A new method for estimating a standardized prevalence of child malnutrition from anthropometric indicators

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Although anthropometric indicators are widely used for assessing the nutritional status of children, lack of consensus on the cut-off points for prevalence estimates has precluded the use of standard analytical methods in population surveys. A simple method for estimating a standardized prevalence of child malnutrition from anthropometric indicators is presented. The method is based on comparing the distribution of the indicator with that of the normalized NCHS reference population, the underlying assumption being that both distributions are nearly normal.

Standardized prevalence is defined as the proportion of cases in the observed population that is outside the normal distribution of the reference values, which can be estimated from the mean and standard deviation of the standardized Z-scores of the population, by using a formula based on the mathematical properties of the normal probability curve. A reference table is included which provides computer-estimated prevalence rates for different mean Z-scores and standard deviations of normally distributed anthropometric indicators.

Introduction

Nutritional anthropometry remains the most practical and useful means for the assessment of the nutritional status of the population, particularly among infants and young children (1, 2). In cross-sectional surveys, the use of appropriate anthropometric indicators allows the identification of the nature and extent of energy-protein malnutrition in the community. Repeated assessments are also useful for follow-up of populations, comparisons between groups, evaluation of programmes, and statistical comparisons in epidemiological research (3, 4).

Despite the popularity and recognized usefulness of nutritional anthropometry in assessments of health and nutrition, there have been many discussions and conflicting recommendations about the cut-off points to be used for estimating the prevalence of anthropometric abnormality which is conventionally taken to indicate "undernutrition" (1-10).

Different cut-off points and classification systems have been proposed and used for estimating the prevalence of malnutrition in population surveys; thus the reported rates are often not comparable and sometimes questionable. This confusion and the consequent lack of standard analytical methods have apparently legitimized an unfortunate tendency to leave every country (or group) open to set up its own criteria, depending on the local circumstances (political or other), for the sake of practicality. However, as stated elsewhere (11), "practical considerations are extraneous to the concept of biometric or functional abnormality" on which true prevalence estimates should be based.

This paper proposes a simple method for estimating a standardized prevalence of malnutrition in cross-sectional population studies. The proposed method makes any further discussion on cut-off points for prevalence estimates irrelevant. While the method could be applied regardless of the source of "reference values" (a topic which is not discussed in the paper), it does require the availability of a healthy, well-nourished reference population whose distribution of anthropometric values is normalized.
such as the NCHS/CDC (U.S. National Center for Health Statistics/Centers for Disease Control) growth reference. It also requires expressing the anthropometric indicator as the difference between the observed value and the age/sex reference value, in units of standard deviations (Z-scores) of the reference population.

**Cut-off points for prevalence estimates**

One of the first known attempts to use anthropometric measurements for estimating the prevalence of child malnutrition was the popular Gomez classification (5), which uses 90 per cent weight-for-age as the cut-off point for identifying children with nutrition and health problems. This classification method was originally designed as a guide to the prognosis of hospitalized malnourished children, and not as a yardstick for prevalence estimates, but over the past decades it has been used increasingly in developing countries for the assessment of malnutrition in the community.

With widespread use, questions have been raised about this classification system (12–13), mostly because of its relatively high cut-off point, which is equivalent to about one standard deviation below the reference mean. This appears to grossly overestimate the prevalence of child malnutrition by including a sizeable proportion (about 15.9 per cent) of "false positives" (i.e., those whose weights are within the normal range of the reference population distribution). What has been particularly dubious is the supposed abnormality of those children labeled as having first-degree malnutrition (75 to 90 per cent weight-for-age). This is often circumvented by reporting prevalence rates for cases below 75 per cent weight-for-age, that is, only second and third degree (14–16).

Recognizing these problems, as well as those related to the use of percentages to express anthropometric indicators, the World Health Organization (WHO) advocated expressing the deviation from the anthropometric measurement of the reference median in terms of standard deviations or Z scores, and strongly urged the adoption of the NCHS reference population data (17) as normative values for international use. To use the Z-scores method, the NCHS/CDC growth reference curves had to be transformed into a Z-score representation with approximately normal distribution (18, 19). Normalized growth curves developed at the Centers for Disease Control are being used worldwide since 1978 to assess the nutritional status of populations. WHO also proposed that the normal range for any population should be between plus and minus two standard deviation (±2 S.D.) units of the median (2, 8–10), a range that includes 95.4 per cent of the reference population, and would yield only about 2.3 per cent false positives on each side.

Besides its statistical justification, the WHO cut-off point, below which the values are seen as potentially abnormal, has been further supported by studies of "functional outcomes" showing a significant increase in the risk of death (20–24), as well as a decreased immune response (25) when anthropometric indicators drop below such a point. Thus, the WHO recommendation has been generally adopted (10, 26) and the cut-off point at two standard deviation units below the reference median (or the third percentile) has been widely used lately for estimating the prevalence of malnutrition in national surveys.

As expected, however, the shift of the cut-off point from one to two standard deviations resulted in dramatically lower prevalence rates of malnutrition in developing countries, thus suggesting that, in contrast with the former cut-off point, the latter might tend to underestimate the magnitude of the problem. WHO then suggested (27), as part of its methodology for measuring change in nutritional status, using either one or two standard deviations as the dividing line between normality and abnormality, but adjusting the resulting prevalence by subtracting the proportion of cases expected below such a cut-off point in the normal distribution (either 15.9 per cent or 2.3 per cent).

This adjustment for "false positives" does not really solve the problem, since applying either of the two cut-off points to a given population yields quite contrasting prevalence estimates. As an example, the following disparate figures result from using the two cut-off points and their corresponding adjustments with the weight-for-age data of the 1977–80 Colombian National Health Survey (28):

<table>
<thead>
<tr>
<th>Cut-off points</th>
<th>Measured prevalence (%)</th>
<th>Adjustment (%)</th>
<th>Adjusted prevalence (%)</th>
</tr>
</thead>
<tbody>
<tr>
<td>- 1 S.D.</td>
<td>49.2</td>
<td>-15.9</td>
<td>33.3</td>
</tr>
<tr>
<td>- 2 S.D.</td>
<td>16.9</td>
<td>-2.3</td>
<td>14.6</td>
</tr>
</tbody>
</table>

Clearly, in spite of the WHO-suggested adjustment, arbitrary cut-off points selected for prevalence studies have profound implications, and might be misused for non-scientific purposes to comply with political and other interests. A floating cut-off point could indeed be moved up or down depending on whether the interest is to dramatize the seriousness of the problem or to show that it is of much less magnitude. Keller has recently contended that "if reasonable simple statistical methods were available,
it would be more desirable to compare distributions rather than prevalences, which to some degree distort biological realities” (29).

Nutritional anthropometry as a diagnostic test

Nutritional anthropometry may be conceived as a diagnostic test to identify and count the malnourished by classifying persons as malnourished or well-nourished in relation to a specific level of the diagnostic indicators (4). As such, it would be composed of both an indicator and a cut-off point for that indicator which, as in other diagnostic tests, results in some misclassification of subjects. Thus, while some well-nourished individuals may be wrongly classified as malnourished (false positives), some malnourished persons are classified as well-nourished (false negatives). This is because of the usual overlapping of the distribution of biological indicators among the diseased and the non-diseased individuals. The ideal cut-off point for a given indicator would be one which results in a complete separation of normals from abnormalities within the population (3).

A diagnostic test is supposed to reflect a true underlying reality, usually a disease entity, which is accurately diagnosed or directly measured by other means. However, in the case of nutritional anthropometry, valid external criteria and instruments for a direct measure (diagnosis) of the true reality (e.g., nutritional status/body composition) are not readily available. In the absence of objective criteria for diagnosis, the following three basic approaches are used in clinical epidemiology to set up criteria for abnormality, which may be defined either as being sick, being treatable, or being unusual (30):

(a) The identification of a significant association (and eventually break-off or threshold points) between the test indicator(s) and changes in functional outcomes, such as the risk of health impairment, disability or death. This approach has been attempted in evaluating anthropometric indicators using either concurrent (immune response) or long-term (mortality) functional outcomes (20–25). Unfortunately, these validation criteria are not totally appropriate because such functional outcomes are known to be affected by factors other than nutritional status, which is the true underlying reality of concern.

(b) The demonstration of selective response to a treatment intended to modify a disease determinant in subjects chosen on the basis of the results of the diagnostic test, as in iron-deficiency anaemia (31).*

This approach can rarely be used in population work, and it is clearly of no use with weight indicators because the weight response to increased food intake may well exceed desirable healthy limits.

(c) The so called “normative reality” (3, 30), using probability estimations based on the statistical properties of the normal distribution of values from a supposedly healthy reference population. This implies comparing the observed values of an indicator with those derived from a known normal population (e.g., the NCHS reference values obtained from a well-nourished, healthy population growing under optimal environmental conditions), and considering those values outside the normal population as abnormal.

The normative reference values are seen as representing the underlying reality, and their distribution is supposed to meet the statistical properties of the normal distribution, provided that all the abnormalities and only the abnormals were excluded. The reference population distribution of anthropometric values is thought to reflect only the individual variability of the genetic potential for growth, which is expected to be fully realized under presumably optimal environmental conditions. This normative reality is the implicit basis of anthropometry reference values and provides the best known criteria for identifying the malnourished, and is therefore a useful yardstick for prevalence estimates in cross-sectional assessments.

Method

The prevalence of child malnutrition, as defined by anthropometric abnormality, could be estimated on the basis of the normative reality by using the following well-known simple formula:

\[
SP = MP - FP + FN
\]

where \( SP \) = standardized prevalence, defined as the proportion of individuals in the observed population who are outside the normal distribution of the referent population; \( MP \) = measured prevalence, calculated from the observed population as the proportion of children under a given cut-off point of the reference population; \( FP \) = false positives, estimated as the proportion of values expected under the cut-off point in the reference population; \( FN \) = false negatives, estimated as the excess proportion of subjects above the cut-off point in the observed population as compared to the reference population distribution.

In most populations, the three common anthropometric indicators (weight-for-age, length or height-for-age, and weight-for-height or length) have bell-
shaped, more or less symmetrical distributions (2, 8, 10, 27–29). In developing countries, the distribution of anthropometric indicators is approximately Gaussian but shifted to the left of the normal distribution of the reference population, with only a slight skewness and a variable degree of overlapping depending on the distance between the two distributions. As an example, Fig. 1 shows a hypothetical Gaussian distribution of a population indicator whose mean is one standard deviation to the left of the reference population distribution (i.e., its mean standardized Z-score is -1.0) and its standard deviation is also 1.0. There is some overlapping between the two curves, and their intersection occurs at half the distance between their means; this is always the case when the standard deviation of both distributions is of the same size.

Adjusting only for false positives, as suggested by WHO, would tend to underestimate the prevalence of malnutrition. By adjusting for both false positives and false negatives, a standardized and more accurate estimation of the prevalence would be obtained. Calculating the proportions of false positives at a given cut-off point is a straightforward procedure; they are defined as the proportion of cases found below that point in the normal distribution of the reference population, e.g., 15.9 per cent below one standard deviation and 2.3 per cent below two standard deviations of the reference mean. As seen in Fig. 1, the proportion of false positives (i.e., area (c) for two standard deviations below the mean, and areas (c) plus (d) for one standard deviation) exclusively depends on the cut-off point used, regardless of the distance between the curves; their calculation can be mathematically expressed using the cumulative distribution function (c.d.f. = \( \Phi \)) of the standardized normal curve (32), as FP = \( \Phi (-K) \), where

\[-K = \text{cut-off point.}\]

Unlike the false positives, the proportion of false negatives would depend not only on the cut-off point but also, to a great extent, on the degree of overlapping, i.e., on the closeness of the two curves. False negatives may be defined as the excess proportion of cases found in the observed population above the cut-off point, as compared to the reference population. Thus, in Fig. 1, area (b) would represent the proportion of false negatives for a cut-off point of one standard deviation, and areas (a) plus (b) for two standard deviations. It should be noted that false negatives are located in the interval between the cut-off and the intersection of the two curves.

The estimation of the proportion of false negatives can also be expressed mathematically using the c.d.f. of the normal curve. Both (a) and (b) or any other excess fraction of the observed population distribution can be estimated (from the table of areas under the normal curve (32)) as the difference in the proportion of cases between the corresponding equivalent intervals of the reference and the observed population, provided that the two distributions are Gaussian and the distance between the two curves is expressed in units of standard deviation (Z-scores) of the reference population, i.e., as the mean (or median) standardized Z-score of the observed population indicator.

In Fig. 1, the proportion of false negatives for a cut-off point (K) of -2.0Z can be estimated as the difference between the proportion of the population expected from -1.0Z to +0.5Z as seen in the observed curve at the left (areas a + b + d + e), and that from -2.0Z to -0.5Z as seen in the reference curve at the right (areas d + e). These proportions can be calculated from the Table of areas under the normal probability curve (32), as follows:

\[
\begin{align*}
-1.0Z & \text{ to } 0 & = 0.8413 - 0.5000 & = 0.3413 \\
+0.5Z & \text{ to } 0 & = 0.6915 - 0.5000 & = 0.1915 \\
0.0Z & \text{ to } 0.5Z & = 0.3413 + 0.1915 & = 0.5328 \\
2.0Z & \text{ to } -0.5Z & = 0.9773 - 0.6915 & = 0.2858 \\
(a) + (b) & = 0.5328 - 0.2858 & = 0.2470 & = 24.7 \text{ per cent}
\end{align*}
\]

Similarly, false negatives for \( K = -1.0 \) (area b) would be:

\[
\begin{align*}
+0.5Z & \text{ to } 0 & = 0.6915 - 0.5000 & = 0.1915 \\
-1.0Z & \text{ to } -0.5Z & = 0.8413 - 0.6915 & = 0.1498 \\
(b) & = 0.1915 - 0.1498 & = 0.0417 & = 4.2 \text{ per cent}
\end{align*}
\]

Standardized prevalence rates for different cut-off points and distances between similar Gaussian curves with standard deviations of one Z have been calculated in Table 1, after adjusting the measured prevalence for the proportion of both false positives and false negatives. Theoretical calculations have been made for distances between the two curves (differences between means or medians) equivalent to 1.0, 1.5 and 2.0 standard deviations of the reference
Table 1: Estimated percentage prevalence of malnutrition at selected cut-off points for different distances (in Z-scores) between the observed and the reference population distributions of an anthropometric indicator (when the observed standard deviation is equal to one)

<table>
<thead>
<tr>
<th>Mean Z-score</th>
<th>Cut-off point ((-K))</th>
<th>Measured prevalence (MP)</th>
<th>False positives (FP)</th>
<th>False negatives (FN)</th>
<th>Standardized prevalence (SP)</th>
<th>Difference (MP – SP)</th>
</tr>
</thead>
<tbody>
<tr>
<td>0.5</td>
<td>1.00</td>
<td>30.9</td>
<td>15.9</td>
<td>4.7</td>
<td>19.7</td>
<td>11.2</td>
</tr>
<tr>
<td></td>
<td>1.28 (P10)</td>
<td>21.7</td>
<td>10.0</td>
<td>8.0</td>
<td>19.7</td>
<td>2.0</td>
</tr>
<tr>
<td></td>
<td>1.50</td>
<td>15.9</td>
<td>6.7</td>
<td>10.5</td>
<td>19.7</td>
<td>-3.8</td>
</tr>
<tr>
<td></td>
<td>1.88 (P3)</td>
<td>8.3</td>
<td>3.0</td>
<td>14.4</td>
<td>19.7</td>
<td>-11.4</td>
</tr>
<tr>
<td></td>
<td>2.00</td>
<td>6.7</td>
<td>2.3</td>
<td>15.3</td>
<td>19.7</td>
<td>-13.0</td>
</tr>
<tr>
<td>1.0</td>
<td>1.00</td>
<td>50.0</td>
<td>15.9</td>
<td>4.2</td>
<td>38.3</td>
<td>11.7</td>
</tr>
<tr>
<td></td>
<td>1.28 (P10)</td>
<td>39.0</td>
<td>10.0</td>
<td>9.3</td>
<td>38.3</td>
<td>0.7</td>
</tr>
<tr>
<td></td>
<td>1.50</td>
<td>30.9</td>
<td>6.7</td>
<td>14.1</td>
<td>38.3</td>
<td>-7.4</td>
</tr>
<tr>
<td></td>
<td>1.88 (P3)</td>
<td>18.9</td>
<td>3.0</td>
<td>22.4</td>
<td>38.3</td>
<td>-19.4</td>
</tr>
<tr>
<td></td>
<td>2.00</td>
<td>15.9</td>
<td>2.3</td>
<td>24.7</td>
<td>38.3</td>
<td>-22.4</td>
</tr>
<tr>
<td>1.5</td>
<td>1.00</td>
<td>69.2</td>
<td>15.9</td>
<td>1.4</td>
<td>54.7</td>
<td>14.5</td>
</tr>
<tr>
<td></td>
<td>1.28 (P10)</td>
<td>58.7</td>
<td>10.0</td>
<td>6.0</td>
<td>54.7</td>
<td>4.0</td>
</tr>
<tr>
<td></td>
<td>1.50</td>
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<td>6.7</td>
<td>11.4</td>
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<td></td>
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<td>3.0</td>
<td>22.5</td>
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<td>2.00</td>
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<td>2.3</td>
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<tr>
<td>2.0</td>
<td>1.00</td>
<td>84.2</td>
<td>15.9</td>
<td>0</td>
<td>68.3</td>
<td>15.9</td>
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<td></td>
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<td>76.4</td>
<td>10.0</td>
<td>1.9</td>
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<td></td>
<td>1.88 (P3)</td>
<td>54.8</td>
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<td>16.5</td>
<td>68.3</td>
<td>-13.5</td>
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<tr>
<td></td>
<td>2.00</td>
<td>50.0</td>
<td>2.3</td>
<td>20.6</td>
<td>68.3</td>
<td>-18.3</td>
</tr>
</tbody>
</table>

* SP = MP – FP + FN

\* P10 and P3 refer to the 10th and 3rd percentile, respectively.

values, and for commonly used cut-off points at 1.28 (10th percentile) and 1.88 (3rd percentile) standard deviations below the reference median.

For a given distance between curves, the same standardized prevalence rate is found irrespective of the cut-off points (indeed, there is only one cut-off curve). As expected, the prevalence is a function of the distance between the observed and the reference curve and not of the cut-off points; in fact, these become irrelevant when the prevalence is estimated by adjusting the measured prevalence for the proportions of both false positives and false negatives, as calculated by the method proposed here.

It is also observed in Fig. 1 that, when the standard deviation of the observed distribution is also one, a cut-off point located at half the distance between the two Gaussian curves would yield no false negatives, thus making it possible to obtain standardized prevalence estimates from the measured prevalence adjusted (by subtraction) for false positives only, as proposed by WHO. In this case, SP = MP – FP. Therefore, this adjustment is appropriate only for that particular cut-off point when the observed distribution is nearly normal and its standard deviation is one.

When the above definitions of false positives and false negatives are applied, it then becomes clear that the estimated standardized prevalence is represented by the shaded area in Fig. 1, i.e., by that portion of the observed distribution that does not overlap (it is indeed outside) the reference population distribution. Thus a statistical method could be developed to compare the two distributions as suggested by Keller (29), using a cut-off curve rather than a cut-off point. The method would be based on the presumption that under optimal environmental conditions everybody will grow within the bound-

![Fig. 1. Overlapping of the Gaussian distributions of an anthropometric indicator in the observed and in the reference population. The shaded area represents the standardized prevalence of abnormality in the observed population.](image-url)
Table 2: Estimated prevalence of abnormality for different mean Z-scores and standard deviations of a normally distributed anthropometric indicator

<table>
<thead>
<tr>
<th>Z-score</th>
<th>Mean</th>
<th>Standard deviation</th>
</tr>
</thead>
<tbody>
<tr>
<td>0.00</td>
<td>1.00</td>
<td>1.05</td>
</tr>
<tr>
<td>0.05</td>
<td>1.05</td>
<td>1.10</td>
</tr>
<tr>
<td>0.10</td>
<td>1.10</td>
<td>1.15</td>
</tr>
<tr>
<td>0.15</td>
<td>1.15</td>
<td>1.20</td>
</tr>
<tr>
<td>0.20</td>
<td>1.20</td>
<td>1.25</td>
</tr>
<tr>
<td>0.25</td>
<td>1.25</td>
<td>1.30</td>
</tr>
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<td>1.35</td>
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<td>0.35</td>
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<tr>
<td>0.95</td>
<td>1.95</td>
<td>2.00</td>
</tr>
</tbody>
</table>

For example, for a Z-score of 0.00, the mean is 1.00 and the standard deviation is 1.05. This allows straightforward calculations based on the observed mean Z-score and standard deviation. This formula makes use of the cumulative distribution function (c.d.f.) of the normal probability curve; thus the underlying assumption is that the observed distribution is nearly normal. The estimated stan-
standardized prevalence (SP) can be obtained by using the following formula:

$$SP = \Phi_0\left(\frac{Z - \sigma \sqrt{Z^2 + 2\sigma^2 \ln \sigma - 2 \ln \sigma}}{1 - \sigma^2}\right) + \Phi_0\left(\frac{Z\sigma - \sqrt{Z^2 + 2\sigma^2 \ln \sigma - 2 \ln \sigma}}{1 - \sigma^2}\right) \quad (\sigma > 1)$$

where $\Phi_0$ = c.d.f. of the standardized normal distribution; $Z$ = mean standardized Z-score of the observed population; $\sigma$ = standard deviation of the standardized Z-scores of the observed population.

For the special case of $\sigma = 1$,

$$SP = 2\Phi_0\left(\frac{Z}{2}\right) - 1$$

The calculation of Z-scores of anthropometric indicators usually requires computer facilities and software (e.g., the CDC software package for the analysis of anthropometric data (33)). To facilitate a rapid assessment of prevalence whenever the observed distribution of Z-scores is approximately normal, Table 2 shows the mathematically estimated prevalence rates for increasing mean Z-scores (from zero to 2.50) and standard deviations (from 1.00 to 2.00) of the observed distribution. These ranges would cover most, if not all, probable values to be found in anthropometric studies of prevalence. As an example, for a population whose mean Z score and standard deviation for an anthropometric indicator are 1.50 and 1.20, respectively, the estimated prevalence of malnutrition would be 50.9 per cent, as indicated by the intersection of the two values in Table 2. Estimates were obtained using a special computer program.

The accuracy of these estimates to reflect the true standardized prevalence rates is obviously contingent upon the extent to which both the reference values and the observed Z-scores are normally distributed. In most populations the distribution of height-for-age is approximately normal, whereas those of weight-for-age and weight-for-height are somewhat skewed (2, 8, 10, 27–29). The original NCHS/CDC reference distributions of weight-for-age and weight-for-height were slightly skewed; thus in constructing the normalized NCHS reference tables (18) the population was divided into two halves at the median, and standard deviations were calculated for each half.

The frequent skewness in the distributions observed in developing countries may introduce some underestimation in the calculations; however, exact estimations applying our method to actual data from nutrition surveys in developing countries showed that the magnitude of the error is negligible (under 10% of the total prevalence) compared with the one resulting from the presence of false positives and false negatives when using conventional cut-off points. Therefore, distributions of anthropometric indicators can be compared to the normalized NCHS/CDC reference, and standard analytical tests based on the assumption of a normal distribution can be applied to the Z-values so derived (34). Although adjusting for skewness in prevalence estimates is theoretically feasible, for practical purposes this would be an unnecessary sophistication.

The differences in the prevalence estimations between the method proposed here and the Gomez and WHO methods are graphically shown in Fig. 2, using estimates for increasing negative mean Z-scores with standard deviation of 1.0Z. The largest differences occur between 0.5Z and 2.0Z, which is the range covering most common situations in developing countries, and become negligible above 3.0Z, which is likely to be found only in extreme famine conditions.

**Discussion**

The method here proposed for estimating the standardized prevalence of child malnutrition in population studies provides a useful tool for standardizing
the analysis of anthropometric data from cross-sectional surveys for the assessment of the nutritional status in the community. The method yields useful estimates of the population prevalence by comparing the observed and the reference population distributions of the anthropometric indicator, as suggested by Keller (29), using a cut-off curve rather than a cut-off point. The same method can be used for estimating a standardized prevalence of overweight. For comparison purposes, standard statistical tests can be applied to the mean Z-scores and standard deviations of the observed distributions.

Standardized prevalence rates can be obtained from Table 2 for any of the anthropometric indicators, provided that it is expressed in terms of Z-scores of the normalized NCHS/CDC reference population and that its distribution is nearly normal and not grossly skewed. Standardized prevalence is defined as the proportion of cases in that portion of the observed distribution which does not overlap the normal reference population distribution, and its estimation is based on the mathematical properties of the normal probability curve, even when the standard deviation of the observed distribution is different from one (indeed, it is usually greater than one).

Our concept of standardized prevalence challenges the traditional epidemiological dogma calling for case definition and counting of individual cases to estimate disease prevalence. Indeed, the case definition approach is impractical when there are no feasible means to individually identify "false positives" and "false negatives" so as to count only the true diseased, as is the case in nutritional anthropometry. A different approach for estimating a standardized population prevalence is used which does not look at individual cases but at the whole distribution of groups of individuals. The principles of this "mixed distribution analysis" method have been used for estimating the prevalence of anaemia as the proportion of individuals whose haemoglobin values are shifted downwards relative to a distribution of haemoglobin values of non-anaemic individuals (35, 36).

By using this method, cut-off points become irrelevant for prevalence estimates, thus making any further controversy on the topic actually unnecessary. Cut-off points would remain important for screening purposes, when the aim is setting targets for action rather than estimating prevalence rates; in this case, the best level for screening would be the one that yields just the proportion of individuals for which the resources suffice (3). Cut-off points may also be useful for educational purposes, such as in the charts commonly used in growth monitoring.

The proposed method is obviously not applicable for the individual assessment of nutritional status. As it is totally based on the mathematical properties of the normal probability distribution, its outcome is a standardized population estimate and not an individual diagnosis. In fact, for a given individual value of an indicator within the area of overlapping, it will be practically impossible with that information alone to ascertain whether or not it belongs to the reference population; this is also true with the adjustment for false positives suggested by WHO (27). The individual assessment of nutritional status should be based on longitudinal observations of growth (incremental growth, growth curves), complemented by clinical and other evaluations.

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Résumé

Nouvelle méthode pour évaluer la prévalence normalisée de la malnutrition infantile à partir des indicateurs anthropométriques

Les mesures et indicateurs anthropométriques servent couramment à évaluer l'état nutritionnel des individus et des populations. Dans les pays en développement, on les utilise dans des enquêtes transversales pour évaluer la prévalence de la malnutrition chez les enfants. Les estimations de la prévalence sont généralement fondées sur des seuils conventionnels pour les valeurs de référence obtenues dans des populations censées être bien nourries. Toutefois, les divergences d'opinion quant au choix de ces seuils empêchent d'utiliser des méthodes analytiques normalisées pour calculer les taux de prévalence. La correction recommandée par l'OMS pour tenir compte des faux positifs produit des résultats non concordants lorsque la valeur seuil utilisée est différente. Des seuils "flottants" pourraient être utilisés à des fins non scientifiques.

Une méthode normalisée a été mise au point pour estimer la prévalence de la malnutrition (caractérisée par des indicateurs anthropométriques inférieurs à la norme) à l'aide de la
La formule suivante :

\[ SP = MP - FP + FN \]

avec :

- SP = Prévalence normalisée, définie par la proportion des individus de la population observée qui sont en dehors de la distribution normale de la population de référence ;
- MP = Prévalence mesurée, calculée comme étant la proportion d’individus au-dessous d’un seuil donné de la population de référence ;
- FP = Faux positifs, soit la proportion estimée d’individus que l’on s’attend à trouver au-dessous du seuil de la population de référence.
- FN = Faux négatifs, soit la proportion excédentaire de sujets qui se trouvent au-dessus du seuil dans la population observée par comparaison avec la distribution de la population de référence.

La prévalence estimée est essentiellement fonction de la distance entre la distribution observée et la distribution de référence. Une méthode statistique a été mise au point pour comparer les deux distributions et estimer un taux de prévalence normalisée, selon la définition ci-dessus. La formulation mathématique fait appel à la fonction de distribution cumulative de la courbe normale de probabilité ; elle est fondée sur les écarts moyens (Z-scores) observés et sur l’écart-type. L’hypothèse fondamentale est que les distributions de la population observée et de la population de référence sont à peu près normales.

Pour faciliter l’évaluation rapide de la prévalence, on a établi à l’aide d’un ordinateur une table qui indique les taux de prévalence estimés mathématiquement pour des valeurs négatives croissantes de l’écart moyen et de l’écart-type, et qui couvrent les valeurs les plus susceptibles d’être rencontrées dans les études anthropométriques de prévalence. Les valeurs estimées sont plus faibles que celles obtenues par la méthode de la classification de Gomez et plus élevées que celles qui résultent de l’application de la méthode recommandée par l’OMS, méthode qui consiste à fixer le seuil à deux écarts-types au-dessous de la moyenne de la population de référence.

Notre conception de la prévalence normalisée remet en question le dogme épidémiologique traditionnel qui repose sur une définition des cas et sur le comptage des cas individuels pour estimer la prévalence d’une maladie. Notre méthode ne consiste pas à examiner les cas individuels, mais à appliquer les principes de l’analyse des distributions mixtes et à comparer les distributions en considérant le seuil comme une ligne plutôt qu’un point. De même que la correction recommandée par l’OMS pour tenir compte des faux positifs, cette méthode ne s’applique évidemment pas à l’évaluation de l’état nutritionnel des individus ; elle fournit une estimation normalisée de l’état de la population, et non un diagnostic individuel.

References
