veloped even further any satisfactory genetic theory would have to invoke a new type of biological uncertainty principle. In the discussion which followed Bohr stood up, and much in the manner used in seminars so often by Delbrück, stated simply "I don't believe a word of it".

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Influenza viruses and comets

SIR—Henderson *et al.*¹ congratulate themselves in the belief that they have demolished our hypothesis that influenza viruses may be connected with comets². Their argument, ostensibly based on phylogeny, is contingent on constraints that they themselves have imposed. Consequently, their conclusions have no relevance to our original cometary model. The assumption that "the simplest comet model is that different isolates of H1 influenza are carried on different comets, having developed independently . . ." is not one to which we ourselves would subscribe, nor are any of the subsidiary postulates they consider.

Contrary to the statement that there is a lack of a "slow-mixing compartment in the atmosphere", we have repeatedly shown that viral-sized particles introduced into the upper atmosphere from outside have a residence time of a decade or more. Such particles are pulled down seasonally, following closely the patterns of atmospheric circulation on a global scale. Seasonal influenza peaks separated by six months in opposite hemispheres are fully consistent with this picture.

There is no requirement in our model for viral additions from comets to take place any more frequently than about once a decade, corresponding to the observed major genetic shifts in the influenza virus. The more frequently occurring changes (designated genetic drift), which are essentially what Henderson *et al.* have mapped, are in our view no more than a sorting out of an initial viral mix according to developing immunities in host populations.

With each cometary inoculation a wide range of closely related viral sequences will be introduced into the upper atmosphere to be pulled down subsequently to ground level. The immunity systems of host species are thus confronted on a seasonal basis with a range of viral genotypes, but only one or two would be permitted to 'take' in any particular season. Such a selective response of the lymphoid system, which is the basis of the immune mechanism, would appear to be well documented. As immunity evolves, influenza sub-types circulating earlier will become replaced in subsequent seasons by

sub-types that would appear to be slightly altered. The 'evolutionary' changes charted by Henderson *et al.* are therefore irrelevant to the evolution of the virus but are connected with a progressive development of immune responses in host species.

Next, it is worth noting that the number of independent comets responsible for carrying the influenza virus need not be as large as it has been assumed. We have recently speculated that emissions from different parts of the same comet occurring in different transits may contribute to inoculations that lead to the observed genetic shifts³.

The strongest evidence against a purely Earth-bound theory of influenza is to be found in data that in our view goes decisively against a simple person-to-person transmission hypothesis. All the available epidemiological evidence is consistent with a model where the causative agent (or a trigger for it) is airborne and is brought down seasonally from a reservoir established in the stratosphere⁴.

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Values in Taylor's law of spatial distribution

SIR—Downing¹ has recently recommended that the values of b in Taylor's^{2,3} empirical law $s^2 = am^b$, describing the relationship between the sample variance s^2 and the sample mean m of the numbers of animals or plants of a species, obtained from groups of replicate samples, should not be used in comparing different mechanisms underlying the spatial distribution of natural populations, owing to statistical bias. However, if different probability models lead to different ranges of values of the parameter β in a relationship of the form $\sigma^2 = \mu^\beta$, where μ and σ^2 denote the true (population) mean and variance of the counts within a group rather than their sample estimates, it may nonetheless be pertinent to use β as a basis for distinguishing between models. Downing uses the slope of a linear regression of $\log s^2$ against $\log m$ as his estimator b of β , and this may well be a biased procedure. However, the estimator b is not the only estimator of β to be used in the literature⁴, nor does bias in b preclude the existence of more reliable estimators of β . Indeed, simply applying bias-correcting techniques to b , such as the jack-knife or bootstrap, might be expected to yield better results. Furthermore, the bias of potential estimators of β in

small studies could be directly investigated, by examining their performance when used with randomly chosen subsets of the large datasets for *Papillia japonicum* and *Pyrausta nubilalis* discussed by Downing¹.

Choosing the correct model underlying spatial distribution is a difficult problem; distinguishing between parameters and their estimates, as elsewhere⁵ in ecology, at least makes the problem clearer.

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Against 'pragmatype'

SIR—The problem experienced by R. H. L. Disney (*Nature* **326**, 251; 1987) is real and encountered by many fellow researchers. A type specimen has to ensure the continued and correct recognition of members of sibling species groups too.

The problem is, what procedure should be followed if the holotype of the first described species of the complex could be assigned with certainty to any of the newly discovered siblings. It is true that a new suitably preserved specimen has to be selected, but do we need a new type of category for this? *The International Code of Zoological Nomenclature* (Vol. 163, Recommendation 75E; 1985) suggests the nomination of neotypes in the case of *nomina dubia* even if type specimens of the nominal species exist.

But do we need to create a new type category, such as Disney's suggested 'pragmatype', to mark such specimens? After all, the holotype of *Megaselia pulicaria* (Fallén) on a pin was in its time as much a pragmatic designation as the same on a slide today. Moreover, the new slide preparation would become an impediment to sensible decisions itself as soon as somebody splits the same taxon further, based on for example electrophoretic characters. A new type would have to be designated again, and if we are consistent yet again under a new type category.

The code covers exactly this and similar situations. It is recommended that neotypes should be designated for *nomina dubia* if, despite the existence of a holotype or a lectotype, it is not possible to resolve a complex zoological problem.

I think our problem and the aims of zoological nomenclature are best served by following the offered solution.

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