

Figure 2. Circuit diagram of the pulse-amplifier P.

the density in the cylinder quite low, especially when presetting a small number.

Experience has shown that the counting error in replicates of 100 *Artemia* larvae per vial is less than 2%, each vial being filled in about 20 seconds, sampled from a batch with approximately 5 nauplii/ml.

The counter can also be used to determine the density of organisms in a batch, simply by presetting the counter at a certain number and determining the volume poured through the system in calibrated cylinders.

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A note on the estimation of the species-area curve

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In a recent paper Holthe (1975) considered the problem of estimating points on the so called speciesarea curve. The formula arrived at, was constructed for the following practical situation: N samples are drawn from a population. It is understood that the samples are comparable, that is, obtained by approximately the same method of sampling. We are only concerned with the presence or absence of species in each particular sample, so that the abundance of each species is not necessarily known. The problem is now to estimate the total number of species expected to be found if $n \leq N$ samples were taken. By arguments taken from the set theory, Holthe arrived at the formula

$$s_n = \sum_{r=1}^{n} \left[\frac{\binom{n}{r}}{\binom{N}{r}} (-1)^{r+1} \sum_{i=1}^{s} \binom{p_i}{r} \right], \qquad (1)$$

where s_n is the estimated mean number of species found when *n* samples are taken, *s* is the total number of species found in all *N* samples together, and p_t is the number of samples in which species no. *i* is represented. When *N* and *n* are large, it is quite laborious to carry out the numerical calculations, and Holthe has pointed out to me (personal communication) the need for simplification of (1).

Holthe applied the result to marine biological data, but the formula would also be suitable for analysing plant communities, since it is often difficult to make a distinction between individual plants, or the concept of individual plants is not valid at all. In Holthe's argument, and in the one to be presented, no assumptions are made about the distribution of individuals in the field, whether it is random or contagious. The fact that our knowledge about spatial distributions is often poor obviously amplifies the need for models like this. Notice, as a special case, that if the individuals are randomly distributed in the field we may very well define each individual as a sample itself, even if they are sampled in groups.

It turns out, as will be shown below, that (1) may be written in the much simpler form

$$s_{n} = s - \sum_{i=1}^{s} \frac{\binom{q_{i}}{n}}{\binom{N}{n}}$$

= $s - \sum_{i=1}^{s} \frac{q_{i}(q_{i}-1)\dots(q_{i}-n+1)}{N(N-1)\dots(N-n+1)}$, (2)

where $q_i = N - p_i$.

The species-area curve estimated by (2) can now be compared to theoretical curves deduced assuming certain patterns in the species abundances (Fisher, Corbet & Williams, 1943; Engen, 1974). Hence, conclusions about the underlying structure of the community under consideration may be drawn.

We first derive (2) by a probability argument, and then show the equivalence between (1) and (2). Define the random variables X_i , i = 1, 2, ..., s, by

 $X_i = \begin{cases} 1 & \text{if species no. } i \text{ is represented in at least one} \\ & \text{of } n \text{ samples drawn at random from the} \\ & \text{total of } N. \end{cases}$

Then
$$s_n = E\left(\sum_{i=1}^{N} X_i\right) = \sum_{i=1}^{N} E(X_i).$$

Now $E(X_i) = Pr(X_i = 1) = 1 - \frac{\binom{q_i}{n}}{\binom{N}{n}}.$

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By summation (2) follows immediately.

To show that (1) and (2) are really equivalent, we first change the order of summation in (1), giving

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$$s_n = \sum_{i=1}^{s} \sum_{r=1}^{n} \frac{\binom{n}{r}\binom{p_i}{r}}{\binom{N}{r}} (-1)^{r+1}.$$
 (3)

Now, writing m for any of the p_i 's, the equivalence follows by proving that

$$\sum_{r=1}^{n} \frac{\binom{n}{r}\binom{m}{r}}{\binom{N}{r}} (-1)^{r+1} = 1 - \frac{\binom{N-m}{n}}{\binom{N}{n}}, \quad (4)$$

$$n, m \leq N.$$

That (4) holds may be shown by a "balls in box" model. Let there be N balls, m blacks, and N - m whites. We draw n balls at random and write A for the event that at least one of them is black. Further, let B_j , j = 1, 2, ..., n, denote the event that the j'th ball selected at random is black. Then

$$A=\bigcup_{j=1}^n B_j.$$

We can immediately write down that

$$Pr(A) = 1 - \frac{\binom{N-m}{n}}{\binom{N}{n}},$$

which is the right side of (4). By a general theorem (Feller, 1968; p. 99) we also have

$$Pr\left(\bigcup_{j=1}^{n} B_{j}\right) = \sum_{i=1}^{n} Pr(B_{j}) - \sum_{j < k} Pr(B_{j} \cap B_{k}) + \dots + (-1)^{n+1} Pr(B_{1} \cap B_{2} \dots \cap B_{n}).$$

Now,
$$Pr(B_{i,1} \cap B_{i,2} \cap \ldots \cap B_{i,r}) = \frac{\binom{m}{r}}{\binom{N}{r}}$$
, and the

sum in which terms of this type are involved has $\binom{n}{r}$ terms. It follows that

$$Pr\left(\bigcup_{j=1}^{n} B_{j}\right) = \sum_{r=1}^{n} \frac{\binom{n}{r}\binom{m}{r}}{\binom{N}{r}} (-1)^{r+1},$$

which proves that the two formulas are identical.

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