amc technical brief

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Fitting a linear functional relationship to data with error on both variables

It is fairly well known that a basic assumption of regression is that the y-values (the dependent- or response variable) are random variables while the x-values (the independent- or predictor variable) should be error-free. This model often prevails (or is approximated to) in analytical chemistry applications, for example in many calibrations. If the condition is violated, however, the results of the regression are in principle incorrect and in practice can be sufficiently incorrect to be misleading. What is far less well known is that a general method, functional relationship estimation by maximum likelihood (FREML), is available for use when the regression assumption is incorrect. FREML provides estimates of the intercept (*a***) and slope (***b***) of the line, plus their standard errors, that do not suffer from the biases introduced by the inappropriate use of regression. The method is symmetric in that the** *x***- and** *y***-variables can be interchanged without affecting the outcome. It is capable of handling heteroscedastic data, that is, data points with different precisions.**

Regression and functional relationship models

Normal weighted regression is based on a model of the paired data $(x_i, y_i, i = 1, ..., n)$ such that

 $y_i = a + bx_i + e_i$

where **a** and **b** are the parameters describing the true line and e_i is a random normal error of variance var (y_i) . Estimates (*a*,*b*) of *a* and *b* are obtained by minimising the function

$$
\sum_{i=1}^{n} (y_i - a - bx_i)^2 / \text{var}(y_i)
$$

with respect to *a* and *b*. The minimisation is done by a simple application of calculus to give the familiar regression equations.

In functional relationship estimation we use a different model, namely

 $x_i = u_i + e_i$ $y_i = v_i + h_i$ $v_i = a + bu_i$

where e_i and h_i are independent, normally distributed errors of variances \mathbf{k}_i and \mathbf{l}_i respectively. The functional relationship is found by minimising

$$
\sum_{i=1}^n (x_i - u_i)^2 / \mathbf{k}_i + \sum_{i=1}^n (y_i - a - bu_i)^2 / \mathbf{l}_i.
$$

This formulation follows from the maximum likelihood principle, which is a statistical estimation procedure that is more general than the familiar least squares method. Unlike regression, however, the above minimisation cannot be solved algebraically, but requires an

iterative numerical method. Details of the procedure can be found elsewhere.¹ Fortunately it is simple to program: both a Minitab macro and a compiled Fortran program to carry out FREML are available in AMC Software.

Analytical applications of FREML

Typical applications of FREML in analytical chemistry are (i) calibration with solid reference materials (where the uncertainty on the reference value may be considerable) and (ii) comparing the results of two methods (or analysts, or laboratories, etc.) over an appreciable concentration range and characterising the bias, if any, between them. Both of these activities may require tests of significance on *a* and *b* and for lack of fit. FREML can accommodate these requirements by providing standard errors $se(a), se(b)$ and a lack of fit statistic.

For example, we could test the hypothesis $H_0: \mathbf{a} = 0$ (*i.e.*, that the line passes through the origin of the graph) by calculating $z_a = a$ /se (a) . Likewise we could test H_0 : $\mathbf{b} = 1$ (that the slope of the line is unity) with $z_b = (b-1)/\text{se}(b)$. The *z*-values can be interpreted as a standard normal distribution, so for 95% confidence we should use a critical value of 1.96 for $|z|$.

The lack of fit statistic is the sum of the squares of the scaled residuals, which we can treat approximately as a chi-squared variable with *n*-2 degrees of freedom. A significantly high value of this statistic suggests either that the variance estimates were optimistically low (a common failing) or lack of fit. The latter could be brought about *inter alia* by uncorrected interference or by non-linearity in the true form of the relationship. An examination of a plot of scaled residuals would help to elucidate that difference.

Example

Consider results from the determination of fat in 11 different foodstuffs by two different methods. The experiment was carried out to determine whether there was bias between the results of the two methods over the whole of the usual concentration range. Each material was analysed by one of the two methods in a number of different laboratories, and Table 1 shows the mean result and the variance of the mean result for each material and both methods. The wide range of the variances is due mainly to the variation in the number of results that provide the mean. The general level of relative standard deviation is high, because the data reflect reproducibility (between laboratory) precision.

An *x-y* plot of the results and the fitted FREML line are shown in Figure 1. The error bars show the 95% confidence interval of each mean. The statistics derived from the FREML fit are shown in Table 2. (The same outcome is obtained if the *x*- and *y*-variables are interchanged.) Taking a critical value of $|z| = 1.96$ for an approximately 95% confidence level, we see that the intercept is clearly significantly different from zero, indicating the presence of a rotational (constant) bias between the methods over the concentration range studied. In contrast, the slope of the line is not significantly different from unity, showing that there is no