A full account of our work will be published elsewhere.

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Economy in Cell Counts

IT is often necessary in clinical work to determine the relative abundance of two or more species of cells. Examples are counts of the percentage of atypical cells, such as reticulocytes, siderocytes or punctate basophilia, in the blood erythrocytes. In these cases the required result, F, is a fraction. If P and Q are the numbers counted of the two types of cell, $F = P/(P + Q)$. In other estimations, such as the 'platelet ratio', or the proportion of megakaryocytes to nucleated white cells in a marrow smear, the required result is a ratio, $R = P/Q$. F cannot exceed unity, while R may have any numerical value.

The frequencies of the two species of cells are often widely different, making it necessary to count thousands of the common type to include a moderate number of the rarer. The questions arise, Can one save time and labour by counting the abundant cells in a fraction $1/a$ of the area sampled for the rarer type? What would be the precision of a value of F or R so obtained? And what are the best values of P and Q to secure a desired precision with a minimum amount of counting?

There are various algebraically equivalent formulæ for the standard deviation of a ratio or a fraction. The forms most useful for the present purpose are

$$\frac{\text{Standard deviation of } R}{R} = \sqrt{\frac{1}{P} + \frac{1}{Q}} \quad . \quad (1)$$

$$\frac{\text{Standard deviation of } F}{F(1 - F)} = \sqrt{\frac{1}{P} + \frac{1}{Q}} \quad . \quad (2)$$

Now it can be shown that when P and Q are sampled on different scales, so that $R = P/aQ$ or aP/Q, and $F = P/(P + aQ)$ or $aP/(aP + Q)$, formulæ 1 and 2 are still true and applicable. It can further be proved that, for any given value of the standard deviation, the number of cells required to be counted is a minimum when $P = Q$. Hence the simple practical rule: choose that value of $1/a$ which will make the counts of the two kinds of cell as near equality as possible.

It is easy to see the commonsense justification of this rule. There is no point in laboriously measuring Q to an accuracy of 1 in 1,000 when P is accurate only to within 1 in 10.

When there is a big disparity in the frequencies of the two kinds of cell, the time saved by this method of 'balanced sampling' is very great. For example, in blood containing 2 siderocytes per 1,000 red corpuscles, a count of 80 cells by balanced sampling will give an answer as precise as a direct count of 10,000 cells. In general, if a is chosen to make $P = Q$, the total number of cells to be counted in balanced sampling is the fraction $4a/(a + 1)^2$ of the number needed in a direct count, for the same precision of estimate.

This method has the further advantage that a count of a given size always yields an estimate with approximately the same relative precision. One can therefore work out once and for all the numbers to be counted for any desired limits of significance, and choose the appropriate size of count for each particular purpose. There will then be no need to calculate standard deviations and significances of differences separately for each estimate.

I am publishing elsewhere a full account, giving details of the practical use of the method in cell counting. It is obvious that balanced sampling has many other uses. The technique here described is a special application of a general theory of weighted and stratified sampling, to be published elsewhere.

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Empirical Data on Hilbert's Inequality

IT is known that

$$\sum_1^\infty \sum_1^\infty \frac{a_r a_s}{r + s - 1} \leqslant \pi \sum_1^\infty a_r^2,$$

π being the best possible constant, and it has recently been shown by H. Frazer[1] that

$$\sum_1^N \sum_1^N \frac{a_r a_s}{r + s - 1} \leqslant \left(N \sin \frac{\pi}{N}\right) \sum_1^N a_r^2.$$

Frazer's result, however, is not the best possible, as may be seen from the numerical data below, in which λ is the maximum value of

$$\sum_1^N \sum_1^N \frac{a_r a_s}{r + s - 1}$$

for a normalized vector a_r. We are indebted to the Royal Aircraft Establishment, Farnborough, and to Mr. Fairthorne for the computation of these data.

N	λ		
1	1		
2	1·267	591	879
3	1·408	318	927
4	1·500	214	280
5	1·567	050	691
10	1·751	919	657
20	1·907	134	681

Approximate relations of the form

$$\frac{1}{\pi - \lambda} = a \log (N + b) + c$$

can be obtained to fit these data, with errors at the most of 0·001 up to $N = 10$, but an error of 0·005 for $N = 20$. It is evident from the behaviour of the errors that the formula is incomplete.

The values of λ for all values from 1 to 20 are at present being calculated for us at the National Physical Laboratory. The results will be published as soon as available.

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