement means will contain a one-half portion of WRME (from all chemical processing stages), IRV, IBV, and a full portion all all forms of BRSE other than BRSME (RBV and/or SRLV), and a one-half portion of WRME (RBV and/or SRLV) for only one reagent blank and/or only one slope that are being run under otherwise standard conditions, and there is no VSAM to be captured. In this case, no BRSME (RBV and/or SRLV), is being generated by the WRME (RBV and/or SRLV). This BAV-variance of the measurement means so determined at Q2-level is then multiplied by 2, in order to have it apply to the variation inherent in the premeasurement-equivalent of a single determination on a regular sample. The resulting BAV-variance will contain the a full portion of WRME (from all chemical processing stages), IRV, IBV, but will have a double portion of all forms of BRSE other than BRSME (RBV and/or SRLV), and a full portion of WRME (RBV and/or SRLV) for only one reagent blank and/or only one slope being run under otherwise standard conditions, and there is no VSAM to be captured. However, it will not contain any BRSME (RBV and/or SRLV) since the WRME (RBV and/or SRLV) isn't generating any due to the fact that a non-traditional calculation procedure is being used. This BAV-variance is then converted to a BAV-standard deviation in PPM at Q2-level by taking the square root. It is further converted to PPM at M-level by multiplying by the standard "c" factor. This overall BAV-standard deviation of the measurement means

cannot be used as a predefined program variable in the DPSP since it cannot be applied to the traditional calculation procedure for which this system is intended, not to mention that it could have an extra portion of all forms of BRSE other than BRSME (RBV and/or SRLV) that might go undetected by the outlier testing and the ANOVA testing. However it might be used for some form of significance testing if its respective data set does not contain outliers.

(6) Utilizing the difference between the measurements obtained for RC-A and RC-B over several analytical runs using the non-traditional calculation procedure (WAV-Sampling), Formula-2 is used to calculate a WAV-standard deviation in PPM at Q2-level. This WAV-standard deviation will contain the correct proportion of WRME (from all chemical processing stages), IRV and IBV, and there is no VSAM to be captured. It does not capture any form of between-run systematic error (BRSE) but it captures the correct proportion of WRME (RBV and/or SRLV) for only one reagent blank and/or only one slope being run under otherwise standard conditions. The exception would be non-random systematic error occurring between the two measurements but this is considered to be ruled out here. The two control samples should be run serially adjacent to each other to reduce the probability of this occurring. The WAV-standard deviation so determined at Q2-level is then multiplied by the standard "c" factor for the specific analytical chemistry method to convert it to PPM at M-level and applied to the variation inherent in the premeasurement-equivalent of a single determination on a regular sample. Unlike the WAV-standard deviation determined in paragraph (3), this WAV-standard deviation would not need correction by having added to it any term for the variation being generated by the WRME (RBV and/or SRLV) before using it as a predefined program variable in the DPSP, provided that the traditional calculation procedure is being used in the respective analytical chemistry method under the restricted condition that only one reagent blank and/or only one slope are being run under standard conditions. This WAV-standard deviation could be useful for significance testing if its respective data set does not contain outliers.

Two X-charts, an X-bar-chart and a range-chart are included for the traditional calculation procedure and two X-charts, an X-bar-chart and a range-chart are included for the non-traditional calculation procedure. An outlier test is included for all and their respective pop-up histograms are available on the form.

One-way ANOVA is done automatically, and cumulatively on the form for both the traditional calculation procedure and the non-traditional calculation procedure with each new analytical run. [Note: ANOVA cannot be done using "chain-link-sampled" duplicates.] Each column in the one-way ANOVA classification table contains the two measurements, RC-A and RC-B, in PPM at M-level for one pair of recovery constant duplicates per analytical run. There are only two rows in the table, one for RC-A (row 1) and one for RC-B (row 2).

The ANOVA done for the traditional calculation procedure is used to detect any significant BRSE in the means of the duplicate recovery constants but note that any BRSME (RBV and/or SRLV) being generated by the WRME (RBV and/or SRLV) of the reagent blank(s) and/or slopes(s) that are being run under standard conditions will be included in those means. The ANOVA for the non-traditional calculation procedure will not contain that (BRSME (RBV and/or SRLV) and so it is better suited to the detection of extreme values in the means that would indicate erroneous measurements.

See note concerning the RC-form and RS-form. The same comments apply here.

SRM-form: Standard Reference Material Form. Note: A separate form is required for each separate SRM sample and only one such SRM sample is allowed to be run on each form per analytical run. The measurement for each SRM control sample must be obtained under the standard processing conditions specified in the analytical chemistry method and calculated at M-level according to the traditional calculation procedure. The traditional calculation procedure will involve using one reagent blank (or the average of

two or more reagent blanks), if any is being run, and one slope (or the average of two slopes); whatever combination is required and specified as standard processing conditions in the analytical chemistry method. The SRM control samples must have nominally equal sample weights or volumes from one analytical run to another. Stratification, such as is required on the SAM-DUP form, is not required on this form since the SRM samples are being run at a specifically targeted measurement level.

Utilizing the measurements obtained for the SRM control sample over several analytical runs using the traditional calculation procedure (BAV-Sampling), Formula-1 is used to calculate a BAV-standard deviation in PPM at M-level. This BAV-standard deviation will contain the correct proportion of VSAM, WRME (from all chemical processing stages), IRV and IBV, and between analytical runs, all forms of between-run systematic error (BRSE), including any between-run systematic measurement error, BRSME (RBV and/or SRLV), that is being generated by the WRME (RBV and/or SRLV) of the reagent blank(s) and/or slopes(s) that are being run under standard conditions. This BAV-standard deviation could be used as a predefined program variable in the DPSP if it is certain that there is no VSAM present in the SRM control sample that does not exist in the regular samples and the data set must not contain outliers. Note that the "c" factor for the SRM control sample may be different from that of the regular samples (non-standard). If it is, the BAV-standard deviation determined on this form must first be corrected by dividing it by the "f" factor before using it as a predefined program variable in the DPSP or for significance testing. The "f" factor is explained in the Theory Section. Because the standard deviation is re-calculated with each new analytical run, the SRM-form and the SRM control sample may be continued to be run as a regular quality control sample. An X-chart in terms of PPM, outlier test and pop-up histogram are available on the form.

SRM-DUP form: This is an abbreviated version of the SRM-DUP-SPECIAL form (found below) for running duplicate SRM's, the measurements of which are obtained during the regular chemical analysis of routine samples under the standard processing conditions specified in the analytical chemistry method and calculated at M-level according to the traditional calculation procedure. The traditional calculation procedure will involve using one reagent blank (or the average of two or more reagent blanks), if any is being run, and one slope (or the average of two slopes); whatever combination is required and specified as standard processing conditions in the analytical chemistry method. Note: A separate form is required for each separate SRM sample and only one pair of SRM duplicates is allowed to be run on each form per analytical run. This is due to the kind of ANOVA testing being done on the form and for other reasons. Note that the "c" factor for the SRM duplicates may be different from that of the regular samples (non-standard). If it is, all the standard deviations that are determined on this form must first be corrected by dividing them by the "f" factor before using them as predefined program variables in the DPSP or for significance testing. The "f" factor is explained in the Theory Section. The SRM duplicates only need to have nominally equal sample weights or volumes. The SRM duplicates are labelled SRM-A and SRM-B. Stratification, such as is required on the SAM-DUP form, is not required on this form since the SRM samples are being run at a specifically targeted measurement level. Both BAV-Sampling and WAV-Sampling are used on the form. To rule out any form of non-random systematic error occurring between the two measurements, it is recommended that the duplicate SRM's be run serially adjacent to each other.

(1) Utilizing the measurements obtained at M-level for each of the SRM-A series and the SRM-B series, over several analytical runs, using the traditional calculation procedure (BAV-Sampling), Formula-1 is used to calculate a BAV-standard deviation in PPM at M-level for each series. The rest of the particulars are exactly the same as in paragraph (1) for the SRM-DUP-SPECIAL form.

(2) Utilizing the measurement means calculated for SRM-A and SRM-B over several analytical runs using the traditional calculation procedure (BAV-Sampling), Formula-1 is

used to calculate a BAV-standard deviation in PPM at M-level. The rest of the particulars are exactly the same as in paragraph (2) for the SRM-DUP-SPECIAL form.

(3) Utilizing the difference between the measurements obtained for SRM-A and SRM-B over several analytical runs using the traditional calculation procedure (WAV-Sampling), Formula-2 is used to calculate a WAV-standard deviation in PPM at M-level. The rest of the particulars are exactly the same as in paragraph (3) for the SRM-DUP-SPECIAL form.

Two X-charts, an X-bar-chart and a range-chart are included on the form. An outlier test is included for each and their respective pop-up histograms are available on the form.

One-way ANOVA is automatically, and cumulatively done on the form with each new analytical run. [Note: ANOVA cannot be done using "chain-link-sampled" duplicates and only one pair of SRM duplicates is allowed to be run per analytical run.] Each column in the one-way ANOVA classification table contains the two measurements at M-level for one pair of SRM duplicates (SRM-A and SRM-B) per analytical run. There are only two rows in the table, one for SRM-A (row 1) and one for SRM-B (row 2).

The basic idea of the ANOVA is to detect any significant BRSE in the means of the SRM duplicates (but note that any BRSME (RBV and/or SRLV) is included in the BRSE) and/or any extreme value in the SRM means that would indicate erroneous measurements. This form would not likely be used if there is significant BRSME (RBV and/or SRLV) variation being generated by the WRME (RBV and/or SRLV) of the reagent blank(s) and/or slopes(s) that are being run under standard conditions, especially from the slopes. In that case, the SRM-DUP-SPECIAL form should be used.

SRM-DUP-SPECIAL form: PAF-form for running duplicate SRM's, labelled SRM-A and SRM-B. Note: A separate form is required for each separate SRM sample and only one pair of SRM duplicates is allowed to be run on each form per analytical run. This is due to the kind of ANOVA testing being done on the form and for other reasons. The measurements of the SRM duplicates must be obtained under the standard processing conditions specified in the analytical chemistry method and calculated at M-level but according to both the traditional calculation procedure and a non-traditional calculation procedure and (unlike most of the other PAF-forms) both of these pairs of calculated measurements must be entered into their respective columns on the spreadsheet form. In order to be able to utilize both of these calculation procedures, two (or more) reagent blanks must be run and two (or more) runs on the calibration standards must be made in order to obtain two calibration slopes. The traditional calculation procedure will involve using one reagent blank (or the average of two or more reagent blanks), if any is required by the method at all, and one slope (or the average of two slopes); whatever combination is required and specified as standard processing conditions in the analytical chemistry method. For the non-traditional calculation procedure, the SRM duplicates will have been labelled SRM-A and SRM-B, so likewise, two of the reagent blanks must be labelled RB-A and RB-B, and the calibration slopes must be labelled SL-A and SL-B. Then, RB-A is to be subtracted from SRM-A, and the result is to be divided by SL-A. Likewise, RB-B is to be subtracted from SRM-B, and the result is to be divided by SL-B. Both BAV-sampling and WAV-sampling are used on this form. Stratification, such as is required on the SAM-DUP form, is not required on this form since the SRM duplicates are being run at a specifically targeted measurement level. [Note: Any form of "chain-link-sampling," as explained in the Theory Section, is not allowed to be used to obtain the duplicates for this form.] To rule out any form of non-random systematic error occurring between the two measurements, it is recommended that the duplicate SRM's be run serially adjacent to each other.

This form is similar the RC-DUP-SPECIAL form in some respects and to the SRM-DUP form in other respects. Note that the "c" factor for the SRM duplicates may be different from that of the regular samples (non-standard). If it is, all the standard deviations that are determined on this form that are to be used as predefined program variables in the DPSP or for significance testing must first be corrected by dividing them

by the "f" factor. The "f" factor is explained in the Theory Section. The SRM duplicates only need to have nominally equal sample weights or volumes.

For the sake of simplicity, only the instruction to calculate the measurements for both pairs of SRM duplicates at M-level before entering them into the form, has been given. But it is also possible to enter the duplicate reagent blanks as on the RB-DUP form and the duplicate slopes as on the CAL-DUP form and their respective standard deviations can then be determined on this same form. For this to be possible, the standard "c" factor for the specific analytical chemistry method must also be entered on the form. This form should then be programmed to be able to do both, giving the user the choice. But if the user has been using the RB-DUP and CAL-DUP forms already, he should continue to enter the duplicate reagent blank and duplicate slope data into those respective forms so as to continue the process of calculating their respective standard deviations on the same forms. The same reagent blank and slope data must not be entered into both the RC-DUP-SPECIAL form and the other forms (RB-DUP and/or CAL-DUP forms). The variances (and standard deviations) from both forms would then be partly duplicated (overlapped) and not be independent. But if this is not done, then the respective variances from each form could be pooled and then converted to a standard deviation by taking the square root.

(1) Utilizing the measurements obtained for SRM-A over several analytical runs using the traditional calculation procedure (BAV-Sampling), Formula-1 is used to calculate a BAV-standard deviation in PPM at M-level. This BAV-standard deviation will contain the correct proportion of VSAM, WRME (from all chemical processing stages), IRV and IBV, and between analytical runs, all forms of between-run systematic error (BRSE), including any between-run systematic measurement error, BRSME (RBV and/or SRLV), that is being generated by the WRME (RBV and/or SRLV) of the reagent blank(s) and/or slopes(s) that are being run under standard conditions. The same thing can be said about the BAV-standard deviation calculated in terms of PPM at M-level from the measurements for SRM-B over several analytical runs. These two standard deviations (converted to variances) should not be pooled using the general equation for the pooled variance, since the two variance estimates are not entirely independent. However, if only one reagent blank and/or only one slope is being run under standard conditions, a pooled variance may be obtained from paragraph (4). If two or more reagent blanks are being run and/or two or more slopes are being obtained and neither of these two submeasurement random variables are highly variable, it might be permissible to pool the variances but it cannot be recommended here. Either of these two BAV-standard deviations for the SRM-A series or for the SRM-B series can be used as a predefined program variable in the DPSP if it is certain that there is no VSAM present in the SRM samples that does not exist in the regular samples and their respective data sets do not contain outliers. Note that the "c" factor for the SRM duplicates may be different from that of the regular samples (non-standard). If it is, the BAV-standard deviation to be used as a predefined program variable in the DPSP must first be corrected by dividing it by the "f" factor. This would also likely have to be done for the purpose of significance testing. The "f" factor is explained in the Theory Section.

(2) Utilizing the measurement means calculated for SRM-A and SRM-B over several analytical runs using the traditional calculation procedure (BAV-Sampling), Formula-1 is used to calculate a BAV-variance in PPM^2 at M-level. This BAV-variance of the measurement means will contain a one-half portion of VSAM, WRME (from all chemical processing stages), IRV and IBV, and a full portion all forms of BRSE, including any between-run systematic measurement error, BRSME (RBV and/or SRLV), that is being generated by the WRME (RBV and/or SRLV) of the reagent blank(s) and/or slopes(s) that are being run under standard conditions. This BAV-variance so determined at M-level is then multiplied by 2, in order to have it apply to the variation inherent in the premeasurement of a single determination on a regular sample. The resulting overall BAV-variance will contain the correct proportions of VSAM, WRME (from all chemical processing stages), IRV and IBV, but will have a double portion of all forms of BRSE,

including any between-run systematic measurement error, BRSME (RBV and/or SRLV), that is being generated by the WRME (RBV and/or SRLV) of the reagent blank(s) and/or slopes(s) that are being run under standard conditions. This BAV-variance is then converted to a BAV-standard deviation in PPM at M-level by taking the square root. This overall BAV-standard deviation is not recommended to be used as a predefined program variable in the DPSP, even if it is certain that: (1) there is no VSAM present in the SRM sample that does not exist in regular samples, (2) its respective data set does not contain outliers and (3) the ANOVA testing does not result in any outcome of significance; since it could have an extra portion of BRSE, including any between-run systematic measurement error, BRSME (RBV and/or SRLV) that might go undetected. If the "c" factor for the SRM duplicates is different from that of the regular samples (non-standard), this BAV-standard deviation would likely need to be corrected by dividing it by the "f" factor before using it for the purpose of significance testing.

(3) Utilizing the difference between the measurements obtained for SRM-A and SRM-B over several analytical runs using the traditional calculation procedure (WAV-Sampling), Formula-2 is used to calculate a WAV-standard deviation in PPM at M-level. This WAV-standard deviation will contain the correct proportion of VSAM, WRME (from all chemical processing stages), IRV and IBV. It does not capture any form of between-run systematic error (BRSE) or any of the between-run systematic measurement error, BRSME (RBV and/or SRLV), being generated by the WRME (RBV and/or SRLV) of the reagent blank(s) and/or slopes(s) that are being run under standard conditions. The exception would be non-random systematic error occurring between the two measurements but this is considered to be ruled out here. The two control samples should be run serially adjacent to each other to reduce the probability of this occurring. The WAV-standard deviation so determined at M-level is then applied to the variation inherent in the premeasurement of a single determination on a regular sample. This WAV-standard deviation, once corrected, might be used as a predefined program variable in the DPSP if it is certain that no VSAM is present in the SRM samples that does not exist in the regular samples. This WAV-standard deviation would also need correction by having added to it the appropriate term for the variation being generated by the WRME (RBV and/or SRLV) of the reagent blank(s) and/or slopes(s) that are being run under standard conditions, before it can be used as a predefined program variable in the DPSP and its respective data set must not contain outliers. If the "c" factor for the SRM duplicates is different from that of the regular samples (non-standard), this WAV-standard deviation would need to be corrected by dividing it by the "f" factor before using it in the DPSP or for the purpose of significance testing.

(4) Utilizing the measurements obtained for SRM-A over several analytical runs using the non-traditional calculation procedure (BAV-Sampling), Formula-1 is used to calculate a BAV-standard deviation in PPM at M-level. This BAV-standard deviation will contain the correct proportion of VSAM, WRME (from all chemical processing stages), IRV and IBV, and all forms of BRSE other than BRSME (RBV and/or SRLV), and a full portion of WRME (RBV and/or SRLV) for only one reagent blank and/or only one slope being run under otherwise standard conditions. In this case, no BRSME (RBV and/or SRLV), is being generated by the WRME (RBV and/or SRLV) for the control samples. The same thing can be said about the BAV-standard deviation, calculated in terms of PPM at M-level from the measurements for SRM-B, over several analytical runs. These two standard deviations can then be pooled (as their respective variances which are independent) by using the general equation for the pooled variance. The resulting standard deviation will have twice as many degrees of freedom as either one alone and contains the same sources of variation. These BAV-standard deviations have a restricted use as predefined program variables in the DPSP. Although they are obtained from basically the same kind of statistical sampling used in paragraph (1) for each individual control sample series, the two control samples series have different reagent blanks and slopes (which is why their variances are independent). Consequently, no BRSME (RBV and/or SRLV) is being generated by the WRME (RBV and/or SRLV) and the kind of WRME (RBV and/or SRLV)

that is present is only equivalent to one reagent blank and/or one slope being run under otherwise standard conditions. Therefore, they can only be applied (pooled or unpooled) to the traditional calculation procedure under the restricted condition that only one reagent blank and/or only one slope are being run under standard conditions. If the "c" factor for the SRM duplicates is different from that of the regular samples (non-standard), these BAV-standard deviations would need to be corrected by dividing them by the "f" factor before using them as predefined program variables in the DPSP or for the purpose of significance testing.

Basically, the statistical sampling, called "one on one," meaning one premeasurement to one of the submeasurements, will be the same here as in paragraph (1) only if only one reagent blank and/or only one slope are being run. Also, in paragraph (1), if more than one reagent blank and/or more than one slope are being run, the statistical sampling is still "one on one," that is, one premeasurement to one of the average submeasurements. In the case of the non-traditional calculation procedure that is being used in paragraph (4), that will not be the case, as neither of the two submeasurements are being averaged at Q1-level or Q2-level before being applied to the premeasurement. Therefore, the kind of WRME (RBV and/or SRLV) that is present is only equivalent to one reagent blank and/or one slope being run under otherwise standard conditions.

(5) Utilizing the measurement means calculated for SRM-A and SRM-B over several analytical runs using the non-traditional calculation procedure (BAV-Sampling), Formula-1 is used to calculate a BAV-variance in PPM^2 at M-level. This BAV-variance of the measurement means will contain a one-half portion of VSAM, WRME (from all chemical processing stages), IRV, IBV, and a full portion all all forms of BRSE other than BRSME (RBV and/or SRLV), and a one-half portion of WRME (RBV and/or SRLV) for only one reagent blank and/or only one slope that are being run under otherwise standard condition. In this case, no BRSME (RBV and/or SRLV) is being generated by the WRME (RBV and/or SRLV). This BAV-variance so determined at M-level is then multiplied by 2, in order to have it apply to the variation inherent in the premeasurement of a single determination on a regular sample at M-level. The resulting overall BAV-variance will contain the correct proportions of VSAM, WRME (from all chemical processing stages), IRV and IBV, and a double portion of all forms of BRSE other than BRSME (RBV and/or SRLV), and a full portion of WRME (RBV and/or SRLV) for only one reagent blank and/or only one slope that are being run under otherwise standard conditions. However, it will not contain any BRSME (RBV and/or SRLV) since the WRME (RBV and/or SRLV) isn't generating any due to the fact that a non-traditional calculation procedure is being used. This BAV-variance is then converted to a BAV-standard deviation in PPM at M-level by taking the square root. This overall BAV-standard deviation of the measurement means cannot be used as a predefined program variable in the DPSP since it cannot be applied to the traditional calculation procedure for which this system is intended, not to mention that it could have an extra portion of all forms of BRSE other than BRSME (RBV and/or SRLV) that might go undetected by the outlier testing and the ANOVA testing. If the "c" factor for the SRM duplicates is different from that of the regular samples (non-standard), this BAV-standard deviation would likely need to be corrected by dividing it by the "f" factor before using it for the purpose of significance testing.

(6) Utilizing the difference between the measurements obtained for SRM-A and SRM-B over several analytical runs using the non-traditional calculation procedure (WAV-Sampling), Formula-2 is used to calculate a WAV-standard deviation in PPM at M-level. This WAV-standard deviation will contain the correct proportion of VSAM, WRME (from all chemical processing stages), IRV and IBV. It does not capture any form of between-run systematic error (BRSE) but it captures the correct proportion of WRME (RBV and/or SRLV) for only one reagent blank and/or only one slope that are being run under otherwise standard conditions. The exception would be non-random systematic error occurring between the two measurements but this is considered to be ruled out here. The two control samples should be run serially adjacent to each other to reduce the

probability of this occurring. This WAV-standard deviation so determined in PPM at M-level is applied to the variation inherent in the premeasurement of a single determination on a regular sample. Unlike the WAV-standard deviation determined in paragraph (3), this WAV-standard deviation would not need correction by having added to it any term for the variation being generated by the WRME (RBV and/or SRLV) before using it as a predefined program variable in the DPSP, provided that the traditional calculation procedure is being used in the respective analytical chemistry method under the restricted condition that only one reagent blank and/or only one slope are being run under standard conditions. If the "c" factor for the SRM duplicates is different from that of the regular samples (non-standard), this WAV-standard deviation would need to be corrected by dividing it by the "f" factor before using it as a predefined program variable in the DPSP or for the purpose of significance testing.

Two X-charts, an X-bar-chart and a range-chart are included for the traditional calculation procedure and two X-charts, an X-bar-chart and a range-chart are included for the non-traditional calculation procedure. An outlier test is included for all and their respective pop-up histograms are available on the form.

One-way ANOVA is automatically, and cumulatively done on the form for both the traditional calculation procedure and the non-traditional calculation procedure with each new analytical run. [Note: ANOVA cannot be done using "chain-link-sampled" duplicates and only one pair of SRM duplicates is allowed to be run per analytical run.] Each column in the one-way ANOVA classification table contains the two measurements at M-level for one pair of SRM duplicates (SRM-A and SRM-B) per analytical run. There are only two rows in the table, one for SRM-A (row 1) and one for SRM-B (row 2).

The ANOVA done for the traditional calculation procedure is used to detect any significant BRSE in the means of the SRM duplicates but note that any BRSME (RBV and/or SRLV) being generated by the WRME (RBV and/or SRLV) of the reagent blank(s) and/or slopes(s) that are being run under standard conditions will be included in those means. The ANOVA done for the non-traditional calculation procedure will not contain that (BRSME (RBV and/or SRLV) and so it is better suited to the detection of extreme values in the means that would indicate erroneous measurements.

Important Note: If multiple (averaged) instrument sub-readings are a part of standard processing conditions (that is, they are done on each regular or control sample extract, each replicate subsample extract, and each calibration standard), then these same multiple sub-readings must be done when determining the various standard deviations on all of the various PAF-forms, including the standard deviation of the instrument as it is being determined on the STAN-DUP, CAL-DUP or CAL-DATA forms. In the latter case though, the standard deviation of the instrument could alternatively be determined as the parent random variable of the instrument (that is, considering each individual non-composite reading to be a single outcome from the instrument) and then the variance thereof (obtained from multiple consecutive individual non-composite instrument readings using a single sample extract or standard solution) can be adjusted so as to comply with the number of multiple sub-readings which are standard. Only the respective standard deviation determined from that variance so adjusted can be entered as an alternative predefined program variable into the DPSP once it is converted to PPM at M-level by multiplying by the standard "c" factor for the specific analytical chemistry method. On the other hand, the standard deviation of "y" given "x" (also the standard deviation of the instrument response variable) determined from each run on the calibration standards, would normally be calculated from the standard number of instrument sub-readings already having been made on each calibration standard so that it would not normally need to be adjusted before entering it as a predefined program variable into the DPSP, it having been converted to PPM at M-level by multiplying by the standard "c" factor for the specific analytical chemistry method. For the following STAN-DUP, CAL-DUP and CAL-DATA forms, it is assumed that the standard number of instrument sub-readings have already been made on each calibration standard.

STAN-DUP form: PAF-form for obtaining duplicate readings on a selected instrument calibration standard (one per form) in addition to the readings used to prepare the calibration graph. This form differs from all the preceding ones in that the calibration standards, which are the control samples here, have not passed through any of the chemical processing stages of the analytical chemistry method, other than the instrument reading step itself. Do not use this form with any calibration standards that have passed through any of the chemical processing stages of the analytical method. The main purpose of this form is to determine, over several analytical runs, the standard deviation of the instrument response variable, it having been converted to PPM, by having brought through the calibration graph already prepared for the run, an extra reading on one of the calibration standards, so that duplicate readings of the same calibration standard may be expressed in terms of PPM at Q2-level at the particular instrument measurement level for the chosen calibration standard. Note that one reading has already been made for the chosen calibration standard (but not converted to PPM) in order to obtain the calibration (regression) line. It is only an extra duplicate reading of it that is required. Both readings are then to be brought through the calibration (regression) line, once it has been prepared, and both are to be entered into the form in terms of PPM at Q2-level without averaging. The extra reading for the chosen calibration standard could also alternatively be obtained from a second run on the calibration standards during the same analytical run provided there is no change in the PRLV. Note that in gas chromatography (and certain other forms of chemical instrumentation) the variation in injected volume (of sample extract or calibration standard) that is input into the instrument is considered to be an integral part of the variation, and thus also the standard deviation, of the instrument.

Utilizing the difference between the readings in PPM per analytical run obtained for over several analytical runs (WAV-Sampling), Formula-2 is then used to determine a WAV-standard deviation of the instrument response variable in terms of PPM at Q2-level and then converted to PPM at M-level by multiplying by the standard "c" factor for the specific analytical chemistry method. This WAV-standard deviation is roughly equivalent to the standard deviation of "y" given "x" (assuming it to be constant about the regression line) that can be calculated from the calibration points of the calibration standards (Spiegel 1961). The standard deviation of "y" given "x" is not calculated on the form because the calibration points are not entered onto the form. But if the WAV-standard deviation determined on the form is substituted for it, the standard deviation of the slope (at Q2-level) can be computed manually. This is obtained (Morrison 1983) by dividing the WAV-standard deviation by the square root of $\Sigma_i(x_i)^2$ where the x_i are the concentrations for the calibration standards and "i" refers to the subscript for each of the calibration standards (S_1, S_2, S_3, for example). Note that (S_0) is excluded since it is passing through the origin of the calibration graph, a known point on the calibration line. Therefore, if the concentrations of the calibration standards are held exactly the same from analytical run to analytical run and if the sensitivity of the instrument is also held constant from analytical run to analytical run as explained below for the CAL-DUP form, the standard deviation and grand mean of the slopes may both be estimated. These calculations are to be done manually by the system administrator, laboratory supervisor or analytical chemistry method developer. Stratification, such as is required on the SAM-DUP form, is not required on this form since the chosen calibration standard is being run at a specifically targeted measurement level. Chain-link-sampling (as explained near the end of the Theory Section) can be used to acquire the duplicates (at Q2-level) for this form if more than one run is been made on the calibration standards (unchanging PRLV) or more than one extra reading is being obtained for the chosen calibration standard. There can be more than one set of duplicates entered into the form per analytical run. A range-chart, outlier test and pop-up histogram are available on the form.

CAL-DUP form: PAF-form for recording the slopes from duplicate runs on the calibration standards that are being done as part of the standard processing conditions specified in the analytical chemistry method. As for the STAN-DUP form, this form is not to be used with any calibration standards that have passed through any of the chemical processing

stages of the analytical chemistry method. The slopes can be calculated by the chemical analyst before being entered into the form (for example, if the calibration lines are being drawn "by eye") or they can be calculated by the form if the concentrations and respective readings for the calibration standards are being entered into the form. The values for each of the two slopes are recorded or calculated on the form in terms of (AU, XAU, or AREA) per PPM at Q-level. Note that in gas chromatography (and certain other forms of chemical instrumentation) the variation in injected volume (of sample extract or calibration standard) that is input into the instrument is considered to be an integral part of the variation, and thus also the standard deviation, of the instrument.

Utilizing the difference between the slopes from duplicate runs on the calibration standards obtained over several analytical runs (WAV-Sampling), Formula-2 is then used to determine a WAV-standard deviation for the slopes, in terms of the dimensional units just mentioned at Q-level. The standard deviation of the slope at Q-level does not need to be converted to M-level since it is a random variable only in a relative sense. But it is necessary to calculate a special variance term for the slope to be added, along with the WAV-variance for the reagent blank or average reagent blank at M-level, to the WAV-variance for the premeasurement at M-level, in order to obtain the correct overall variance at M-level for the overall measurement (see the general equation for the overall variance of a single of average determination at the end of the Theory Section). The numerator of the special variance term contains the square of the standard deviation for the parent random variable of the slope or average slope times the overall measurement level, squared. The denominator of the special variance term contains an estimate of the population mean of the slopes, squared. There are two possible sources for the estimate of this population mean of the slopes. One, of course, is the individual or mean slope for the analytical run. This might not be considered to be very accurate. It might be suggested to obtain a grand mean for the slopes over several runs. It is not correct, by way of comparison, to think in terms of getting a grand mean for the regent blanks over several runs, because, as every chemical analyst knows, the population mean of the reagent blanks "could change significantly" from analytical run to analytical run. For the slopes though, there is often a way to verify that one is getting close to the acceptable value for the slope for the analytical run, by injecting (inputting) a known concentration calibration standard into the instrument at the very beginning of every analytical run to check that one is getting the theoretically correct reading (instrument response). Small changes in alignment usually can be done to maximize and/or adjust the reading. If this is done, the PRLV might be kept to a sufficiently small level between analytical runs to do this. A column to detect outliers (extreme values) in the accumulated values for the slopes is included on the form to help verify the data. The option to calculate this grand mean of the slopes at Q-level is available on the form. The standard deviation of "y" given "x" (the standard deviation of the instrument response variable) and the correlation coefficient are computed for each analytical run provided the slopes are calculated on the form. Both are indices of the "goodness of fit" of the calibration points to the (regression) calibration line. The standard deviation of the slope can also be calculated as explained for the STAN-DUP form (Morrison 1983) provided the slopes are calculated on the form. Note, as is the case with all of the required formulas, the formulas for each of these three parameters are different (Morrison 1983) for a regression line $y = mx + 0$ than for a regression line $y = mx + b$. The ones for the latter case, are the only ones given in most elementary and advanced textbooks on statistics. The system administrator, laboratory supervisor or analytical chemistry method developer will be the ones making the choices about which options are chosen on the form and whether or not to manually calculate some of the parameters. Stratification, such as is required on the SAM-DUP form, is not required on this form since the duplicate slopes of the calibration standards are being obtained in a sufficiently narrow measurement range. Chain-link-sampling (as explained near the end of the Theory Section) could be used to acquire the duplicates if more that two runs are being done on the calibration standards in the same analytical run provided that there is no change in the PRLV. In that case, the slopes would be labelled A, B, C, and so on, in serial order, according to when the calibration standards are being run in succession during the analytical run. There can be more than

one set of duplicates entered into the form per analytical run. Any repeated running of the calibration standards (including the duplicate run) during the instrument reading step should be spaced out so as to bracket blocks of regular samples in between them so that the average of the bracketing slopes can be applied to the included block of samples using the traditional calculation procedure. A range-chart, outlier test and pop-up histogram are available on the form.

CAL-DATA form: PAF-form for recording the data generated by each run on the instrument calibration standards. The concentrations of the calibration standards and their respective instrument readings (per calibration run) are recorded on the form. Do not use this form with any calibration standards that have passed through any of the chemical processing stages of the analytical method. The standard deviation of the instrument response variable for each calibration run is calculated as the standard deviation of "y" given "x" in terms of (AU, XAU, or AREA) at Q1-level. This can then be divided by the individual or mean slope for the analytical run or the grand mean of the calibration slopes over several analytical runs (see comments about this grand mean of the slopes in the CAL-DUP form) in order to express it in terms of PPM at Q2-level. From there it is converted to PPM at M-level by multiplying by the standard "c" factor for the specific analytical chemistry method. The standard deviation of the slope is also determined and is calculated in terms of (AU, XAU, or AREA) per PPM at Q-level. Each of these two standard deviations are individually and cumulatively pooled (in terms of their respective variances) over each succeeding analytical run on the form. One nice thing about this form is that it doesn't require any additional control samples to be run or any additional readings to be made on behalf of the chemical analyst. Plus the form itself does all the calculations required to determine the calibration (regression) line in the first place and, in addition, calculates all the related variables and stores them on the form. Thus, it accomplishes the same tasks as the STAN-DUP form and the CAL-DUP form but in a different manner. Note that in gas chromatography (and certain other forms of chemical instrumentation) the variation in injected volume (of sample extract or calibration standard) that is input into the instrument is considered to be an integral part of the variation, and thus also the standard deviation, of the instrument.

Along with the standard deviation of "y" given "x" (the standard deviation of the instrument response variable), the correlation coefficient is also computed for each analytical run. Both are indices of the "goodness of fit" of the calibration points to the (regression) calibration line. Note that the formulas for all of the parameters mentioned here are different (Morrison 1983) for a regression line $y = mx + 0$ than for a regression line $y = mx + b$. The ones for the latter case, are the only ones given in most elementary and advanced textbooks on statistics.

RB-WAV form: PAF-form for running several replicate (within-run) reagent blanks, the measurements of which are obtained under the standard processing conditions specified in the analytical chemistry method. The readings for the replicate reagent blanks are obtained at Q1-level and converted to Q2-level by dividing by the single or average slope of a common calibration line. The standard deviation of the submeasurement random variable of the reagent blanks is first calculated in terms of PPM at Q2-level using Formula-1 but with $(n - 1)$ in the denominator instead of $(k - 1)$. It is then converted to M-level by multiplying by the standard "c" factor for the specific analytical chemistry method. An X-chart, outlier test and pop-up histogram are available on the form. This form is used to acquire the respective standard deviations with the required degrees of freedom more quickly than can be done on the other forms.

RC-WAV form: PAF-form for running several replicate (within-run) recovery constants, the measurements of which are obtained under the standard processing conditions specified in the analytical chemistry method. The readings for the replicate recovery constants are obtained at Q1-level and converted to Q2-level by dividing by the single or average slope of a common calibration line. The standard deviation of the premeasurement-equivalent random variable of the recovery constants is first calculated

in terms of PPM at Q2-level using Formula-1 but with (n - 1) in the denominator instead of (k - 1). It is then converted to PPM at M-level by multiplying by the standard "c" factor for the specific analytical chemistry method. An X-chart, outlier test and pop-up histogram are available on the form. This form is used to acquire the respective standard deviations with the required degrees of freedom more quickly than can be done on the other forms.

Some Examples of Significance Testing:

Significance testing can be done on the WAV- and BAV-variances obtainable from the various PAF-forms taking into account the various sources of variation that are contained in them provided that the "c" factors and other conditions that were used in determining them are exactly equivalent. For example, various F-ratio tests can be constructed. These would normally be done by the system administrator, laboratory supervisor or analytical chemistry method developer. For example, suppose it is desired to know whether or not a newly purchased SRM sample contains any VSAM (non-homogeneity). A variance capturing VSAM could be divided by a variance not capturing any VSAM to give an F-ratio which can then be tested at significance level ($\alpha = 0.05$). This F-ratio can be obtained in various ways:

An SRM-BAV-variance at M-level from the SRM-form could be divided by an RC-BAV-variance at M-level from the RC-form. An SRM-WAV-variance at M-level from the SRM-DUP form could be divided by an RS-WAV-variance at M-level from the RS-DUP-form.

An SRM-BAV-variance at M-level for the SRM-A series (paragraph 1) from the SRM-DUP-SPECIAL form could be divided by an RC-BAV-variance at M-level for the RC-A series (paragraph 1) from the RC-DUP-SPECIAL form. An SRM-BAV-variance at M-level for the SRM-A series (paragraph 1) from the SRM-DUP-SPECIAL form could be divided by an RC-BAV-variance at M-level for the RC-A series (paragraph 1) from the RC-DUP-SPECIAL form. If both of these tests are being done, then each of the F-ratio tests should be done at significance level ($\alpha = 0.025$), so that, in applying the theory of multiple tests, a result of significance in either one will be at ($\alpha = 0.05$). An SRM-BAV-variance at M-level for the SRM-B series (paragraph 1) from the SRM-DUP-SPECIAL form could be divided by an RC-BAV-variance at M-level for the RC-B series (paragraph 1) from the RC-DUP-SPECIAL form. An SRM-BAV-variance at M-level for the SRM-B series (paragraph 1) from the SRM-DUP-SPECIAL form could be divided by an RC-BAV-variance at M-level for the RC-B series (paragraph 1) from the RC-DUP-SPECIAL form. Likewise, if both of these tests are being done, then each of the F-ratio tests should be done at significance level ($\alpha = 0.025$), so that, in applying the theory of multiple tests, a result of significance in either one will be at ($\alpha = 0.05$). An SRM-WAV-variance at M-level (paragraph 3) from the SRM-DUP-SPECIAL form could be divided by an RC-WAV-variance at M-level (paragraph 3) from the RC-DUP-SPECIAL form. In this case, the F-ratio test should be done at significance level ($\alpha = 0.05$) since it is not a multiple test. An SRM-BAV-variance at M-level for the measurement means (paragraph 2) from the SRM-DUP-SPECIAL form could be divided by an RC-BAV-variance at M-level for the measurement means (paragraph 2) from the RC-DUP-SPECIAL form but note carefully that this test will not be independent from any of the first four tests mentioned above for paragraph 1. And there are other possible combinations, most of which will not be entirely independent from the above.

An SRM-BAV-variance at M-level for the SRM-A series (paragraph 4) from the SRM-DUP-SPECIAL form could be divided by an RC-BAV-variance at M-level for the RC-A series (paragraph 4) from the RC-DUP-SPECIAL form. An SRM-BAV-variance at M-level for the SRM-A series (paragraph 4) from the SRM-DUP-SPECIAL form could be divided by an RC-BAV-variance at M-level for the RC-A series (paragraph 4) from the RC-DUP-SPECIAL form. If both of these tests are being done, then each of the F-ratio tests should be done at significance level ($\alpha = 0.025$), so that, in applying the theory of multiple tests, a result of significance in either one will be at ($\alpha = 0.05$). An SRM-BAV-variance at M-level for the SRM-B series (paragraph 4) from the SRM-DUP-SPECIAL form

could be divided by an RC-BAV-variance at M-level for the RC-B series (paragraph 4) from the RC-DUP-SPECIAL form. An SRM-BAV-variance at M-level for the SRM-B series (paragraph 4) from the SRM-DUP-SPECIAL form could be divided by an RC-BAV-variance at M-level for the RC-B series (paragraph 4) from the RC-DUP-SPECIAL form. Likewise, if both of these tests are being done, then each of the F-ratio tests should be done at significance level ($\alpha = 0.025$), so that, in applying the theory of multiple tests, a result of significance in either one will be at ($\alpha = 0.05$). An SRM-WAV-variance at M-level (paragraph 6) from the SRM-DUP-SPECIAL form could be divided by an RC-WAV-variance at M-level (paragraph 6) from the RC-DUP-SPECIAL form. In this case, the F-ratio test should be done at significance level ($\alpha = 0.05$) since it is not a multiple test. An SRM-BAV-variance at M-level for the measurement means (paragraph 5) from the SRM-DUP-SPECIAL form could be divided by an RC-BAV-variance at M-level for the measurement means (paragraph 5) from the RC-DUP-SPECIAL form but note carefully that this test will not be independent from any of the first four tests mentioned above for paragraph 4. And there are other possible combinations, most of which will not be entirely independent from the above.

The WAV-variances at M-level that do not contain either the between-run systematic measurement error, BRSME (RBV and/or SRLV), that is being generated by the WRME (RBV and/or SRLV) of the reagent blank(s) and/or slopes(s) that are being run or the WRME (RBV and/or SRLV), itself, of the reagent blank(s) and/or slopes(s), are recommended for the above tests. These conditions are satisfied on the SRM-DUP, RS-DUP, SRM-DUP-SPECIAL (paragraph 3) and the RC-DUP-SPECIAL (paragraph 3) forms.

Another possible example would be to test for any form of between-run systematic error (BRSE) over and above that of the between-run systematic measurement error, BRSME (RBV and/or SRLV), that is being generated by the WRME (RBV and/or SRLV) of the reagent blank(s) and/or slopes(s) that are being run under standard conditions. The F-ratio test for this could be constructed by dividing the BAV-variance at M-level from the RC-DUP-SPECIAL form (paragraph 5) by the WAV-variance at M-level from the RC-DUP-SPECIAL form (paragraph 6) or by dividing the BAV-variance at M-level from the SRM-DUP-SPECIAL form (paragraph 5) by the WAV-variance at M-level from the SRM-DUP-SPECIAL form (paragraph 6). The former would be recommended, if possible, since the latter could have extra variation due to VSAM. This kind of significance testing is also being done automatically by the ANOVA testing on the respective forms but one might want to check that the ANOVA is working or do the test in more detail using power calculations. The respective variances are described below:

The BAV-variance at M-level from the RC-DUP-SPECIAL form (paragraph 5) will not contain any BRSME (RBV and/or SRLV) since the WRME (RBV and/or SRLV) isn't generating any due to the fact that a non-traditional calculation procedure is being used. But it will have a double portion of all forms of BRSE other than BRSME (RBV and/or SRLV) and a full portion of WRME (RBV and/or SRLV) for only one reagent blank and/or only one slope being run under otherwise standard conditions.

The WAV-variance at M-level from the RC-DUP-SPECIAL form (paragraph 6) does not capture any form of between-run systematic error (BRSE) but it captures the correct proportion of WRME (RBV and/or SRLV) for only one reagent blank and/or only one slope being run under otherwise standard conditions.

The BAV-variance at M-level from the SRM-DUP-SPECIAL form (paragraph 5) will not contain any BRSME (RBV and/or SRLV) since the WRME (RBV and/or SRLV) isn't generating any due to the fact that a non-traditional calculation procedure is being used. But it will have a double portion of all forms of BRSE other than BRSME (RBV and/or SRLV) and a full portion of WRME (RBV and/or SRLV) for only one reagent blank and/or only one slope being run under otherwise standard conditions. It will also contain a full portion of VSAM, if any is present.

The WAV-variance at M-level from the SRM-DUP-SPECIAL form (paragraph 6) does not capture any form of between-run systematic error (BRSE) but it captures the correct proportion of WRME (RBV and/or SRLV) for only one reagent blank and/or only one slope being run under otherwise standard conditions. It will also contain a full portion of VSAM, if any is present.

References

Annis C., Central Limit Theorem Summary, <http://www.statisticalengineering.com/central_limit_theorem_(summary).htm>

Day R. A. Jr., Underwood A. L., 1967 Quantitative Analysis, 2nd ed, Prentice-Hall, Inc., p. 15.

Dixon W. J., Massey F. J. Jr., 1957 Introduction to Statistical Analysis, 2nd Edition. McGraw-Hill Book Company, Inc., pp. 76, 109.

Morrison D. F., 1983 Applied Linear Statistical Methods. Prentice-Hall, Inc., pp. 53-54.

Pearson E. S., Hartley H. O., 1942 The probability integral of the range in samples of "n" observations from a normal population. Biometrika **32**(3):309.

Spiegel M. R., 1961 Schaum's Outline Series: Theory and Problems of Statistics. McGraw-Hill Book Company, Inc., p. 252.

Watkins T., The Distribution of Linear Regression Coefficients, <http://www.applet-magic.com/sampleregress.htm>

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