

Model To Predict Gypsy Moth (*Lepidoptera: Lymantriidae*) Defoliation Using Kriging and Logistic Regression

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ABSTRACT Outbreaks of the gypsy moth, *Lymantria dispar* (L.), typically occur over large areas but are difficult to predict. Most gypsy moth management programs base suppression decisions on models that predict defoliation from pre-season counts of egg masses in a given stand. In this study we developed a statistical model that used spatially stratified egg mass samples to predict gypsy moth defoliation on a regional scale, rather than on a stand level. The model was developed from historical defoliation sketch-map data and counts of gypsy moth egg masses under burlap bands at irregularly distributed plots in Massachusetts. These counts were used to generate interpolated surfaces of egg mass counts in grid cells (2 by 2 km) throughout the state. Maximum-likelihood procedures were used to parameterize a logistic regression model that predicted the probability of defoliation in each grid cell as a function of interpolated egg mass counts, the presence of defoliation in the previous year, and the 30-yr frequency of defoliation. Predicted probability surfaces tended to align mostly with the distribution of actual defoliation in each year. The model appeared to perform better than a previous model that was based on three-dimensional kriging of defoliation.

KEY WORDS *Lymantria dispar*, egg mass, outbreak

THE GYPSY MOTH, *Lymantria dispar* (L.), is probably the most important forest-defoliating pest in the northeastern United States. Defoliation and tree mortality associated with gypsy moth outbreaks can cause a multitude of ecological and economic effects (Twery 1991, Gottschalk 1993).

Every year, >250,000 ha of forest land in the United States are sprayed to minimize the adverse effects of defoliation by the gypsy moth (USDA Forest Service 1992). Most gypsy moth management programs base population suppression decisions on models that predict defoliation from pre-season counts of egg masses (Ravlin et al. 1987). Several very similar nonlinear models have been developed that predict gypsy moth defoliation at the stand level from estimates of egg mass density (Gansner et al. 1985, Montgomery 1990, Williams et al. 1991, Liebhold et al. 1993). Unfortunately, these models tend to be imprecise because of the difficulty of estimating egg mass densities and the erratic nature of gypsy moth populations (Elkinton & Liebhold 1990, Liebhold et al. 1993). In addition, these types of models have largely ignored the spatial dependencies inherent in gypsy moth outbreak dynamics (Gage et al. 1990, Hohn et al. 1993b, Liebhold et al. 1993).

In an attempt to address these concerns and develop a more precise method of predicting gypsy moth defoliation, Hohn et al. (1993a, b) developed a geostatistical model that predicted future defoliation maps from historical defoliation maps. The resulting landscape-level predictions of defoliation took into account the spatial and temporal dynamics of gypsy moth outbreaks but the predictions were generally inadequate because the regional magnitude of defoliation tended to lag behind actual values. Liebhold et al. (1995) compared historical counts of egg masses, pupae, and adult males in pheromone traps at a network of plots irregularly distributed in Massachusetts with historical defoliation maps and found that counts of over-wintering egg mass populations exhibited the greatest spatial correlation with defoliation. They concluded that it may be possible to incorporate this type of census data into a regional model of defoliation, such as developed by Hohn et al. (1993b), to generate a more precise model.

The objective of this study was to develop a model that uses both historical defoliation patterns and egg mass counts to predict defoliation on a regional level. We parameterized a logistic model that predicts the probability of defoliation using the same historical Massachusetts defoliation and egg mass count data used by Hohn et al. (1993a, b) and by Liebhold et al. (1995).

Materials and Methods

Defoliation Data. Aerial sketch maps of gypsy moth defoliation were prepared yearly from 1961

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to 1991 by the Massachusetts Department of Environmental Management. As described by Hohn et al. (1993b), these maps are sketched during a series of low-level reconnaissance flights made in late July during peak defoliation. Approximately 30% defoliation is considered the lower threshold for detection from the air (R. Acciavatti, USDA Forest Service, personal communication). In situations where there was doubt as to the cause of the defoliation, ground checks for the presence of gypsy moth life stages were made. The aerial sketch maps were initially overlaid on standard U.S. Geological Survey (1:24,000) topographical maps that were then used to generate a composite mosaic map for the entire state at 1:760,000 scale. Each composite defoliation map was converted to a raster matrix file using a digital scanner set at 150 dots per 2.54 cm (1 in) resolution.

A geographic information system, IDRISI (Eastman 1992), was used to assemble and collate the defoliation data. Defoliation maps, and all other spatial data were registered using an azimuthal equal-distant projection (Snyder 1987). A coarse spatial resolution of rasters (2 by 2 km) was used in this study because of the likely presence of data errors in defoliation maps caused by variation in the mapping processes by region and year. Each map layer was 198 cells wide by 93 cells high. Only 6,075 of these cells actually fell within the state boundaries and were coded with defoliation data. The remaining cells were treated as missing data and were not included in subsequent analyses. Because defoliation was originally mapped as presence/absence, the defoliation raster data were coded as either 0 or 1; this binary variable indicated whether the defoliation threshold (30%) was exceeded. During the period from 1961 to 1991, very little of Massachusetts was aerially sprayed (<5% of the defoliated area) and, therefore, spraying was ignored in our analysis.

Forest Susceptibility Data. The gypsy moth is highly polyphagous, but in New England, the oak-hickory and oak-pine forest types are historically the most susceptible to defoliation (Houston & Valentine 1977). A forest-type group map published in Eyre (1980) depicts seven forest-type groups occurring in the state of Massachusetts (Fig. 1A). These forest-type group data could have been used as a class variable in the logistic regression model developed (below) for predicting defoliation. However, the forest-type groups shown in Fig. 1 are very broad; each may encompass many more specific forest types (Eyre 1980). Liebhold et al. (1994) showed that these forest type groups provide only approximate estimates of gypsy moth susceptibility. Therefore, as an alternative we overlaid historical defoliation maps from 1961 to 1991 to calculate the frequency with which each cell was defoliated (Fig. 1B). Some areas of the state were clearly more susceptible to defoliation than others (Liebhold & Elkinton 1989). The historical frequency of defoliation may reflect not

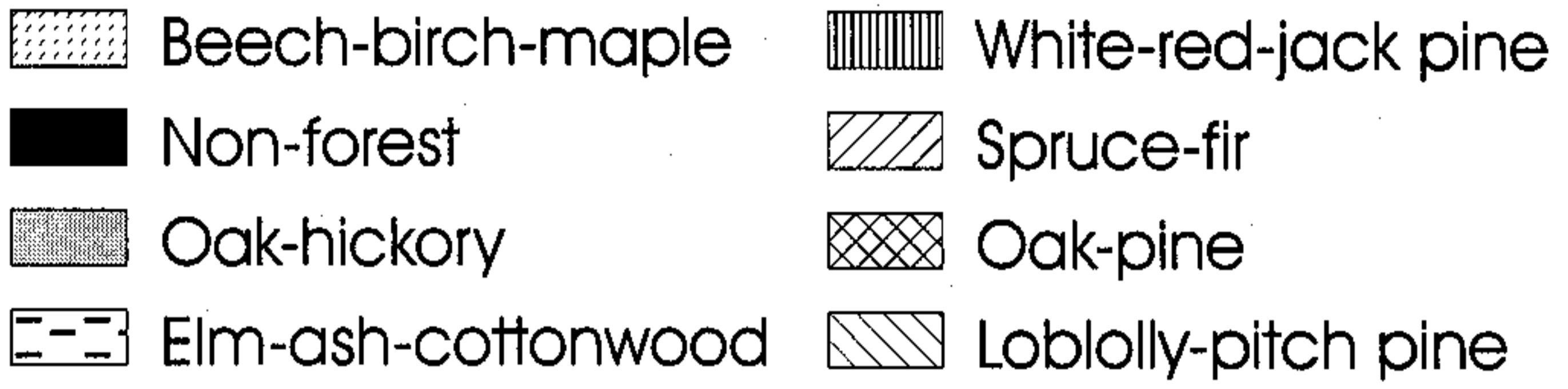
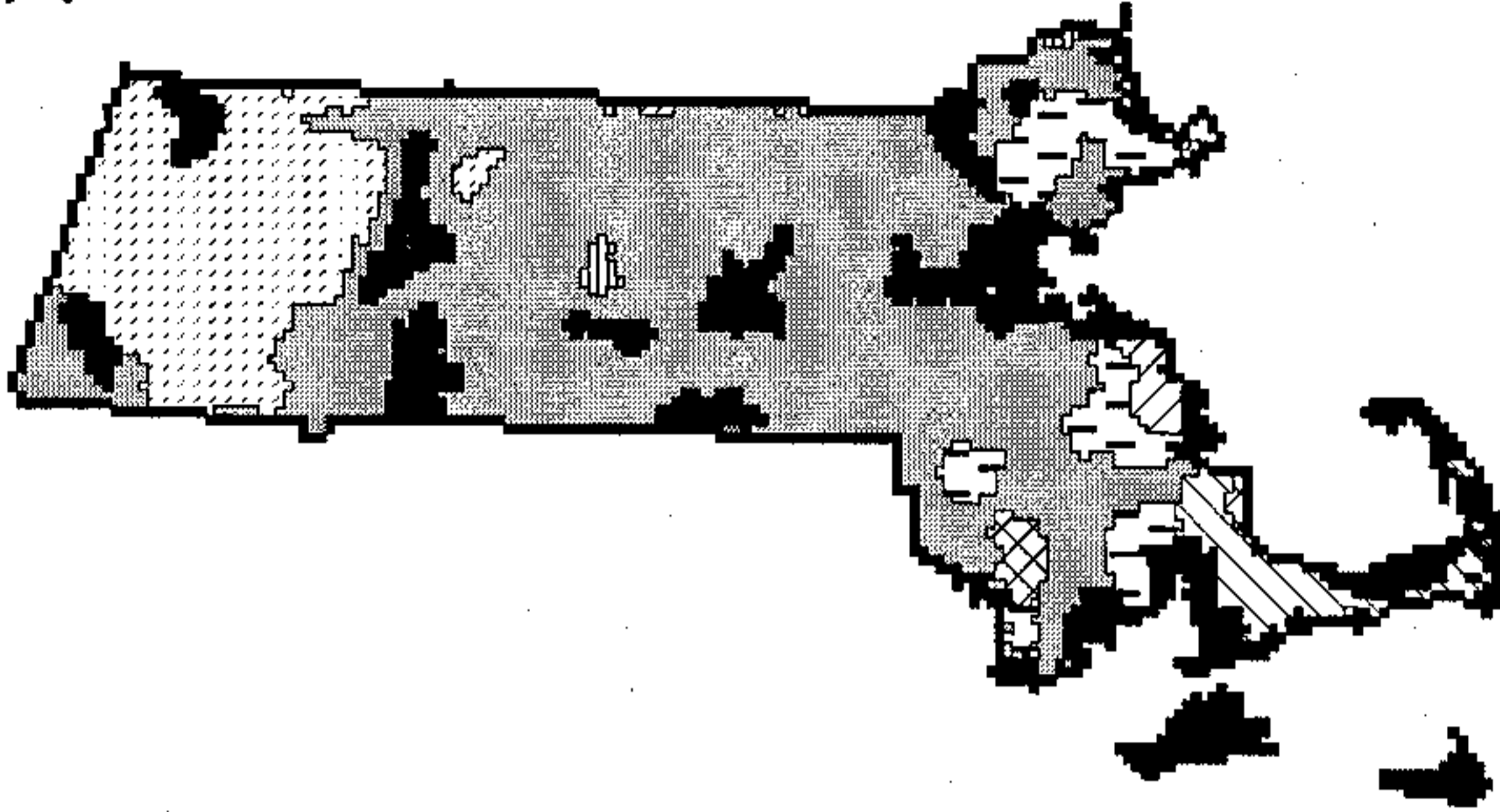
only the local forest-type but also any other biological, climatic, or physiographic landscape features that may influence gypsy moth population behavior (Liebhold et al. 1994). Thus, frequency of defoliation was used as a measure of forest susceptibility and was used in defoliation prediction models described below.

Egg Mass Data. In 1984, the University of Massachusetts and the Massachusetts Department of Environmental Management established a network of 167 plots irregularly distributed throughout the state (Fig. 2). Plots were located in forest stands that were considered susceptible to gypsy moth defoliation. Substantial numbers of gypsy moth egg masses can be found under burlap bands placed around the boles of trees even when population densities are low and other egg mass sampling methods yield mostly zero counts (Bellinger et al. 1990). Therefore, on each plot, burlap bands were placed around the boles of 20 oaks >6-cm diameter breast height (dbh) closest to the plot center. In the late summer of each year, counts were made of all egg masses under the burlap bands. Average numbers of egg masses per banded tree were calculated after excluding counts from trees where bands were missing. Data were not collected from every plot in every year; however, at least 125 plots were sampled each year.

The number of egg masses per tree was estimated for every grid cell (2 by 2 km) within state boundaries by interpolating values sampled at the irregularly spaced sample locations. This was accomplished using two-dimensional ordinary point *kriging*, a geostatistical technique that forms interpolated estimates as weighted averages of values at nearby locations (Isaaks & Srivastava 1989, Kemp et al. 1989, Liebhold et al. 1991, Roberts et al. 1993). The weight given to an individual observation is dependent on its distance and direction from the point being estimated. Kriged estimates represent a best estimate because weights are calculated to minimize the error variance of the estimate.

Before kriging, the spatial dependence of the data was determined by fitting a model to a *variogram* of the data (Isaaks & Srivastava 1989, Liebhold et al. 1991, Rossi et al. 1992). A variogram is a plot of $\gamma(h)$ versus h , where h represents a distance between pairs of points and $\gamma(h)$ represents half the average squared difference between paired data values separated by that particular distance (Hohn 1988, Isaaks & Srivastava 1989, Rossi et al. 1992). In this study, distance was expressed as the number of cells separating the centers, or grid nodes, of sampled cells. For example, if two adjacent cells were both sampled, then the distance between samples was 1. If these two cells were situated diagonally from each other, the distance was 1.414. When two sampled cells were separated by another cell, the distance between the sampled cells was 2, and so on. The variogram statistic is defined as

A



B

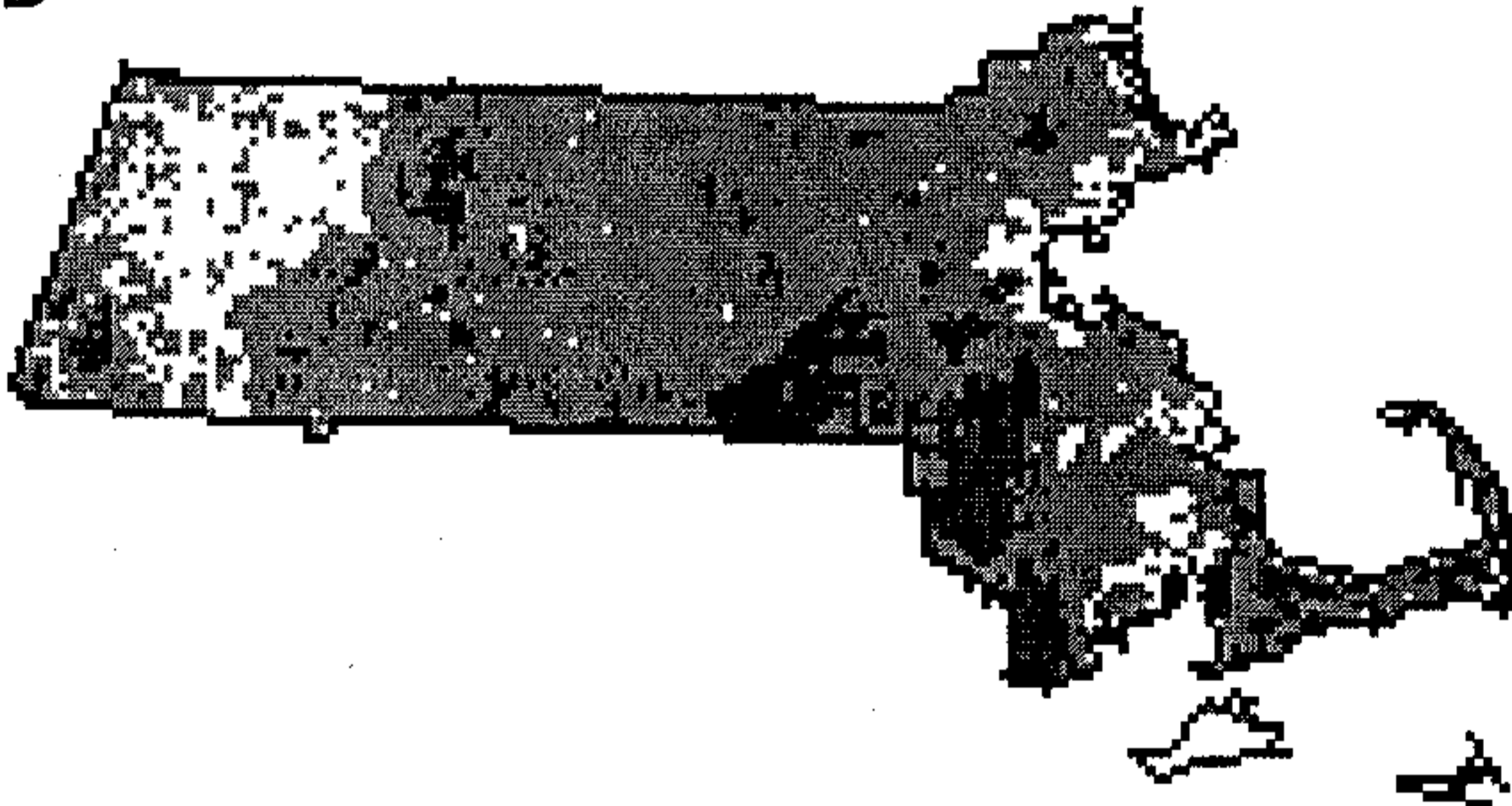


Fig. 1. (A) Forest type designation for each cell (2 by 2 km) within the state of Massachusetts from Eyre (1980). (B) Total number of years each cell (2 by 2 km) was defoliated from 1961 to 1991.

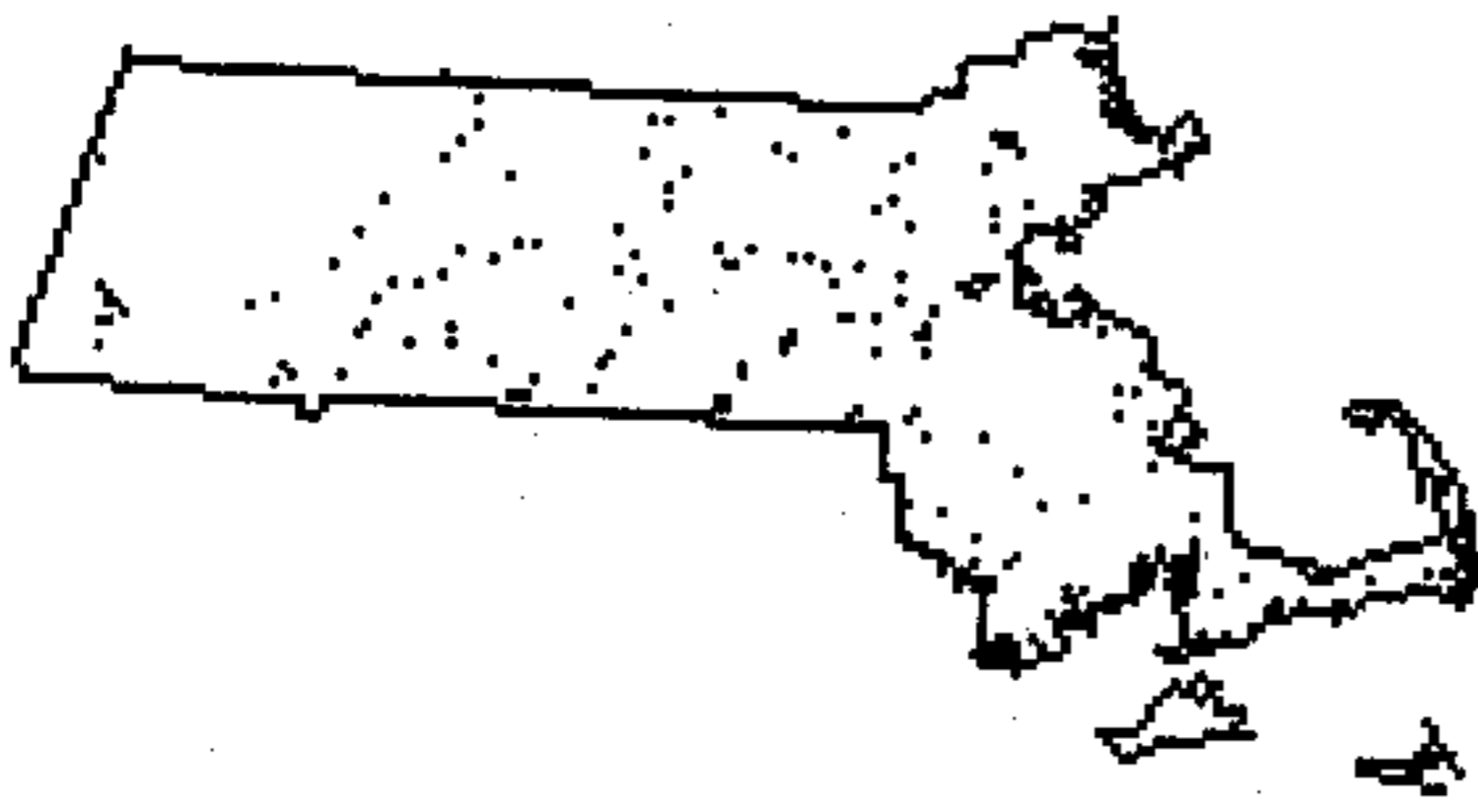


Fig. 2. Locations of egg mass sample plots.

$$\gamma(h) = \frac{1}{2n} \sum_{k=1}^{n_h} [z(x_k) - z(x_k + h)]^2 \quad (1)$$

where n_h is the number of pairs of cells separated by a distance of h , $z(x_k)$ is the observed egg mass count at location x_k , and $z(x_k + h)$ is the observed count at a location h units from x_k . In the presence of strong spatial dependence, the difference between $z(x_k)$ and $z(x_k + h)$ will be relatively small when h is small. However, as the distance between samples (h) increases, the difference between $z(x_k)$ and $z(x_k + h)$ can be expected to increase. In other words, egg mass counts from cells very close to one another can be expected to be very similar, whereas counts from cells separated by greater distances can be expected to become more dissimilar as the distance increases. At some distance, the difference between counts fails to increase further and the variogram levels off. This distance is referred to as the *range* of the variogram. The value of $\gamma(h)$ at the range is called the *sill*.

Spatial anisotropy is the term given to the condition in which the correlation among samples depends on their spatial orientation (Isaaks & Srivastava 1989, Rossi et al. 1992). For example, egg mass counts from plots oriented in a north-south direction along the top of a ridge may tend to be more similar than counts from plots oriented in an east-west direction perpendicular to the ridge. Given a sufficient number of samples, anisotropy in the data can be detected by calculating separate variograms for interpoint vectors falling in the 0, 45, 90, and 135° angle classes using a tolerance of 22.5° in each direction (Liebhold et al. 1991). Substantial differences in the shape or magnitude of these variograms indicate the presence of anisotropy. Because of the limited number of observations in the Massachusetts egg mass data set, tests for anisotropy could not be conducted. Therefore, only a single omnidirectional variogram was calculated. Previous analyses of gypsy moth defoliation in this same region (Hohn et al. 1993b, Liebhold et al. 1995) failed to detect any anisotropy and, thus, support the use of an isotropic model for egg mass populations.

As with most insect count data, histograms of egg mass count data revealed a skewed distribution

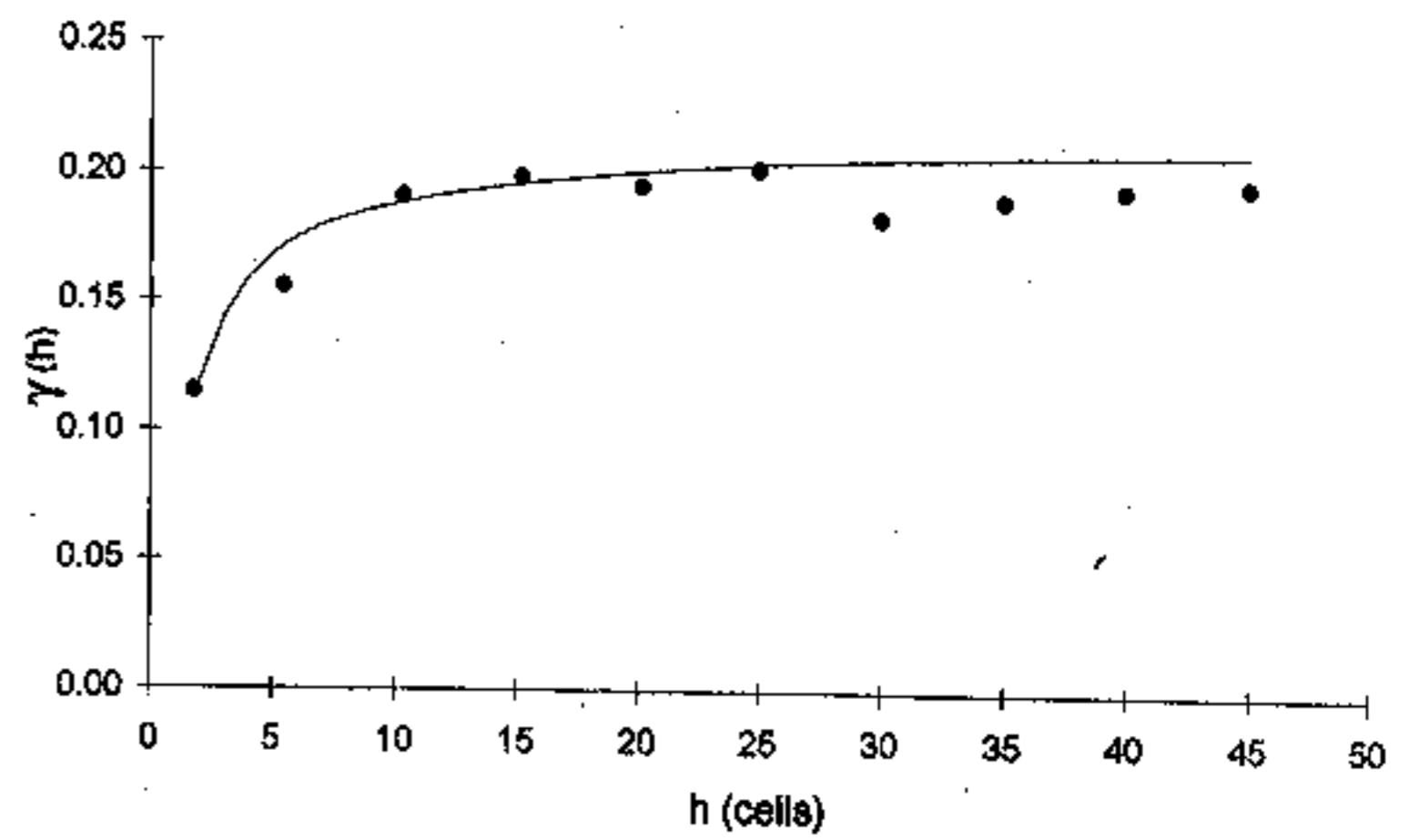


Fig. 3. Omnidirectional variogram calculated from the 1984 to 1990 egg mass census data. Solid line is the variogram model defined in equation 8.

with many low or zero values and a few very high values. Therefore, a $\ln(z + 1)$ transformation of the data was used before calculation of the variogram and kriging. Because variogram statistics are calculated for only discrete distance classes, it is necessary to fit a model to $\gamma(h)$ as a function of h for the purpose of obtaining values of $\gamma(h)$ for all values of h (Liebhold et al. 1991). In this study, the variogram was fit with a single, isotropic, nested exponential model of the form

$$\gamma(h) = c_1(1 - e^{-h/a_1}) + c_2(1 - e^{-h/a_2}) \quad (2)$$

where c_1 and a_1 are the sill and the range of the first exponential term and c_2 and a_2 are the sill and the range of the second exponential term. The model was fit iteratively by eye using procedures outlined by Hohn (1988).

Results of the variogram analysis were then used to calculate weights to be used in the ordinary kriging of egg mass sample data. Kriged estimates are weighted averages of values at nearby locations

$$z^* = \sum_{j=0}^n w_j \cdot z_j \quad (3)$$

where z^* is the interpolated value being estimated, $z = [z_1, z_2, z_3, \dots, z_n]$ is the vector of values at nearby locations and $w = [w_1, w_2, w_3, \dots, w_n]$ is the vector of corresponding weights to be used in averaging the values. Because the kriging procedure minimizes the variance of the errors, the weight matrix can be estimated as

$$w = C^{-1} \cdot D \quad (4)$$

where C is the $(n + 1)$ by $(n + 1)$ covariance matrix for all the z values from nearby samples and D is the $n + 1$ vector of covariances of z values between the point being estimated and the nearby samples. The covariances can be computed directly from the variogram as

$$\text{cov}(h) = c - \gamma(h) \quad (5)$$

where c is the variogram sill.

Logistic Regression. A logistic regression model that predicted the probability of defoliation in a

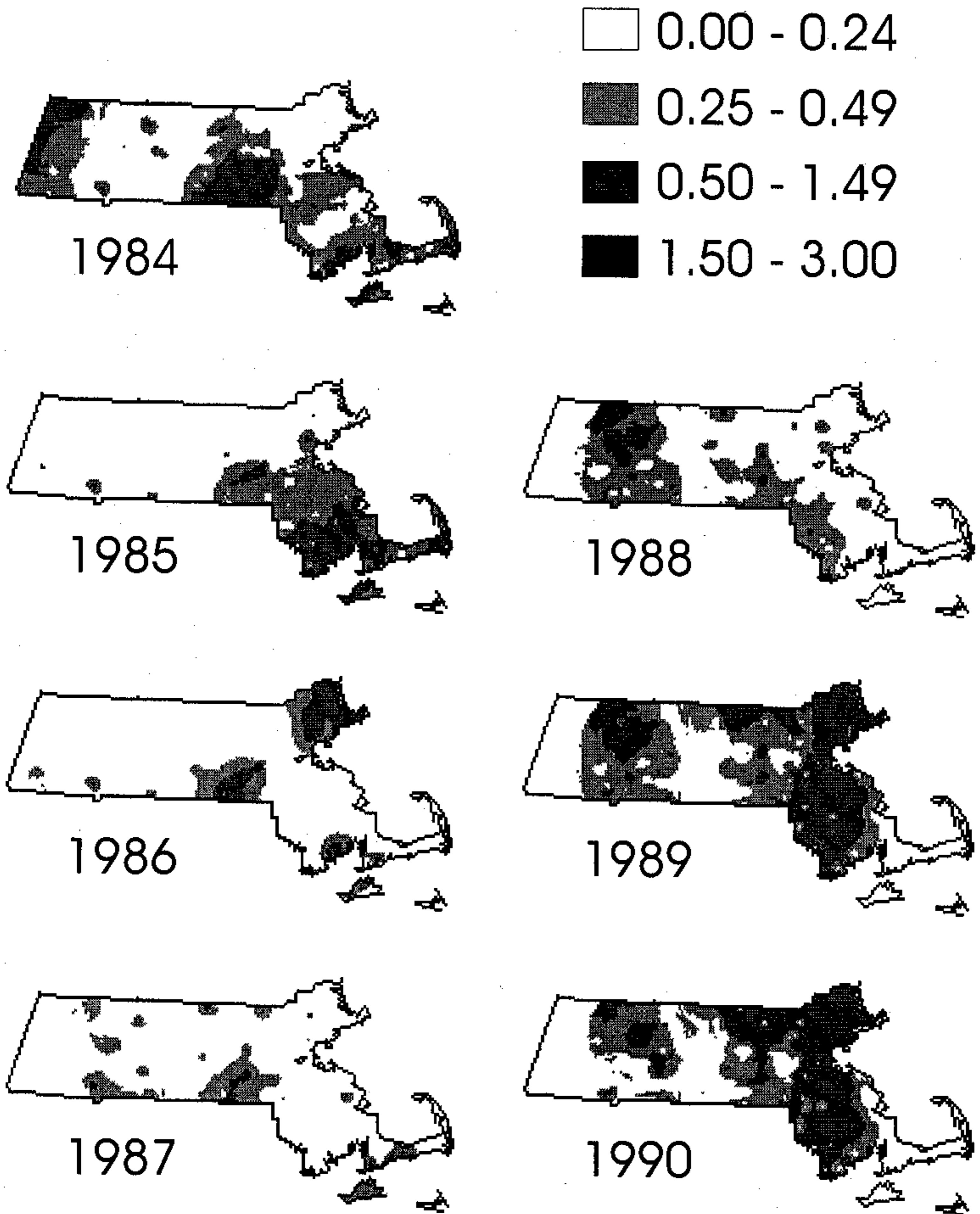


Fig. 4. Kriged egg mass density estimates for the years 1984–1990 [$\ln(1 + \text{egg masses per tree})$].

given grid cell was fit using data from each cell in all 6 yr of the study (1985 to 1991). The kriged estimates of log egg mass density, defoliation presence (0, 1) in the previous year, and the total number of years of defoliation within each cell were used as independent variables in the regression.

The LOGISTIC procedure of SAS, which fits linear logistic regression models for binary response data by maximum likelihood, was used in this analysis (Hosmer & Lemeshow 1989, SAS Institute 1992). The logit link function was selected for use so the linear logistic model had the form

Table 1. Logistic regression parameters and associated statistics from maximum likelihood estimation

Variable	Parameter estimate	SE	Wald chi-square	P > chi-square	Standardized estimate
Intercept	-5.1547	0.0608	7,198.25	0.0001	n/a
ln(egg masses/tree)	2.6036	0.0828	989.32	0.0001	0.3523
Defoliation frequency	0.3256	0.0131	619.83	0.0001	0.2976
Presence of defoliation in previous year	2.0613	0.0611	1,138.48	0.0001	0.2496

$$\text{logit}(p) = \ln\left(\frac{p}{1-p}\right) = a + B'x \quad (6)$$

where p is the response probability (in this case the probability that the cell will be defoliated), a is the intercept parameter, and $B'x$ is the vector of slope parameters. The value of p could then be calculated as:

$$p = \frac{e^{\text{logit}(p)}}{1 + e^{\text{logit}(p)}} \quad (7)$$

Results

Kriging of Egg Mass Sample Data. The sample variogram calculated from egg mass counts from all years is shown in Fig. 3. The fitted variogram model, which is shown in the figure as a solid line, is

$$\gamma(h) = 0.16(1 - e^{-h/1.7}) + 0.05(1 - e^{-h/12}). \quad (8)$$

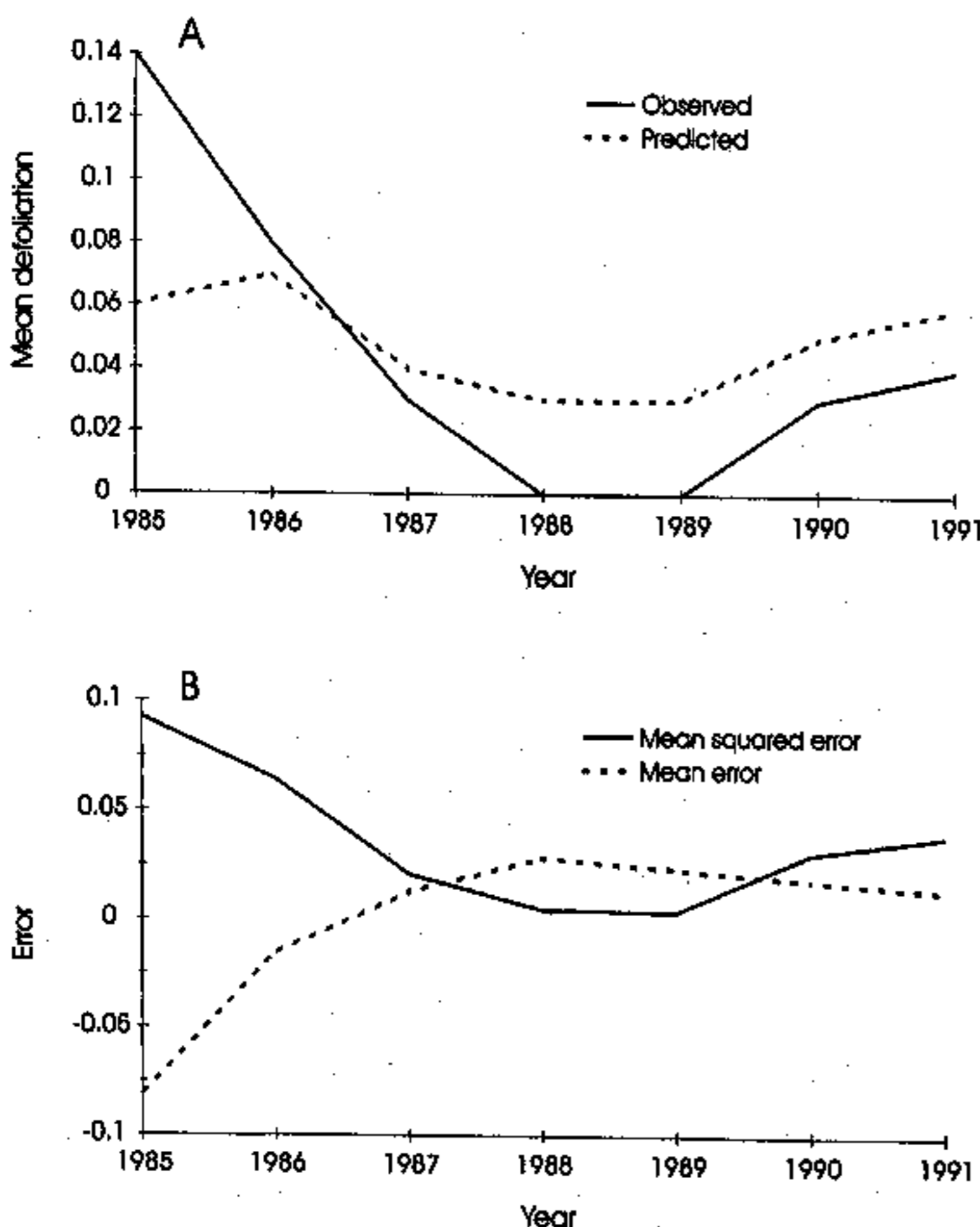


Fig. 5. Yearly observed and predicted defoliation from 1985 to 1991. (A) Observed frequency of defoliation and mean probability of defoliation, in Massachusetts. (B) Mean errors and mean squared errors of the predictions.

Maps of the kriged estimates for 1985–1991 are shown in Fig. 4.

Logistic Regression. The maximum-likelihood procedure converged on a vector of parameters shown in Table 1. The probability of defoliation should be positively related to counts of over-wintering egg mass populations because high densities of egg masses will produce high densities of larvae which will in turn cause defoliation. The probability of defoliation should also be correlated with the historical frequency of defoliation because defoliation is more likely in areas where forests are historically more susceptible. Defoliation probability should also be positively related to the presence (0, 1) of defoliation in the same cell in the previous year because defoliation is statistically autocorrelated in time (Hohn et al. 1993b).

Composite Wald chi-square statistics indicated that all three independent variables were significant at the 0.01 level (Table 1). Tests of association (Hosmer & Lemeshow 1989) indicated that 85.8% of the estimates were concordant with the actual defoliation values, 13.0% were discordant, and 1.2% were tied. Mean observed defoliation and mean predicted probability of defoliation were calculated for each year (Fig. 5). Though the mean observed defoliation level varied from 0 to 14%, predicted defoliation varied from 3 to 7%. Because the model was fit using a least-squares approximation, it did not correctly predict the extremes that occurred in the actual data. Hohn et al. (1993b) noted a 1-yr lag in defoliation predictions made from the same data using a three-dimensional kriging model. No such lag is discernible in the estimates made here. In addition, for each year, both the mean error

$$\frac{\sum_{k=1}^n P^*(x_k) - v(x_k)}{n} \quad (9)$$

and the mean squared error:

$$\frac{\sum_{k=1}^n [P^*(x_k) - v(x_k)]^2}{n} \quad (10)$$

were calculated (Fig. 5B). In these equations, $P^*(x_k)$ is the predicted probability of defoliation in cell x_k , $v(x_k)$ is the actual, or observed, defoliation in cell x_k , and n is the number of cells for which a prediction was made. Overall, the model tended to underpredict slightly in years of heavy defoliation

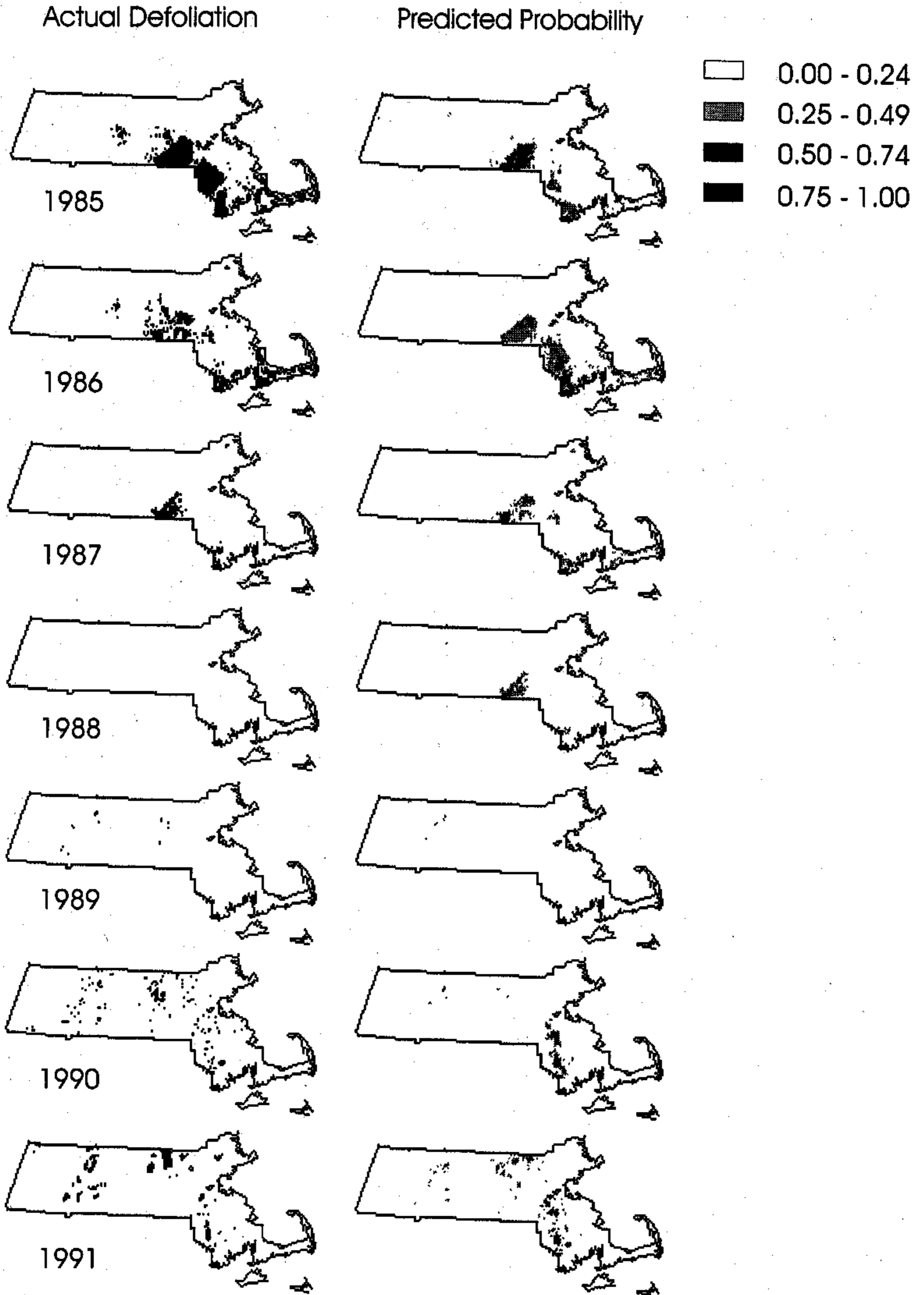


Fig. 6. Predicted defoliation probabilities and actual defoliation maps for Massachusetts from 1985 to 1991.

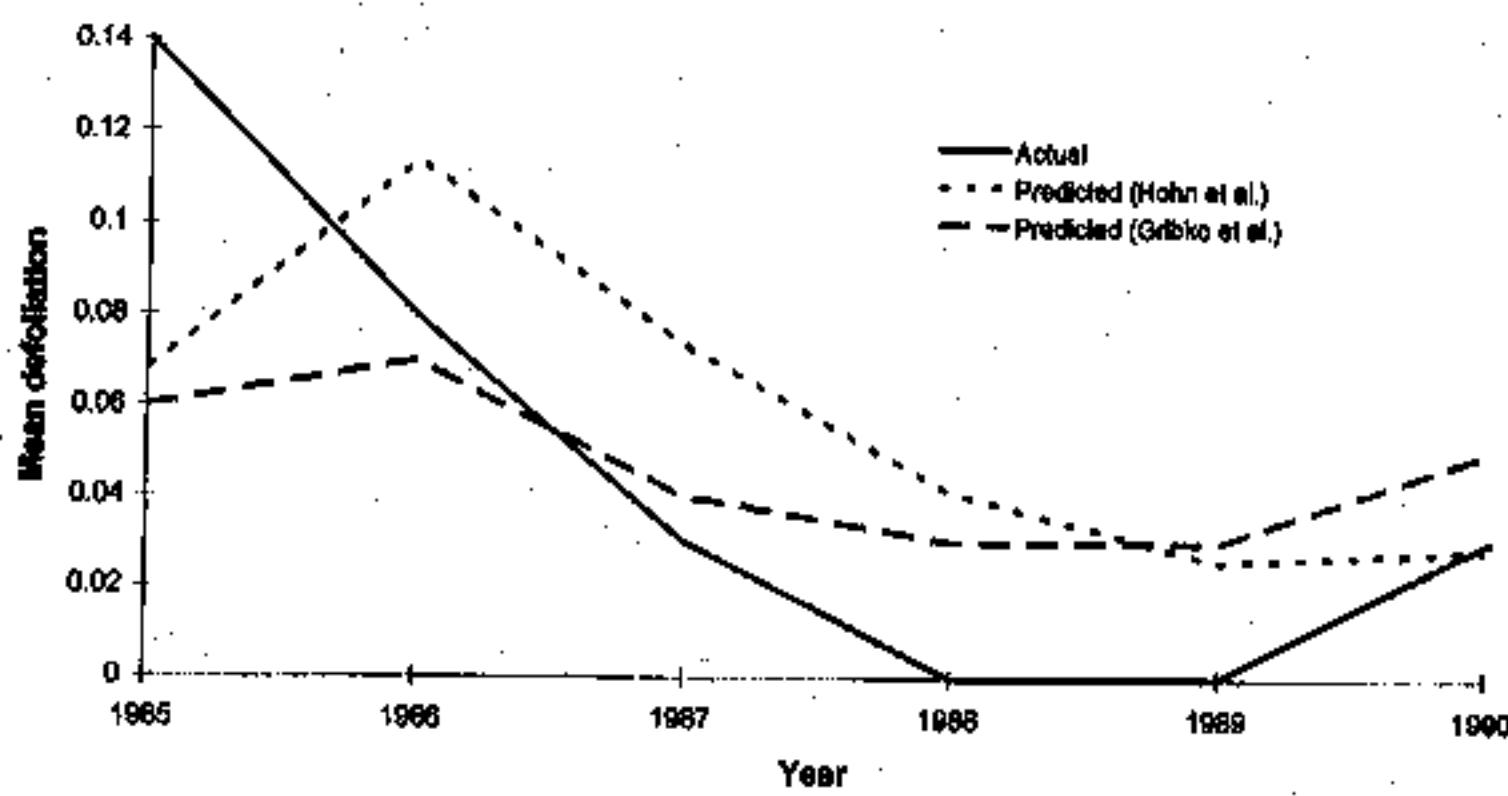


Fig. 7. Actual defoliation frequency and mean probability of defoliation predicted through the use of three-dimensional kriging (Hohn et al. 1993b) and logistic regression (see *Results*).

(1985–1986) and overpredict slightly in years of lighter defoliation (1987–1991) (Fig. 5A).

As can be observed in paired maps of actual and predicted defoliation for each year of the study (Fig. 6), there was at least some visual congruence between observed defoliation patterns and predictions from the model. Of particular interest are the maps for 1986 (a year of heavy defoliation) and 1991 (a year of sparse, widely dispersed defoliation), which indicate that this model can be expected to perform well over a wide range of defoliation levels.

Predictions made using the logistic model compare favorably with those obtained by applying three-dimensional kriging to the same data set (Hohn et al. 1993b). Specifically, mean defoliation probabilities from the logistic model more closely tracked the actual proportion of cells defoliated (Fig. 7). This is particularly evident from 1987 to 1989, a period of low regional defoliation. Predictions made for this period using three-dimensional kriging gradually decreased from 1987 to 1989 and then increased only slightly in 1990. In contrast, the defoliation predictions made using the logistic model more closely matched the trend observed in the actual data.

Discussion

Results of this study indicate that geostatistical techniques, such as kriging, can be used in combination with more traditional statistical approaches to produce predictive models of gypsy moth defoliation. The spatial resolution in this study was relatively coarse (cells [2 by 2 km]) and, thus, the model developed here cannot be applied to actual gypsy moth suppression decisions, which are made on individual stands. However, the model developed here can be used to make regional predictions of defoliation probabilities that could be used to trigger more extensive surveys in specific stands. Furthermore, the same type of analysis could easily be applied to data collected on a finer scale to produce a model that could make predictions of defoliation in individual stands. Kriging previously

has been used to interpolate gypsy moth egg mass counts collected at a much finer spatial scale (Liebhold et al. 1991). We expect that this sort of model will ultimately provide more reliable predictions of defoliation than is currently achieved with models that predict defoliation from average egg mass density alone (Gansner et al. 1985, Montgomery 1990, Williams et al. 1991, Liebhold et al. 1993) because more information (e.g., previous defoliation and population levels in surrounding areas) is incorporated.

The model developed here incorporated interpolated counts of egg masses under burlap bands. Liebhold et al. (1995) showed that these counts are spatially correlated with defoliation occurring in the subsequent generation. However, use of counts in 0.01-ha cells is a more commonly used method for assessing egg mass abundance in operational gypsy moth management programs (Ravlin et al. 1987). Although there have been several studies that demonstrated the correlation of counts of egg masses in 0.01-ha plots with defoliation in the same stand (Gansner et al. 1985, Montgomery 1990, Williams et al. 1991, Liebhold et al. 1993), the spatial correlation with defoliation in surrounding areas has never been evaluated. Because there is generally a good association between counts of egg masses beneath burlap bands with counts in 0.01-ha plots (Wallner et al. 1991), we expect that the spatial correlation of defoliation with egg mass counts in 0.01-ha plots would be similar to the correlation with counts under burlap bands reported by Liebhold et al. (1995). Thus, we expect that models similar to the one presented here could be developed using counts of egg masses in 0.01-ha plots.

In addition, these techniques may also have application in the prediction of outbreaks of other forest insects. In situations where long historical outbreak frequencies are not available at all locations, *surrogate* data such as physiography or forest type may possibly be substituted as these data can be statistically associated with forest susceptibility (e.g., Liebhold et al. 1994).

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