

Forecasting Gypsy Moth (*Lepidoptera: Lymantriidae*) Defoliation with a Geographical Information System

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ABSTRACT Maps of defoliation caused by the gypsy moth, *Lymantria dispar* (L.), as well as point estimates of egg mass density and counts of male moths captured in pheromone-baited traps collected from the Shenandoah National Park and George Washington National Forest from 1989-1992 were assembled in a geographic information system. A maximum likelihood estimation procedure was used to fit 15 logistic regression models that predicted the probability of noticeable defoliation in 1-ha grid cells from various combinations of egg mass densities, counts of males in pheromone traps, presence of defoliation in the previous year, and distance to the expanding gypsy moth population front. Models that incorporated egg mass density estimates and distance to the infested front provided the most reliable predictions of defoliation probability. The performance of these models was comparable with decision errors encountered using various egg mass density thresholds alone. The errors associated with application of egg mass density thresholds and the various models were high and highlighted the need for improved methods for predicting defoliation.

KEY WORDS gypsy moth, sampling, egg mass, model

POPULATIONS OF THE gypsy moth, *Lymantria dispar* (L.), in North America exhibit eruptive behavior; densities vary through several orders of magnitude, often reaching epidemic levels that have spectacular effects on their habitat (i.e., total defoliation of host trees) (Montgomery and Wallner 1988). It is not uncommon for gypsy moth populations to persist for many years at densities that are so low that it may be difficult to detect any life stages except male moths. Occasionally, for unknown reasons, population densities increase, often to defoliating levels of >6,000 egg masses per hectare, within only a few generations. These outbreak populations may persist for several years before collapsing.

Gypsy moth outbreaks often occur over very large areas but are notoriously difficult to predict (Liebhold and Elkinton 1989). Previous models developed for predicting defoliation have been based mostly upon pre-season counts of egg masses (Gansner et al. 1985, Montgomery 1990, Williams et al. 1991, Liebhold et al. 1993b). Though there is a significant relationship between egg mass density and subsequent defoliation at the stand level, the variance about this relationship is great. Consequently, considerable error is encoun-

tered in using this method for prediction of defoliation.

Large areas of forest land are sprayed every year to prevent gypsy moth defoliation; >3 million ha were aerially treated as part of the USDA Forest Service Cooperative Suppression Program over the last 15 yr. One of the major impediments to implementation of an effective integrated gypsy moth management program is the lack of a precise, yet economical procedure for forecasting defoliation. Most gypsy moth management programs rely on stand-level estimates of egg mass densities as the basis for decision-making (Ravlin et al. 1987). The development of a more precise method for prediction of defoliation could greatly improve the efficiency of gypsy moth management programs.

Previous models developed for predicting outbreaks have relied on data collected at individual stands and have largely ignored spatial processes. Thirty years ago, Campbell (1967) recognized that the dynamics of gypsy moth populations are affected by population densities in nearby areas; populations are often synchronized in their yearly fluctuations during the development of gypsy moth outbreaks or outbreaks appear to spread (Liebhold and McManus 1991, Williams and Liebhold 1995, Zhou and Liebhold 1995).

The advent of geographical information systems has opened up the possibility to capture quantitatively these spatial relations to improve the quality of forecasts of gypsy moth defoliation. Hohn et al. (1993) developed a geostatistical model that forecasts probabilities of future gypsy moth defoliation from histor-

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ical spatial patterns of defoliation in the same area; this model quantified the temporal persistence and spread of defoliation in a predictive model. Gage et al. (1990) used a Geographical Information System to develop models for predicting pheromone trap-catch from trap-catch in previous years and demonstrated how trap capture maps were related to defoliation maps. Liebhold et al. (1995) showed that gypsy moth egg mass counts are more highly spatially correlated with subsequent defoliation than are counts of trapped males. Gribko et al. (1995) developed a logistic model and Zhou and Liebhold (1995) developed a series of transition models that incorporated the spatio-temporal autocorrelation of defoliation, and also incorporated the spatial correlation of pre-season egg mass counts with subsequent defoliation to produce predictions of defoliation that were more accurate than the 3-dimensional kriging model of Hohn et al. (1993).

In all of the previous spatial models described above, predictions have been made over a large scale (i.e., ≈ 2 by 2 km cells or greater). Since actual gypsy moth management decisions (i.e., decisions about aerial suppression) are made at a much smaller scale (gypsy moth spray blocks typically range from 10 to 200 ha [Twardus and Machesky 1990]) these models cannot be reliably applied for real management decisions. In this study, we developed several logistic regression models for forecasting gypsy moth defoliation. These models were similar in form to those developed by Gribko et al. (1995), but they were parameterized using data collected over a smaller area and consequently these models can be more reliably applied to actual management decisions.

Methods and Materials

All data used in this study were collected from the Appalachian Integrated Pest Management (AIPM) program. The Appalachian IPM program was a joint program of the USDA Forest Service, and various state and other national agencies from 1988–92 (Reardon 1991). The objective of AIPM was to demonstrate the use of integrated pest management of the gypsy moth in the central Appalachian Mountains in a 5.5 million-ha area in Virginia and West Virginia.

During the AIPM program, a large number of forested areas were aerially sprayed to prevent defoliation by the gypsy moth. Because we wished to develop models for predicting defoliation by the gypsy moth in the absence of spraying, we only used data collected inside of the Shenendoah National Park (SNP) and the George Washington National Forest (GWNF). Most of the SNP and GWNF is composed of forest types susceptible to defoliation by the gypsy moth but aerial suppression was rarely used within these areas. Areas that were within 100 m of a treatment (sprayed) area were not used in this study. Data from the GWNF were used to parameterize models and data from both GWNF and SNP were used to evaluate the accuracy of predictions from these models. The data used to build models consisted of 4 data themes: defoliation,

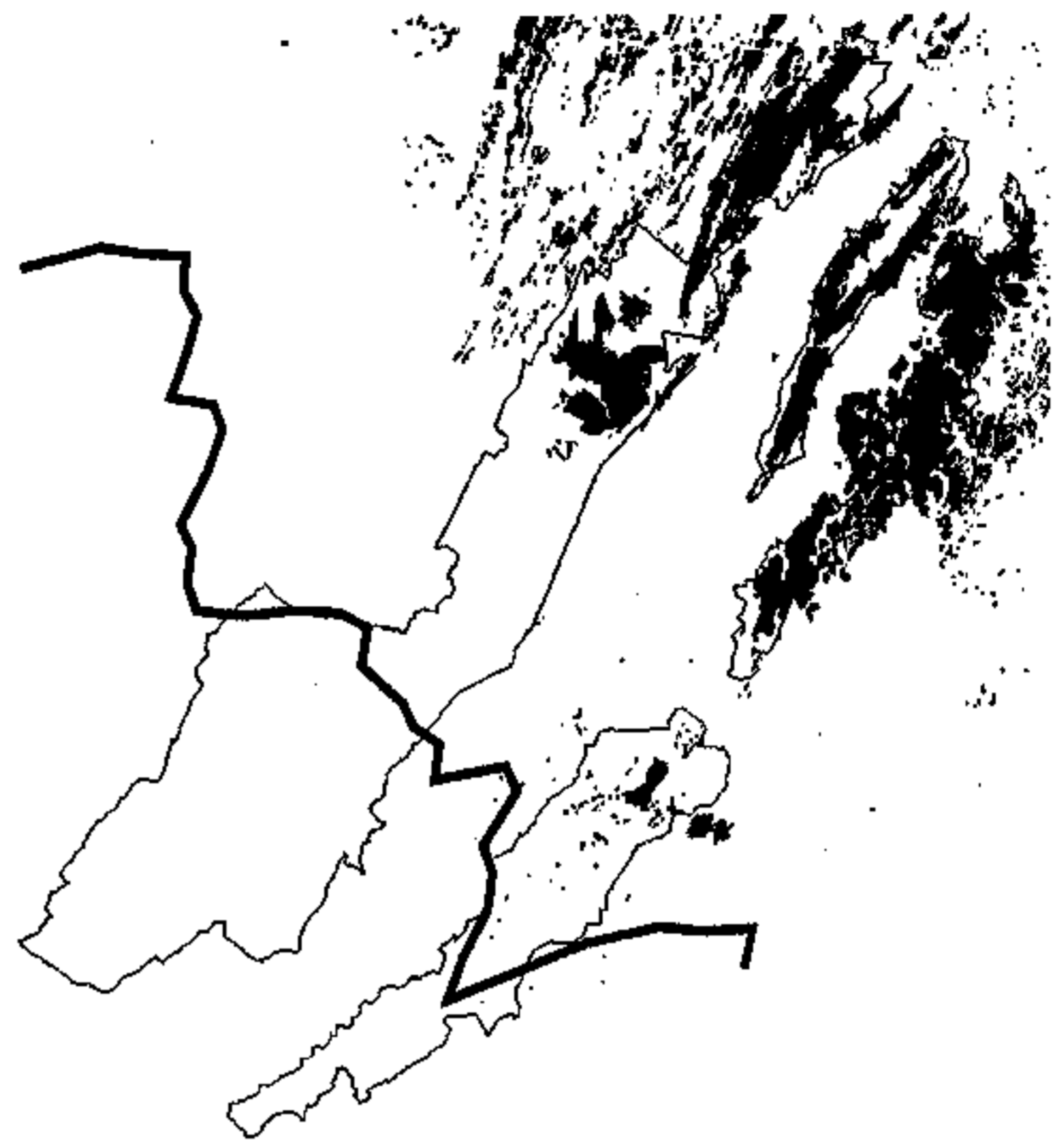


Fig. 1. Distribution of defoliation in SNP and GWNF 1990. Location of the boundary of 10 males per trap in 1990 from Sharov et al. (1995) is shown as a heavy black line.

egg mass densities, pheromone trap counts, and distance from the population boundary.

Defoliation was recorded with the use of high-altitude color-infrared photography (Ciesla and Acciavatti 1982) which was collected at the approximate week of peak defoliation. Optical bar photography was returned to the laboratory and the boundaries of areas with noticeable defoliation were recorded on standard 1:24,000 topographical maps. Defoliation polygons were digitized using a vector-based Geographical Information System, and then imported to the raster Geographical Information System, GRASS (U.S. Army Corps of Engineers 1993), by rasterizing these defoliation polygons using a 1-ha raster system using a universal transverse mercator projection (Snyder 1987). The minimum level for detection of defoliation using this method is approximately 30%. Thus, every 1 ha cell was classified as either 0 or 1, depending on the presence of noticeable defoliation (Fig. 1).

Gypsy moth pheromone traps were deployed annually over the AIPM area on an ≈ 2 - by 2-km grid. These traps were standard disparlure-baited milk carton traps (Schwalbe 1981). At the end of the trapping season, the number of males within each trap was recorded, as were the universal transverse mercator coordinates (estimated from topographical maps). Whenever the number of males per trap exceeded 200, egg mass densities were sampled using 3–10 fixed-radius plots of 0.01-ha (Liebhold et al. 1994) in each 1-km² cell coincident with the trap (Fig. 2). Cells with a catch >500 were sampled first, and cells with a capture of 200–500 male moths were sampled as time allowed (Rutherford and Fleischer 1989, Fleischer et al. 1991). Egg mass sample plots were situated as widely dispersed as possible within each area though

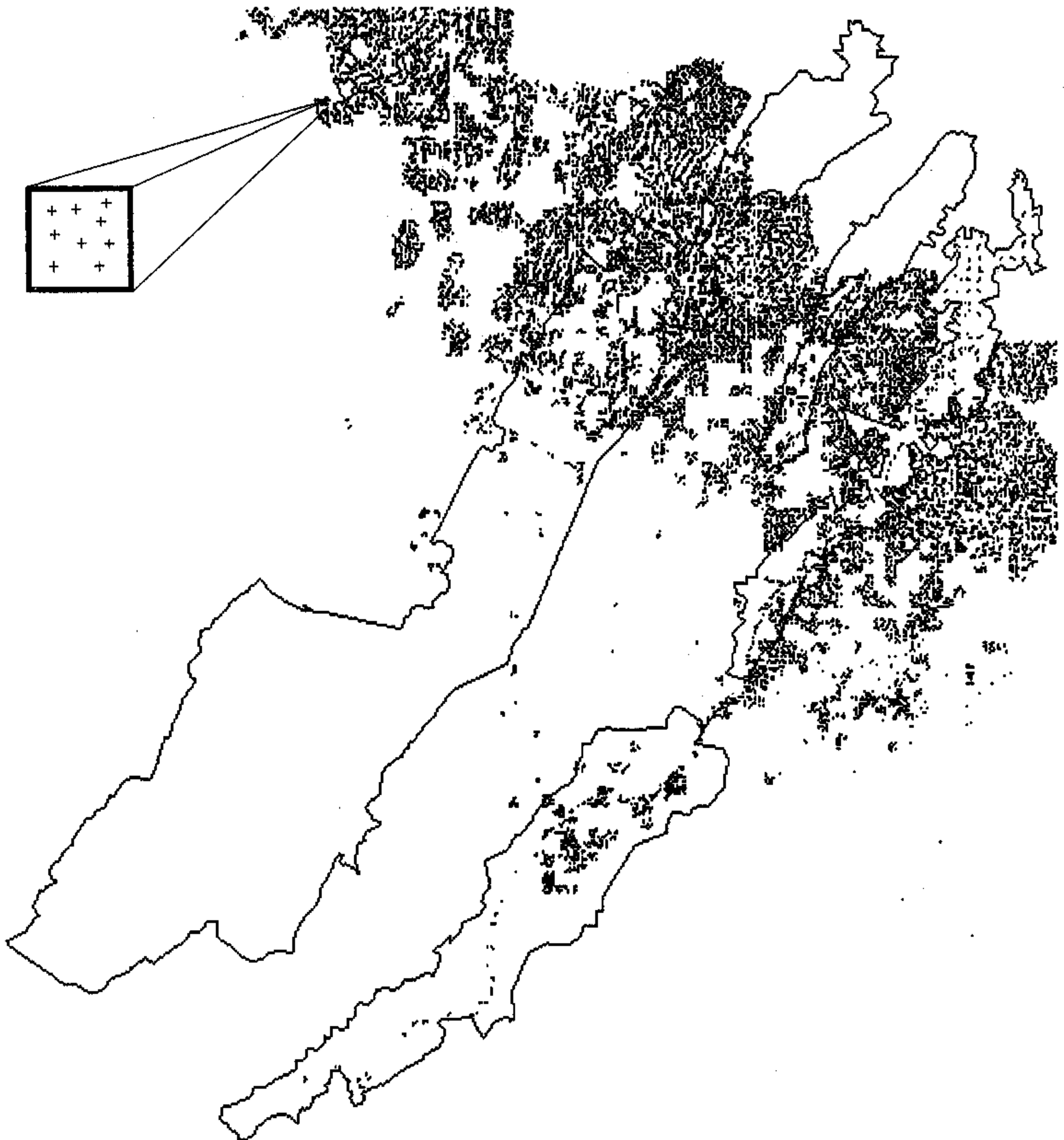


Fig. 2. Posting of 1990 egg mass plot locations in SNP and GWNF.

plots were preferentially located in stands considered capable of supporting gypsy moth populations (i.e., preferred tree species were present) (Rutherford and Fleischer 1989). The universal transverse mercator coordinates of each egg mass plot were estimated from 1:24,000 topographical maps.

We assembled the pheromone trap data from the Appalachian IPM program from each year and estimated an interpolated trap capture at each 100- × 100-m grid node, using ordinary kriging. Ordinary kriging estimates values at unsampled locations as a weighted average of values at nearby locations (Liebhold et al. 1993a, Isaaks and Srivastava 1989). We also used ordinary kriging to create a grid (100 m between

each node) of estimated egg mass densities at each grid cell using egg mass plot data from each year (Liebhold et al. 1991). If a grid node was >500 m from an egg mass plot, data from that node were excluded from the analyses for that year because geostatistical analysis of egg mass data indicated that spatial dependence in egg mass counts rapidly declines at distances exceeding 500 m (Liebhold et al. 1991, Sharov et al. 1996b) and kriged estimates would be unreliable.

The AIPM program was located along the expanding front of gypsy moth distribution in North America. Therefore, most of the outbreaks occurring from 1988 to 1992 were the 1st gypsy moth outbreaks in these areas. Because the timing of defoliation in these areas

was related to their position relative to the expanding front, this information was included in the analysis. For each cell in the GWNF and SNP, we calculated the distance to the boundary of 10 males per trap estimated using the "best classification" method of Sharov et al. (1995) (Fig. 1). Sharov et al. (1996a) found that the 10 males per trap boundary was the most stable and reliable boundary estimated along the expanding front.

Logistic regression was used to predict the probability of defoliation in a manner similar to that used by Gribko et al. (1995). In other studies, we have used 3-dimensional kriging (Hohn et al. 1993) and cellular automata models (Zhou and Liebhold 1995) for forecasting defoliation. Comparison of the performance of all 3 types of models indicated that they yield very similar predictions and we have recommended the use of logistic regression models because of their simplicity of estimation (Liebhold et al. 1996).

Data from all 4 yr of study (1988–1992) in GWNF were pooled to parameterize a single logistic regression model. Data from SNP were reserved for model testing. The logistic model predicted the probability of noticeable defoliation at each 1 ha-cell from several independent variables corresponding to the same cell: log egg mass density estimated at each cell using ordinary kriging, the presence (0,1) of defoliation at the same cell in the previous year, distance to the expanding front estimated from the boundary of 10 males/trap, and log number of males per pheromone trap estimated at each cell using ordinary kriging. The LOGISTIC procedure of SAS, which fits linear logistic regression models for binary response data by maximum likelihood, was used in this analysis (SAS Institute 1992, Hosmer and Lemeshow 1989). The logit function had the form

$$\text{logit}(p) = \ln\left(\frac{p}{1-p}\right) = a + b'x, \quad [1]$$

where p is the response probability (in this case the probability that the cell will be defoliated), a is the intercept parameter, b_1, b_2, b_3, \dots are the vectors of slope parameters, and x_1, x_2, x_3, \dots are the vectors of independent variables. The value of p could then be calculated as

$$p = \frac{e^{\text{logit}(p)}}{1 + e^{\text{logit}(p)}}. \quad [2]$$

Fourteen models that used every combination of the 4 independent variables (log mass density, log number of males per pheromone trap, distance (KM) from the 10 males/trap boundary, presence (0,1) of defoliation in the same cell in the previous year) in equation 1 were estimated from data in GWNF.

We applied each of the 15 logistic regression models to predict defoliation for each of the 4 yr of the AIPM program in both GWNF and SNP and predicted probabilities of defoliation were compared with observed defoliation. In order to use p for decision-making, it is necessary to adopt a threshold probability, p' ; when estimated p is above the threshold, the cell will be

Table 1. Matrix of spray decision outcomes

	No defoliation	Defoliation
Don't spray	X_1 (correct)	X_2 (error)
Spray	X_3 (error)	X_4 (correct)

sprayed, and when estimated $p < p'$ then no action is taken. The selection of a value for p' will depend on managerial constraints, specifically the relative benefits and costs of correct and incorrect decisions. The 2 types of correct and 2 types of erroneous decisions are shown in Table 1. To evaluate the performance of each model, we simulated the use of decision-making with these models using values of p' ranging from 0.1 to 0.9.

We classified each 1-ha cell in GWNF and SNP into 1 of 4 possible outcomes (Table 1), depending on the predicted probability of defoliation (from each model) versus the observed defoliation. We also simulated decision-making by applying 1 of several widely used egg mass density thresholds to kriged egg mass density surfaces. This use of density threshold simulated the application of current gypsy moth management decision-making as is currently programmed in the GypsES decision support system (Foster et al. 1992, Gottschalk et al. 1996). We defined 3 types of errors:

$$\begin{aligned} \text{all errors} &= (X_2 + X_3) / (X_1 + X_2 + X_3 + X_4), \\ \text{error 2} &= X_2 / (X_1 + X_2) \\ \text{error 3} &= X_3 / (X_3 + X_4) \end{aligned}$$

where $X_1 - X_4$ are the frequencies (counts) in each cell in Table 1.

Results and Discussion

A map of kriged estimates of male moth capture is shown in Fig 3. During the AIPM program, the range of the gypsy moth was expanding to the south in this region and this phenomenon can be observed in these maps; counts were generally higher to the north and increased with progressive years (Sharov et al. 1996b). This phenomenon can also be observed in kriged maps of egg mass density (Fig. 4).

We developed 15 logistic regression models that used all possible combinations of the 4 independent variables (log mass density, log number of males per pheromone trap, distance (KM) from the 10 males/trap boundary, presence (0,1) of defoliation in the same cell in the previous year) to predict the probability of defoliation. The values of regression coefficients and regression statistics are shown in Table 2.

All coefficients of these models were significant. The signs of the coefficients made biological sense: The coefficients for log mass density and log number of males per pheromone trap were positive in all models, indicating that the probability of defoliation was positively correlated with counts of over-wintering egg mass populations and counts of adult males. This positive correlation apparently reflects the obvious correlation between the abundance of insects and the

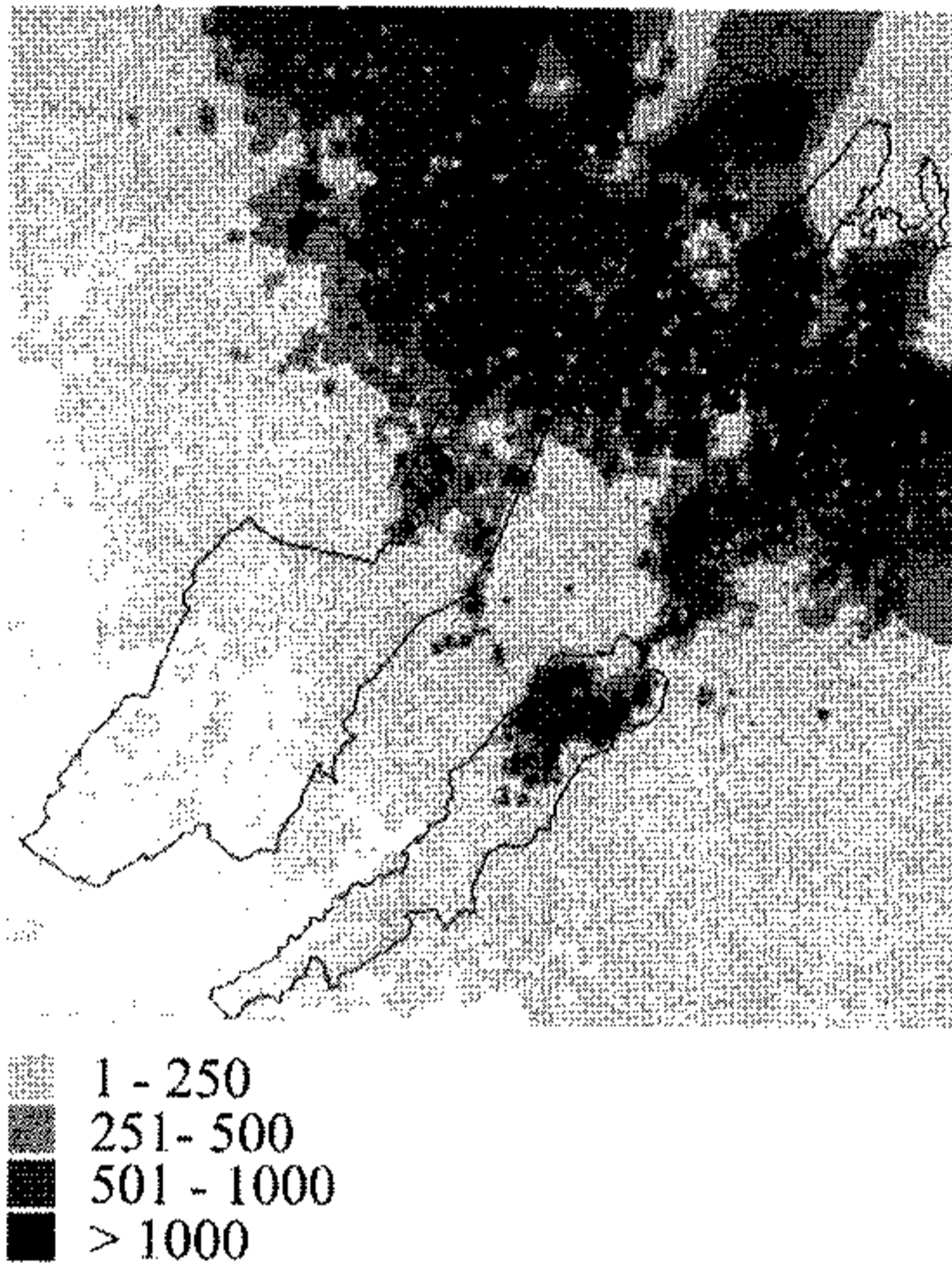


Fig. 3. Maps of pheromone trap counts estimated using ordinary kriging in SNP and GWNF in 1990.

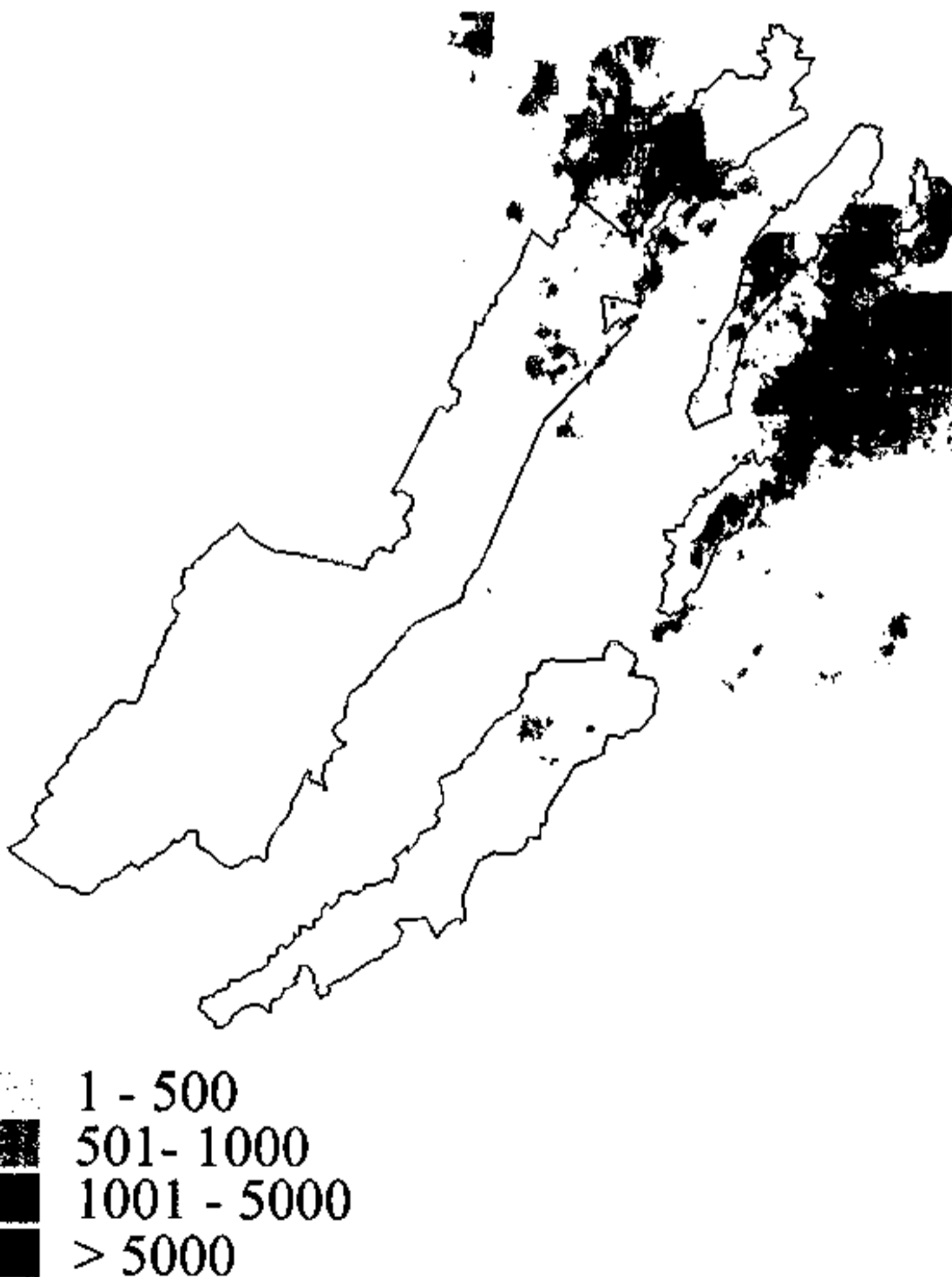


Fig. 4. Maps of egg mass densities estimated using ordinary kriging in SNP and GWNF in 1990.

Table 2. Statistics from maximum likelihood estimation of logistic models

Model Variable ¹	Parameter estimate	Standard error	Wald χ^2	P > χ^2
1 a	-2.11	0.00665	100619	0.0001
EM	0.392	0.00147	70812	0.0001
2 a	-2.77	0.0100	76049	0.0001
DIST	0.0316	0.000149	45362	0.0001
3 a	-12.3	0.0725	28740	0.0001
MALES	1.71	0.0108	25236	0.0001
4 a	-0.844	0.00461	33496	0.0001
DEF	1.00	0.0114	7759	0.0001
5 a	-2.95	0.0106	77208	0.0001
EM	0.317	0.00158	40399	0.0001
DIST	0.0190	0.000163	13603	0.0001
6 a	-9.11	0.0749	14801	0.0001
EM	0.335	0.00153	48311	0.0001
MALES	1.09	0.0113	9285	0.0001
7 a	-1.75	0.00708	61381	0.0001
EM	0.331	0.00157	44662	0.0001
DEF	0.240	0.0131	334	0.0001
8 a	-10.2	0.0777	17323	0.0001
MALES	1.19	0.119	10090	0.0001
DIST	0.0243	0.000162	22650	0.0001
9 a	-9.74	0.0716	18487	0.0001
MALES	1.36	0.0107	16166	0.0001
DEF	0.756	0.0117	4173	0.0001
10 a	-2.18	0.0101	47189	0.0001
DEF	0.132	0.0129	106	0.0001
DIST	0.0259	0.000156	27600	0.0001
11 a	-8.35	0.0776	11595	0.0001
EM	0.294	0.00158	34460	0.0001
MALES	0.864	0.0119	5280	0.0001
DIST	0.0147	0.000173	7190	0.0001
12 a	-8.049	0.074	11846	0.0001
EM	0.283	0.00161	31107	0.0001
MALES	0.978	0.0111	7751	0.0001
DEF	0.192	0.0130	218	0.0001
13 a	-2.54	0.0110	53047	0.0001
EM	0.278	0.00163	29018	0.0001
DIST	0.0180	0.000169	11281	0.0001
DEF	-0.218	0.0137	255	0.0001
14 a	-7.46	0.0766	9500	0.0001
EM	0.256	0.00164	24515	0.0001
MALES	0.788	0.0117	4555	0.0001
DEF	-0.135	0.0136	99	0.0001
DIST	0.0137	0.000180	5754	0.0001
15 a	-8.64	0.0759	12974	0.0001
DIST	0.0194	0.000169	13140	0.0001
MALES	1.03	0.0115	8022	0.0001
DEF	0.217	0.0127	289	0.0001

¹ EM, log egg mass density; MALES, log number of males per pheromone trap; DIST, distance (km) from the 10 males/trap boundary; DEF, presence (0,1) of defoliation in the same cell in the previous year.

amount of food that they consume. Coefficients for distance (km) from the 10 males/trap boundary were also positive for all models, indicating that as distance from the infested front (generally to the south of the area where defoliation was modeled) increased, defoliation probability increased. This phenomenon can be explained by the time lag that occurs between when gypsy moths are first detected in traps and when defoliation first occurs (Sharov et al. 1996a, b). If we had sampled populations farther from the infested front, this relationship may have been inverse, since outbreaks presumably collapse as one moves even farther from the infested front. In areas very far removed from the infested front (e.g., New England),

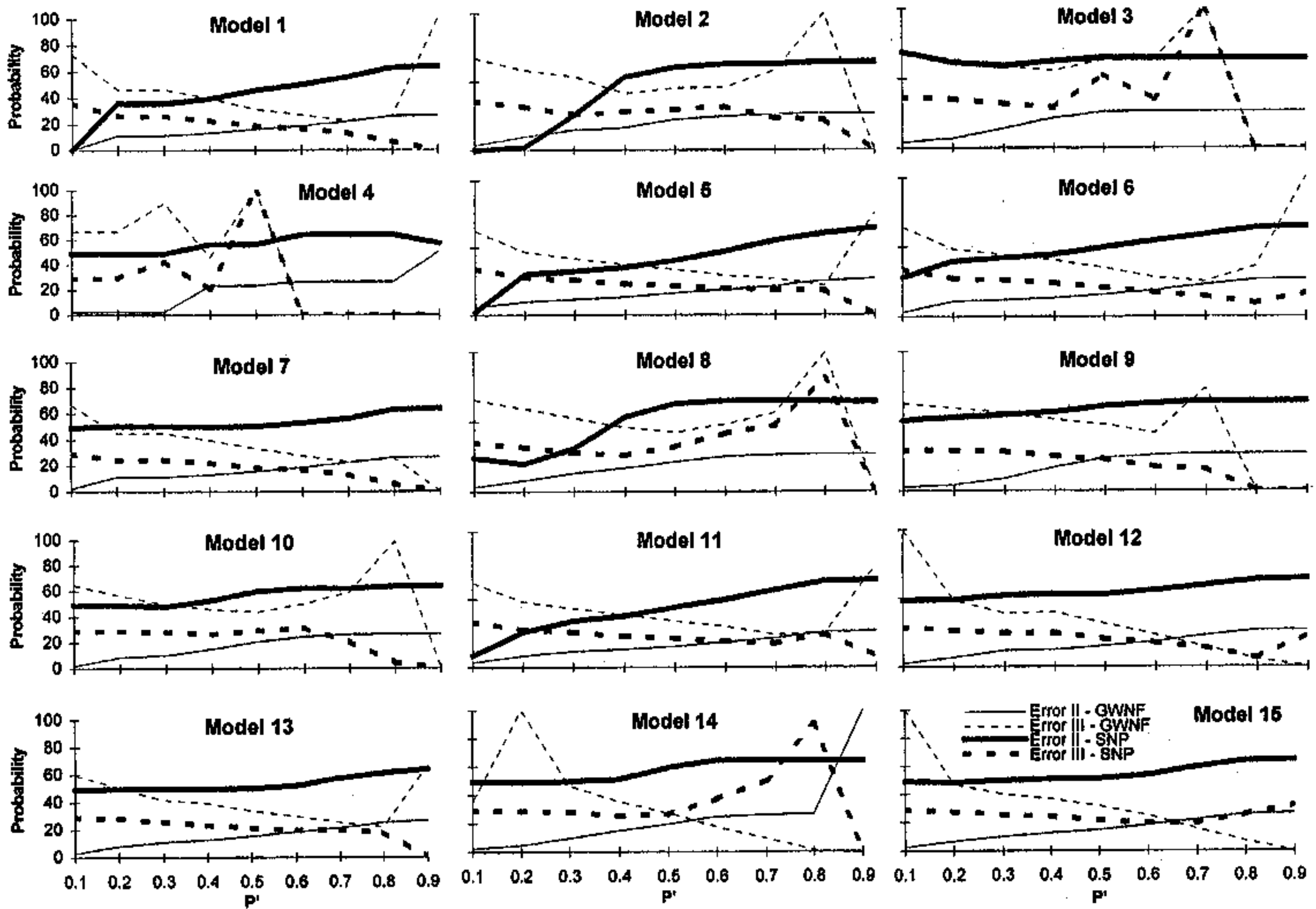


Fig. 5. Plots of simulated spray decision errors (percentages) versus values of probability thresholds, p' used with each of the 15 models.

there is presumably no relationship between defoliation probability and distance from the infested front. Coefficients for presence (0,1) of defoliation in the same cell in the previous year were sometimes positive (models 4, 7, 9, 10, 12, and 15) and sometimes negative (models 13 and 14). This probably reflects the complexity of the relationship between the presence of defoliation in the previous year with the probability of defoliation. When regional populations are rising, the presence of defoliation in the previous year would be positively correlated with the probability of defoliation, but when regional populations are declining, the probability of defoliation is inversely related to the presence of defoliation in the previous year (Liebhold and Elkinton 1989, Hohn et al. 1993, Zhou and Liebhold 1995).

Figure 5 shows simulated values of error 2 and error 3 versus values of p' at GWNF and SNP for each of the 15 logistic models. In all of the models at both GWNF and SNP, as p' increased, error 1 generally increased and error 2 generally decreased. This is logical since error 2 = 0 and error 3 = 1 when $p' = 0$ and error 2 = 1 and error 3 = 0 when $p' = 1$. In most of the models, error 3 was generally less stable relative to p' than was error 2; graphs of error 3 often exhibited a peak value at values of p' other than 0.1 (Fig. 5). For each model, error 2 was generally greater in SNP than it was at GWNF. This probably was caused by the use of GWNF data for model parameterization; parameters

were probably suboptimal for SNP. It is also evident in Fig. 5 that in GWNF, values for error 2 tended to be lower than values for error 3. This probably occurred because in the original data, most cells were not defoliated. The maximum likelihood procedure used for estimation of models 1-15, minimized all errors, and thereby error 2 values had more impact on the selection of model parameters than did error 3 values.

Table 3. Decision error percentages derived by application of models to GWNF and SNP data and setting $p' = 0.5$

Model	GNWF			SNP		
	Error 2	Error 3	All errors	Error 2	Error 3	All errors
1	16.1	31.4	19.2	45.9	18.8	31.9
2	22.3	45.3	25.4	60.4	29.7	49.1
3	26.2	63.0	27.5	64.7	52.5	64.3
4	23.3	100.0	27.4	56.3	100.0	60.2
5	16.3	33.4	19.8	40.3	21.1	28.5
6	15.7	34.5	19.8	49.4	20.5	35.3
7	15.5	33.2	19.3	50.3	18.4	36.3
8	21.3	42.1	24.3	62.7	32.0	54.6
9	23.7	47.4	26.1	60.4	22.7	52.1
10	20.8	43.7	24.6	59.9	29.1	48.3
11	15.3	33.7	19.4	44.0	21.1	30.8
12	15.1	31.1	19.2	52.7	20.0	39.0
13	15.5	33.8	19.5	50.2	21.4	36.1
14	14.7	31.4	18.9	51.0	21.4	37.0
15	19.4	27.1	21.5	59.3	26.5	48.2

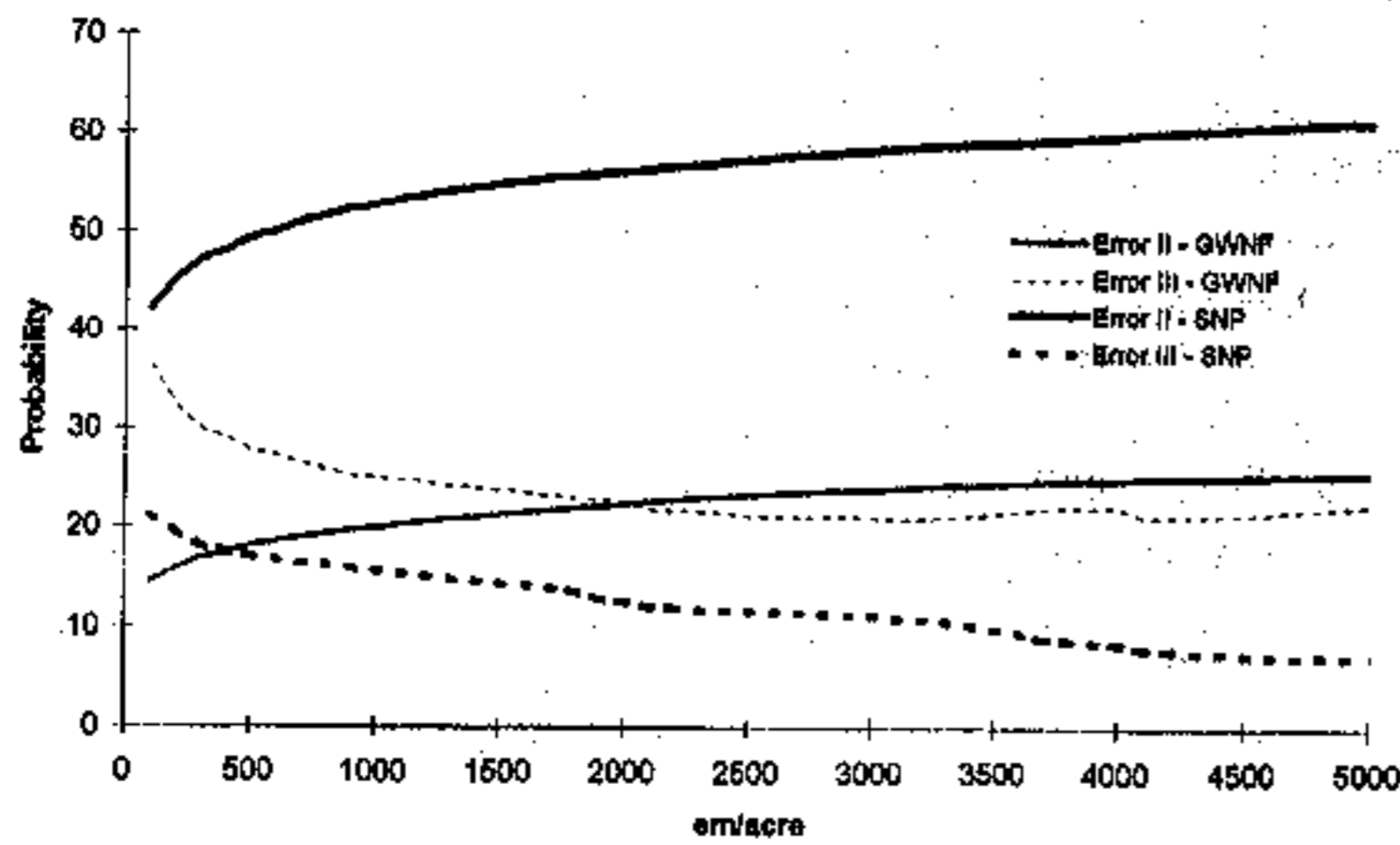


Fig. 6. Plots of simulated spray decision errors (percentages) versus values of threshold egg mass densities.

Table 3 shows values for error 2 and error 3 when $p' = 0.5$. As noted above, there was a tendency for decision error levels to be greater when models were applied at SNP than at GWNF presumably because parameters were chosen using data only from GWNF. Decision errors from GWNF were generally greatest for models that incorporated only one independent variable and were generally lowest for models that incorporated 3 or 4 independent variables. A noteworthy exception to this trend was model 1 which yielded very low decision error rates, especially error 2. Model 1 was also exceptional in its performance using data from SNP as well. When all 15 models were applied to SNP data, models 1, 5, and 11 yielded the lowest total of the 2 decision errors. All 3 of these models included log egg mass density as an independent variable.

Decision errors derived using 624 or 1,250 egg masses per ha treatment decision thresholds were in the same approximate range as errors from models 1, 5, and 11 (Fig. 6; Table 4).

Error 2 was greater at SNP than at GWNF but error 3 was lower. The sum of the 2 errors was greater at SNP than at GWNF. This difference suggests that the greater decision errors observed at SNP using models 1-15 (Table 3) may have been partially due to some inherent lack of association between log egg mass density and defoliation, rather than completely the result of parameterization of models using GWNF data.

The results shown in Tables 3 and 4 indicate that use of traditional egg mass density thresholds may perform as well, or better than, the logistic models presented here. The only exception may be models 5 and 11 which appeared to perform as well or better than the egg mass density thresholds in terms of reducing de-

cision errors. Both models 5 and 11 contain the terms log egg mass density and distance (km) from the 10 males/trap boundary, suggesting that information on the distance of the stand relative to the expanding gypsy moth front may provide information useful for predicting defoliation and making management decisions. Thus, gypsy moth populations appear to reach defoliating densities in a predictable manner, as the leading edge passes through an area (Sharov et al. 1996a) although distance by itself (model 2) provided a poor predictor of defoliation (Table 3). In areas, such as New England, where gypsy moth populations have been established for many years, distance to the expanding front is likely irrelevant to the probability of defoliation and thus these models are only appropriate in areas near the expanding front. Capture of males in pheromone traps, MM, also was a very poor predictor of defoliation in a single term model (model 4, Table 3). Liebhold et al. (1995) found that counts of males in pheromone traps were much lower in spatial correlation with defoliation than were counts of egg masses in Massachusetts. These results support that conclusion. This lack of correlation is probably the result of male moth dispersal over considerable distance (Carter et al. 1992, Ravlin et al. 1991, Liebhold et al. 1995).

Table 4 and Figure 6 illustrate that the choice of an egg mass density threshold for use in treatment decision-making should depend upon the manager's adversity to error 2 relative to error 3. For example, a forest products company may own a stand of high-value veneer trees that is approaching a scheduled harvest event and would therefore be very adverse to any defoliation events that might put those trees at risk to mortality. Thus, the company may choose to use an egg mass density threshold of 100 egg masses per ha or less that minimizes error 2 (Table 4). Because the company will realize considerable profit in the near future when the trees are harvested, it may be willing to spend money on treatments when they may not have been necessary, error 3. In contrast, a private individual may manage a woodlot primarily for its wildlife and scenic value. In this situation, the landowner may be more adverse to unnecessary applications of pesticides (error 3) because of concern over impact on nontarget organisms and other environmental concerns. In this case, the landowner may opt for a treatment threshold of 1,000 egg masses per hectare (≈ 500 egg masses per acre) or greater to minimize error 3 (Table 4). In this case, the landowner may be willing to tolerate a higher frequency of defoliation when the decision was made to not treat an

Table 4. Decision error percentages derived by application of egg mass density treatment thresholds to GWNF and SNP

Egg mass density threshold (egg masses/ha)	GWNF			SNP		
	Error 2	Error 3	All errors	Error 2	Error 3	All errors
625 (250 egg masses/acre)	16.5	30.6	19.2	46.6	18.4	32.5
1,250 (500 egg masses/acre)	18.1	27.8	19.6	49.3	17.0	35.1

area (error 2) because the impacts of defoliation on wildlife and scenic values may be considered less significant.

While this study failed to yield landscape-level models that performed substantially better than the traditional application of egg mass density thresholds (Tables 3 and 4), it is possible that superior landscape-level models may be developed in the future. For example, the models developed here did not incorporate any landscape-level information on forest composition and it seems likely that certain habitat data may aid considerably in predicting future defoliation events. Montgomery (1990) reported that inclusion of data on forest composition increased the predictive power of stand-level defoliation models. Landscape-level data on forest composition over the eastern United States are currently available only at very coarse spatial scales (Liebhold et al. 1997). However, in the future, new map data may become available and these should be useful in models that predict gypsy moth defoliation.

This study represents the first exploration of error rates associated with treatment decisions that are based upon egg mass density thresholds (Fig. 6, Table 4). It is obvious that the use of these thresholds results in very large values of error 2 (16–49%) and error 3 (17–31%). It is perhaps surprising from Figure 6 that the use of egg mass thresholds for gypsy moth treatment decision-making results in such large levels of error. The data used in this study were collected in a rapidly rising gypsy moth population in a highly susceptible forested area and these error probabilities cannot be universally applied elsewhere in the gypsy moth's range. Nevertheless, the conclusion that the use of egg mass density thresholds is an error-prone practice is consistent with recent recognition that the relationship between egg mass density and defoliation is highly stochastic (Montgomery 1990, Liebhold et al. 1993b). These high errors highlight the need for better methods for predicting defoliation so as to develop more effective gypsy moth management practices.

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