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INSTAR IMPACT

A lepidopteran's instar affects its interactions with its natural enemies (e.g., parasitoids), and these ecological interactions have significant impacts on applied research, such as integrated pest management (IPM). For example, parasitoids are commonly used as biological controls for IPM and many parasitoids select their hosts based on host size and instar.

DATA COLLECTION

We studied the red-head fall webworm (FW) morphotype from our colony housed in our laboratory at the University of Denver.

Head capsules are ideal for assessing larval body size because they can only change size during molts between instars. Head capsules exhibit geometric growth patterns, allowing use of successive head capsule widths when estimating the number of instars.

We chose six host plants in three different plant families:

- Alder
- Apple
- Chokecherry
- Broadleaf Cottonwood
- Narrowleaf Cottonwood
- Black Willow

We destructively sampled larvae from each host plant frequently. At the beginning of the growing season, we sampled larvae every day.

SOURCE

Tanino-Springsteen MM, Vyas DK, Mitchell A, Durso C, Murphy SM. Investigating the effect of host plant identity on instar number in fall webworm, a common generalist herbivore. Environ Entomol. 2024 Feb 20;53(1):188-194. doi: 10.1093/ee/nvad126. PMID: 38206676.

Figure 1: Step 1, (Optional) Consider the default model fit. Here it gives non-intuitive instars. Reducing the number of instars under the default caused the first two instars to be merged.

SEED CHOICE FOR FITTING GAUSSIAN MIXTURE MODELS OF INSTAR **CHARACTERISTICS IN LEPIDOPTERANS**

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INSTAR MODEL

We modeled head capsule widths as Gaussian mixture models, with a Gaussian distribution corresponding to each instar. We used the R functions Mclust and emV to estimate the parameters for each Gaussian mixture model (GMM). To promote the fitting of biologically reasonable models, we initialized the means with a geometric sequence of values.



Figure 3: Step 3 Group cases by assigning them to the nearest proposed mean in step 1. For each group, calculate the mean of the group, the proportion of the cases in that group, and the variance of the observations in the group. Use these as the starting model to fit a GMM.



Figure 2: Step 2 Estimate a starting and ending mean for head capsule widths of the first and last instar. This can be done using quantiles, here the 0.05 and 0.95 quantiles, but this can vary depending on the sampling method used for the data. Informed by the Brooks-Dyar concept, construct a sequence of intermediate widths according to a geometric sequence.

Figure 4: Step 4 Fit a GMM to the seed means, proportions, and variances from step 3.

CONCLUSIONS AND EXTENSIONS

For populations that follow a geometric sequence of head capsule widths, this method of fitting a Gaussian Mixture Model to the data quickly and reliably produces a biologically reasonable model.

The choice of the number of instars and the choice of starting and ending points for the geometric seeds could be automated using an information criterion or biological criteria such as Crosby's growth rule.









COMPARISON

Figure 6: Brooks-Dyar

APPLICATION

Figure 7: vectors of successive head capsule widths

Using parametric bootstrapping based on merged data from pairs of diets, we find that the vector of willow population head capsule widths at successive instars is further from those of the alder and chokecherry populations than is typical of samples with the same instar proportions but with

CONTACT INFORMATION