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STATISTICS AND TAXONOMY

by F. Martin Brown

I am sorry that I am not here in person to speak to you about the use-
fulness of statistics to the taxonomist. It would be so much easier for me to
speak directly to you than to write. Statistics can be a wonderful tool in any
research, but it can be a dangerous master if sight is lost of the true goal. The
goal of all of us who work with living things, or in any other field of science,
is orderly understanding of the laws that control all material things. Tax-
onomy is a tiny facet of biology but a very important one. Without names to
apply to each recognizable taxon the geneticist, the physiologist, the compara-
tive anatomist, and a host of others must use cumbersome descriptions. The
taxonomist must make use of every tool to give his decisions lasting quality.
Statistics is a tool that taxonomists have, but use all too infrequently.

Before I go further let me define statistics as I see the subject. It is a
study of error, error in its true sense: — wandering. Statistics allow us to
state with precision the degree to which a measurement wanders from its mean
or average condition. If it were possible to study an entire population we could
measure the wandering, or variation, directly. Unfortunately we cannot study
whole populations. We usually have to be content with minute fractions of
populations, rarely as much as a millionth part. We all know that when we
describe a new taxon from a short series we write a better description than is
possible from a single specimen, the type. But if our short series represents only
a millionth part of the population, how sure are we that any statement about
the taxon is valid? In such a case, statistics becomes a tool for the taxonomist.
There are statistical methods devised to tell just how much chance you are
taking. Once you have learned that, it is up to you to decide whether or not
you are willing to take that chance.

There are two kinds of variation with which we deal as taxonomists —
continuous and discrete. Size is a good example of continuous variation. How
many times do you see in an original description something like this: "The new
subspecies is somewhat larger that subspecies A and smaller than B"? All too
often. And what does it mean? It means only that of the tiny fractions of the

population before the investigator, one appears to be intermediate to the others in size. The difference may be a real one but until that difference is tested statistically its import is vague. A simple statistical procedure will tell you the chance you take if you assume that a pair of measurements are different enough to hold true for a very large series drawn from the same populations.

As an example of the use of statistics with a continuous variant, such as size, let us take DOS PASSOS' subspecies *Plebius sæpiolus gertschi*. Here is DOS PASSOS' statement: "The new race differs from nymotypical specimens in being much smaller — the type series averages about 22 mm." The type series consists of 10 males and 8 females from WILLIS GERTSCH's collection and 20 males and 10 females from my own. Let us see how this type series varies from a similar series of Californian *sæpiolus*. First, DOS PASSOS' measure of expanse is a poor one. It depends upon how the pinned specimens were set. A better measure is the maximum radius of the fore wing. That does not depend upon the mechanics of pinning and spreading. Using that measure for the *gertschi* series, I found that the radius of the left forewing averaged 12.37 mm.—the average is carried to the 0.01 mm. for statistical reasons, not for any real meaning beyond that the radius is a little over 12 mm. A series of the same number of males from McCloud, California, had an average radius for the same wing of 14.32 mm., and another such series from Big Meadows, California, 13.90 mm. By simple statistical procedure I demonstrated to myself that there was less than 1 chance in 10,000 that a series of 30 males caught at random at either McCloud or Big Meadows would average the same size as the males in the type series of *gertschi*. On this basis I am willing to accept size as one of the criteria for *gertschi*. So much for continuous variants.

Here is another kind of statement that often leaves you up in the air: "The new subspecies has more fully developed ocelli than the nymotypical insect". Now this is a different kind of variation. The measures run in whole numbers. You do not find individuals with 1.3 ocelli. There are good statistical methods for determining whether or not there is a real difference between the degree to which one series is marked from another. As an example, while studying the variation that occurs in North American *Cænonympha* I was puzzled by a small series of specimens from the Black Hills in South Dakota. It seemed to combine characteristics of both *C. inornata benjamini* from the prairies of Alberta and Saskatchewan and *ochracea* from the Rocky Mountains. My problem was this: Should I treat the Black Hills material as a strain of *inornata* or as a strain of *ochracea*? The decision rested on the degree to which the sub-marginal ocelli on the under side of the hind wings were developed. Good-sized series of males, 40 to 50, from various Canadian prairie localities showed that from 36.6 to 50.9 percent of the specimens of *benjamini* had ocelli on the under side of the hind wings. Of the 10 males I had from Custer, South Dakota, half of them were ocellate. I have several long series of *ochracea* from stations at the edge of the prairie in Colorado and Wyoming that contain individuals without ocelli. It is wholly possible to collect 10 males at any of these Rocky Mountain stations and have one of the specimens without an ocellus on the under side of the hind wings. I doubt that you would ever get

two such unmarked specimens among 10 caught at random. In fact the smallest series I have in which two do appear has over 100 males collected at one time.

Here is the problem: What is the chance of collecting at random 10 male *ochracea* at a Rocky Mountain station 50% of which bear ocelli on the under side of the hind wings?; and, what is the chance of collecting at random 10 male *Cœnonympha* in the Black Hills, 100% of which bear ocelli on the under side of the hind wings? Let us look at the last situation first. My series of 10 males from Custer has a frequency of 50% for the ocelli in question. Statistics show me that THE NEXT SERIES OF TEN MALES collected at Custer will contain from 3 to 7 ocellated specimens, if I get a "normally" random series. They also tell me that if I continue to pick up groups of 10 random males at Custer I have 1 chance in about 600 for getting a group that is wholly ocellated. This is quite different from the conditions that prevail in the Rocky Mountains but quite like those in the homeland of *benjamini*. Now turn to the first question. According to the statistics about the colonies of *ochracea* in the eastern foothills of the Rockies I have about 1 chance in more than a billion billion (10^{24}) of collecting 10 random males, 5 of which lack ocelli on the under side of the hind wings. For practical purposes my chance of duplicating the Custer situation in the Rocky Mountains is nil. You may agree with me that it is best to refer the Black Hills material to *benjamini* and not to the geographically nearer *ochracea*.

There is a third kind of variation that I would like to bring to your attention. It is a variety — or "subspecies" — of discrete variation, a Poisson population. This is a case where a characteristic is present or absent. It is the sort of diagnostic item that often is found in keys and that Skipper men seem to love. You know, "the microscopic spot that lies between Cu_1 and Cu_2 usually is present and forms the basis for separating species A and B, otherwise the patterns are alike." I'm not bitter, really, only I've been trying to write intelligently about Colorado *Hesperia* this past week. Well, what do you do about the spot? There are two ways of approaching this problem, one statistical, the other intelligent. The use of $\sqrt{npq}$, explained in "Simple Statistics for the Taxonomist" (*Lepid. News,* vol. 5: pp. 4-6, 43-45, 64-66, 112-120) will tell you what chance you assume if you consider it perfectly possible to gather a random series, the same size as the series upon which the statement was based, without spots. The intelligent approach is to turn a binocular microscope upon the location of the spot on those specimens that "lack" it. If the difference is valid, the chances are very good that you will find a few scales of white color that were not visible to the unaided eye.

There is nonsense in statistics just as there is in taxonomy. There are many statistically valid differences that are meaningless when looked at from either the biological or taxonomic angle. There is no mechanical way for you to reach a decision in taxonomy. You just have to use your head and all of the tools available to you. Statistics is one of those tools, and no more important and no more certain than any other. Statistics is a science, but Taxonomy is much more an Art.

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