amc technical brief

Analytical Methods Committee Editor: Michael Thompson No. 18 Dec 2004

GMO Proficiency testing: Interpreting z-scores derived from log-transformed data

In some proficiency tests concerned with measuring the proportion of genetically modified organism (GMO) in food the results produced are log-transformed (converted into logarithms) before z-scores are calculated [1]. The transformation can be justified both theoretically and practically. However, the transformation gives rise to z-scores that are not on the same type of scale as the original data, and are therefore less readily interpreted. A certain amount of background in logarithmic transformation may be helpful.

What is a lognormal distribution?

Figure 1 shows the density of a lognormally distributed variable. It is asymmetric, with a positive skew and all values of *x* necessarily greater than zero. If alternatively we plot the density against the logarithm of *x*, we see the familiar shape of the normal distribution (Figure 2). (Note that logarithms base ten are implied throughout this Brief.)

Definition: a variable *x* is lognormally distributed if log *x* is normally distributed.

While all normal distributions are essentially the same shape, the shape of a lognormal distribution depends on its RSD (relative standard deviation, here expressed as a fraction). For example, the highly-skewed distribution in Figure 1 has an RSD of 0.3, while Figure 3, also a lognormal but with an RSD of 0.1, shows only a slight skew. (For reference, results from a round of a GMO proficiency test commonly have an RSD of about 0.7.)

Data from GMO proficiency testing

At present, nearly all quantitative measurements of a genetically modified species in a food are based on the polymerase chain reaction (PCR). In interlaboratory studies such as the proficiency test, the results almost invariably show a strongly skewed distribution of results, Figure 4 for example. There are *a priori* reasons for expecting this outcome. Firstly the procedure may start with a small number of copies of the gene, so that there is a binomial distribution of copies in the sample taken for PCR. Binomial distributions are positively skewed for small number of copies. If the DNA is associated with a small number of particles, sampling these particles could give rise to a skewed result even if the number of copies of the gene is reasonably large. The calibration function in PCR is log-linear in form and this will tend to produce a lognormal distribution of results from a normal input. Finally there is the usual normal distribution of errors from the instrumental readout system.

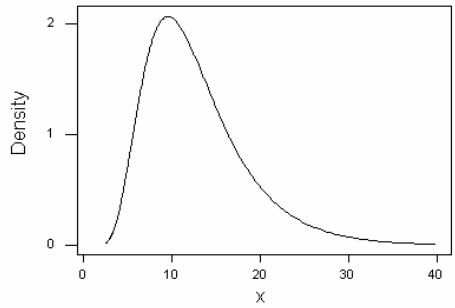

Figure 1. A lognormal distribution with an RSD of 0.3.

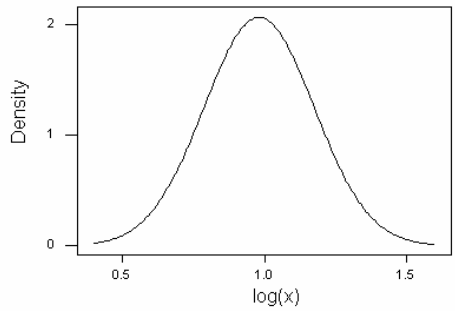

Figure 2. The same distribution as Figure 1, with the density plotted against log *x*.

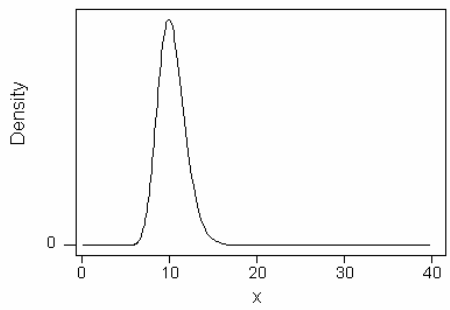

Figure 3. A lognormal distribution with an RSD of 0.1.

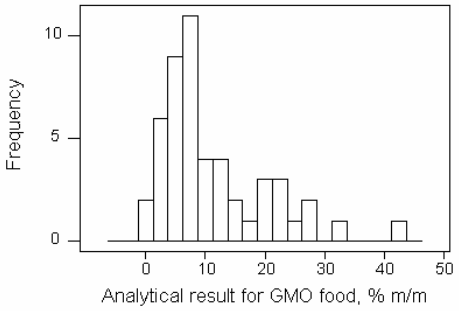

Figure 4. Results from a single round of a proficiency test involving measuring the concentration of GMO soya.

As an outcome of all this, the distribution of errors is expected to be a complex convolution of distribution types, but with a tendency towards a positive skew. It is therefore tempting to suggest that log-transformation of participants' results may be appropriate before the formation of z-scores. A detailed study of proficiency test data has justified this action in practice [2]. But how are we to relate such z-scores to everyday requirements and the performance of an individual laboratory?

Z-scoring in GMO proficiency testing

What we have to bear in mind is that, in quantitative GMO testing, errors seem to be largely multiplicative, rather than additive as in most other analytical work. In that context, a very useful property of log-transformation is that various datasets with the same *relative* standard deviation in the original scale have the same *absolute* standard deviation in the log-scale. In the instance of GMO proficiency testing, this enables providers to set a single σ_p value for the scheme, regardless of the concentration of the analyte (except, of course, where the concentration is zero, or very close to it). A z-score can then be calculated from a result x and an assigned value x_a (both in the original scale) according to the equation $z = (\log x - \log x_a)/\sigma_p = \log(x/x_a)/\sigma_p$.

$\log x_a$ will usually be the robust mean of the $\log x$ values. The σ_p value (the standard deviation for proficiency, previously called the 'target value') should be a fitness-for-purpose criterion, if at all possible.

So if fitness for purpose demanded that a satisfactory result should be within limits of (say) $0.5x_a$ and $2.0x_a$, we would need to set σ_p such that these limiting results produced z-scores of –2 and +2 respectively.

Substituting the corresponding values $z = 2$ and $x = 2.0x_a$ in the equation above gives us

$2 = (\log 2x_a - \log x_a)/\sigma_p$, or

$\sigma_p = \frac{1}{2}\log 2 = 0.1505$.

(Using $z = -2$ and $x = 0.5x_a$ gives the same result: try it!)

Generalising, if limits given by x_a/q and qx_a are required, we need $\sigma_p = \frac{1}{2}\log q$. Furthermore, we can easily toggle between a z-score and the corresponding value of $r = x/x_a$ (the factor by which a result differs from the assigned value) by using the equations $r = 10^{z\sigma_p}$ and $z = \log r/\sigma_p$. For instance, if $z = 3.5$ and $\sigma_p = 0.1505$, we have $r = 10^{0.527} = 3.36$: the result exceeds the assigned value by a factor of 3.36.

In conclusion

The essential point here is that the major errors seem to be multiplicative in quantitative GMO testing based on PCR. As a consequence, the uncertainty on the original measurement scale is not symmetrically disposed around the result. Regardless of this, z-scores based on log-transformed data can still be treated as symmetric: a z-score of –3.5 has the same importance as one of +3.5. Similar considerations might apply to any measurement system (such as quantitative microbiology) based on a multiplicative procedure.

This Technical Brief was prepared for the Analytical Methods Committee by the Statistical Subcommittee (Chairman M Thompson) with support from the Food Standards Agency.

References

1. J Powell and L Owen, *Accred Qual Assur*, 2002, **7**, 392-402.
2. M Thompson et al. (in press).

AMC Health Warning: inappropriate log-transformation could damage your statistics.
Positively skewed datasets, with a greater or lesser resemblance to lognormal, often occur in nature (for example, concentrations of a trace element in randomly selected soils). However, datasets with lognormal *distribution of error* are rarely encountered in chemical measurement. Log-transformation should be used with some caution: in the wrong context, it could provide misleading statistics (as can most other practices). An AMC Report on broader aspects of log-transformation is in preparation and will cover this topic.

