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Short Communication

Difficulties in Processing of Catching Data of Light-Traps

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From 1958 to the present day Jermy-type light-traps operate at every county plant protection and forestry station in Hungary.

The size of a population is different at the various observation posts and the modifying environmental factors are not identical either at all the venues and times of light trapping. Therefore, it is easy to understand that catching the same number of specimens at two different observation posts or at different points of time may stand for varying proportions of the given population. Using relative catch values might solve this problem.

The relative catch is a quotient of the individual caught (dividend) and the average of individual caught of sampling time (submultiple). An instance makes its purport clear. If a nightly catch equivalent to the average of sampling time, then the value of quotient will be 1 [1].

In their investigation the method they most often used was to co-ordinate relative catch values (dependent variable) with the values of some environmental factor (independent variable) prevalent in the same sampling interval.

All the catching data of a given moth species were considered as a sole sample and from this we calculated the relative catch values. The effectiveness of the catch in different swarms and years became comparable in this way.

Both environmental factor and relative catch data were sorted into groups. Within a group, however, it is not reasonable to have big differences in the number of data. We calculated the number of groups according to the method of Sturges [2].

$$k = 1 + 3.3 * 1g\ n$$

where: k = the number of groups, n = the number of catching data.

However, the extreme values of a given group are more similar to the extreme value of a neighboring group than to its own middle value.

Therefore, within each group we used our own method and calculated three point weighted moving averages from the values of the dependent variable. Earlier, there was a problem about moving averaging, namely, that the first and last values, the ones carrying in many cases valuable information on the most important biological impacts were lost. In elaborating our method, we also considered the work of [3]. He came up with a solution to ensure that no data is lost, with every initial data being accompanied by a moving average value. The new method also considers with differing weights the middle, previous and following values. Thanks to this method, our moving averages get weighted with the number of initial data. The 3-point moving average is calculated on the basis of the following formula

The first value: $\frac{7\Sigma x_1 + 4\Sigma x_2 - 2x_3}{7n_1 + 4n_2 - 2n_3}$

The last value: $\frac{7\Sigma x_h + 4\Sigma x_{h-1} - 2\Sigma x_{h-2}}{7n_h + 4n_{h-1} - 2n_{h-2}}$

The remaining values: $\frac{\Sigma x_{i-1} + 2\Sigma x_i + \Sigma x_{i+1}}{n_{i-1} + 2n_i + n_{i+1}}$

where: k = the number of groups, n = the number of observation data.

It is justified to calculate moving averages in all cases where a large amount of data has to be processed. In the next step, the catching data were assigned to the environmental factor groups. Thereafter, were averaged the data pairs of environmental factor and relative catch within all the groups. The results are illustrated in the figures and the confidence intervals are shown in them.

When we only have data on a single or a few light-trap we cannot get significant results. Then the standard deviations are large due to the significantly different catch data on different days. In the other case, some species, especially migrants, appear intermittently. Each day a large crowd, while other times only a few specimens. The standard deviations are extremely large in this case as well.

In our opinion, results that meet two conditions can be considered real. One is that those from several independent samples are essentially the same. The other condition is that they can be interpreted based on our prior knowledge.

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