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ARTICLE

Evaluation of Effectiveness of Fixed-Station Sampling for Monitoring American Lobster Settlement

Bai Li, Jie Cao, and Jui-Han Chang
School of Marine Sciences, University of Maine, Orono, Maine 04469, USA

Carl Wilson
School of Marine Sciences, University of Maine, Orono, Maine 04469, USA; and Maine Department of Marine Resources, 194 McKown Point Road, West Boothbay Harbor, Maine 04575, USA

Yong Chen*
School of Marine Sciences, University of Maine, Orono, Maine 04469, USA

Abstract
The American lobster *Homarus americanus* supports one of the most valuable fisheries in the USA. One of the important monitoring programs is for benthically settled lobsters, which closely relates to recruitment. The lobster settlement sampling program follows a fixed-station design. However, the performance of this design has not been evaluated, and we are unclear if the design can capture the temporal dynamics of settlers, in particular in response to changes in spatial distribution of lobster in the last 2 decades. In this study, we compared the fixed-station design with a random sampling design for the mid-coast region of the Gulf of Maine. We developed a generalized additive model (GAM) to quantify the relationship between habitat variables and density of early benthic phase and older juvenile lobsters by using the data from inshore trawl surveys from 1989 to 2012. The GAM model was then used to simulate putative true populations using the habitat variables. The two different sampling designs were applied to sample the simulated true populations. The fixed-station sampling design tended to underestimate the true density but could capture the temporal trends in settler density. A persistence index analysis suggests that the fixed-station design could identify interannual change of the lobster settler density. This study suggests that fixed-station sampling design is effective in monitoring temporal changes in settler density but could not be used for the estimation of absolute density of settlers.

The American lobster *Homarus americanus* supports one of the most valuable commercial fisheries in the USA, and its management requires continuous monitoring of its abundance and distribution. The landings of American lobster were over 67,800 metric tons and were worth over US$461 million in 2013 (NOAA 2013). More than 85% of the total landings in the USA occur from the inshore waters of the Gulf of Maine (ASMFC 2009; NOAA 2013). However, the distribution and abundance of the American lobster vary along the Gulf of Maine over years (Chen et al. 2006). The distribution of the American lobster has been well studied (Bowlby et al. 2008; Steneck and Wahle 2013; Green et al. 2014) and can be influenced by many environmental variables (Cooper et al. 1975; Cowan et al. 2001; Selgrath et al. 2007; Chang et al. 2010). The spatial and temporal patterns of adult lobster abundance were found to be associated with postlarval settlement indices (Wahle et al. 2004; Xue et al. 2008).

Long-term monitoring of benthic settlers can provide vital information for understanding the recruitment dynamics of the American lobster in the Gulf of Maine. Such a program can collect data about species density and associated environmental and spatial variables at selected sites annually. Initiated in 1989, the

*Corresponding author: ychen@maine.edu
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American Lobster Settlement Index (ALSI) program is an annual diver-based survey of newly settled young of year and older juvenile lobsters in the Northeast USA and Atlantic Canada (Wahle et al. 2010). This settlement survey covers the longest monitoring time series, more than 20 years, in the mid-coast region of the Gulf of Maine. Unlike most of the fishery-independent monitoring programs, which follow stratified random survey designs (NRC 2000; Liu et al. 2009), the ALSI monitoring program follows a fixed-station design with the sampling stations unchanged throughout the survey period. The effectiveness of such a design in capturing the temporal variability of newly settled lobsters has not been evaluated. Thus, it is unclear if this settlement survey can quantify temporal variability of young of year lobsters, particularly in response to changes in the spatial distribution of the Gulf of Maine lobsters in the last 2 decades (ASMFC 2009; Wahle et al. 2010).

There has been debate on the advantages and disadvantages of fixed-station versus random-station sampling designs (Warren 1994; Seng 1951; Quist et al. 2006). A random-station sampling design tends to yield unbiased estimates and is often used for its precision. Fixed-station sampling is often examined for its accuracy in identifying possible biases as a result of lack of randomness in the selection of samples (Warren 1994). One objective of this study was to evaluate whether the fixed-station sampling design that has been used in the ALSI settlement survey can capture the temporal dynamics of lobster settlers. Specifically, we temporally simulated true populations of the distribution of newly settled lobster in the mid-coast region of the Gulf of Maine based on a two-stage generalized additive model (GAM) model and then applied both fixed and random designs to sample the simulated population. We compared the estimated and simulated true population densities for both the fixed and random survey designs to calculate estimation error. The estimation errors were then compared between the fixed and random survey designs to determine their performance in capturing the temporal variability of the lobster settlers. Additionally, persistence indices were calculated to evaluate the fixed-station sampling power of detecting temporal trends in lobster density.

METHODS

The fixed-station sampling data from the ALSI were used in this study for evaluating the performance of the program to detect temporal trends in lobster density. Since we want to compare fixed-station and random-station sampling designs, we need to simulate a true population of American lobster in the mid-coast region of the Gulf of Maine so that both the sampling designs could be applied to sample the simulated population. We used generalized additive model (GAM; Hastie and Tibshirani 1990) to quantify the statistical relationship between the abundance of American lobsters and environmental and spatial variables, and we used the developed the GAM model to project the spatial distribution of the lobsters, which we considered as a true population.

Maine–New Hampshire Inshore Trawl Survey data.—Data from 2000 to 2012 in the fall Maine–New Hampshire inshore bottom trawl survey were used to build the GAM model. The Maine–New Hampshire Inshore Trawl survey has been conducted along the coastal waters of Maine and New Hampshire since the fall of 2000 (Chen et al. 2006). It is a semiannual survey conducted in spring (April–June) and fall (September–November). The trawl survey has a target tow duration of 20 min for each site and collects environmental at each sampling site (e.g., temperature, salinity, and depth) in addition to biological information for each lobster (e.g., carapace length [CL], weight, and sex]. The number of sampling sites covered in a given year varies from 54 to 99 stations within the four depth strata (Figure 1). The standardized lobster density (around 0.01 km^2/tow) was estimated based on the lobster less than 60 mm CL. The data from early benthic phase lobsters and older juveniles we used for developing and validating the habitat model for simulating the distribution of newly settled lobsters.

Environmental and spatial data.—The environmental and spatial data that are associated with potential sampling stations in the mid-coast region were obtained for the development of GAM model. Bottom water temperature, salinity, latitude, longitude, depth, distance offshore, sediment type, and distance to sediment boundary were identified as environmental and spatial variables influencing the distribution and abundance of lobster (ASMFC 2009; Chang et al. 2010), and they were included in the GAM in this study. The bottom water temperature and salinity from the trawl survey were directly used to build the GAM. The bottom water temperature and salinity data associated with potential sampling stations were obtained through spatially interpolating the data from finite-volume, primitive equation community ocean model (FVCOM; Chen et al. 2006). We extracted the depth (m) data from U.S. coastal relief model (NOAA 1999) for the Northeast Atlantic region. The sediment information was gathered from the map of sediment grain-size distribution for the U.S. east coast (Continental Margin Mapping Program; Poppe et al. 2005). The distance to sediment boundary was calculated using Arc GIS 10.3 (Chang et al. 2010).

Lobster settlement data.—We used lobster density data from the ALSI survey program between 1989 and 2013 to evaluate the power of the fixed-station sampling program in detecting temporal trends. Unlike the bottom trawl survey that collects data for multistpecies, the ALSI program targets American Lobster. The program covers coastal areas from Nova Scotia to Rhode Island. This diver-based suction sampling was conducted in all the sites at the end of the settlement season each year. Divers collected lobsters from 12 to 20 quadrats (0.5 m^2/quadrat) by using an air-lift suction sampler (Pershing et al. 2012). The sizes of young of year lobsters are $<$10.5 mm CL, and the sizes of juveniles are 11–60 mm CL (Wahle and Steneck 1992). We chose the mid-coast region of Gulf of Maine as the study area because it has one of the

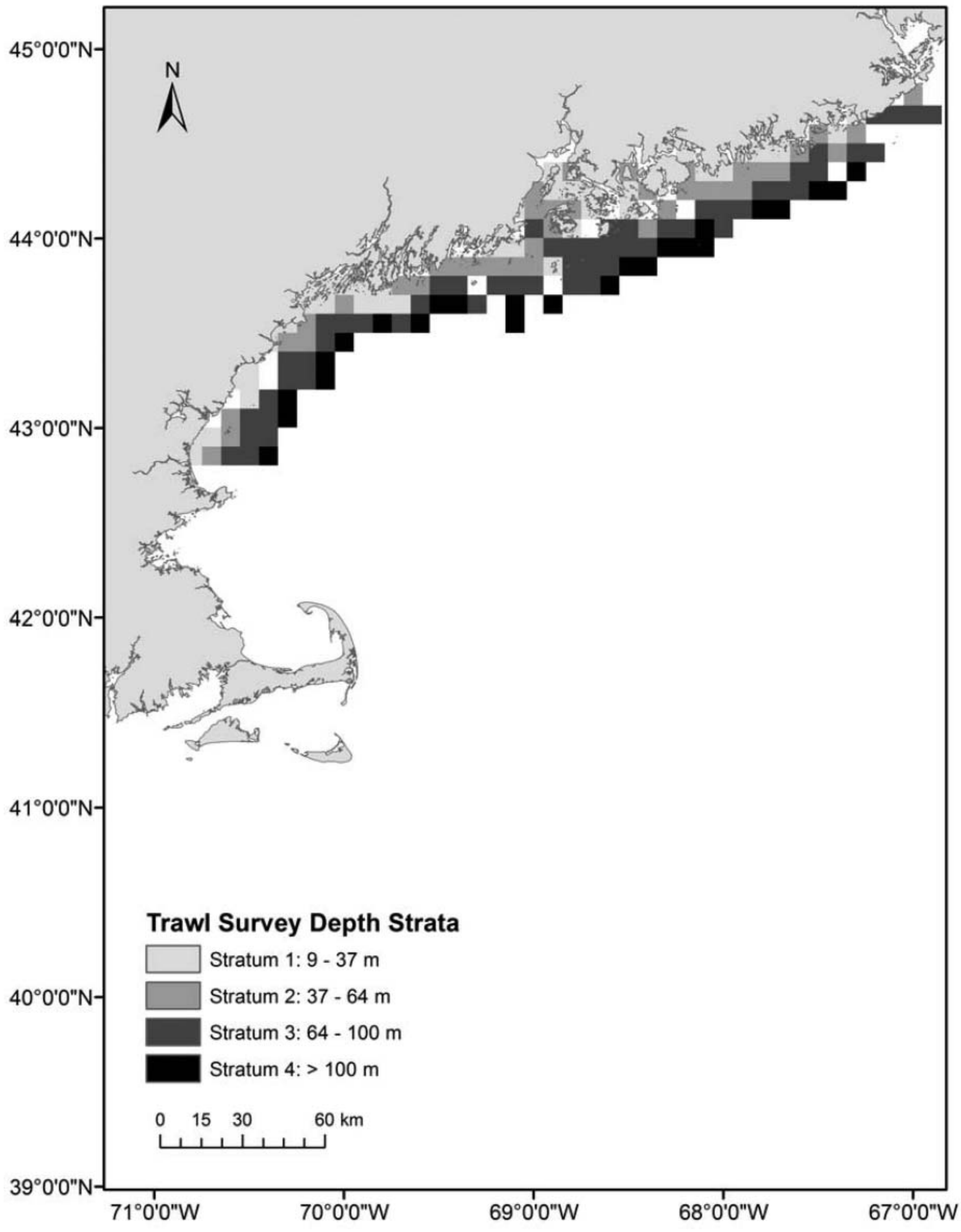

FIGURE 1. American lobster trawl survey area in the Maine–New Hampshire region by four depth strata.

longest time series data in the ALSI program. In this region, 10 fixed sampling stations were revisited every year (Figure 2).

Development of two-stage generalized additive model.— The GAM has been used for predicting density of American lobsters and blue crabs *Callinectes sapidus* as a function of environmental and spatial variables (Jensen et al. 2005; Chang et al. 2010). The GAM can fit nonlinear response curves to individual predictor variables. We developed a two-stage

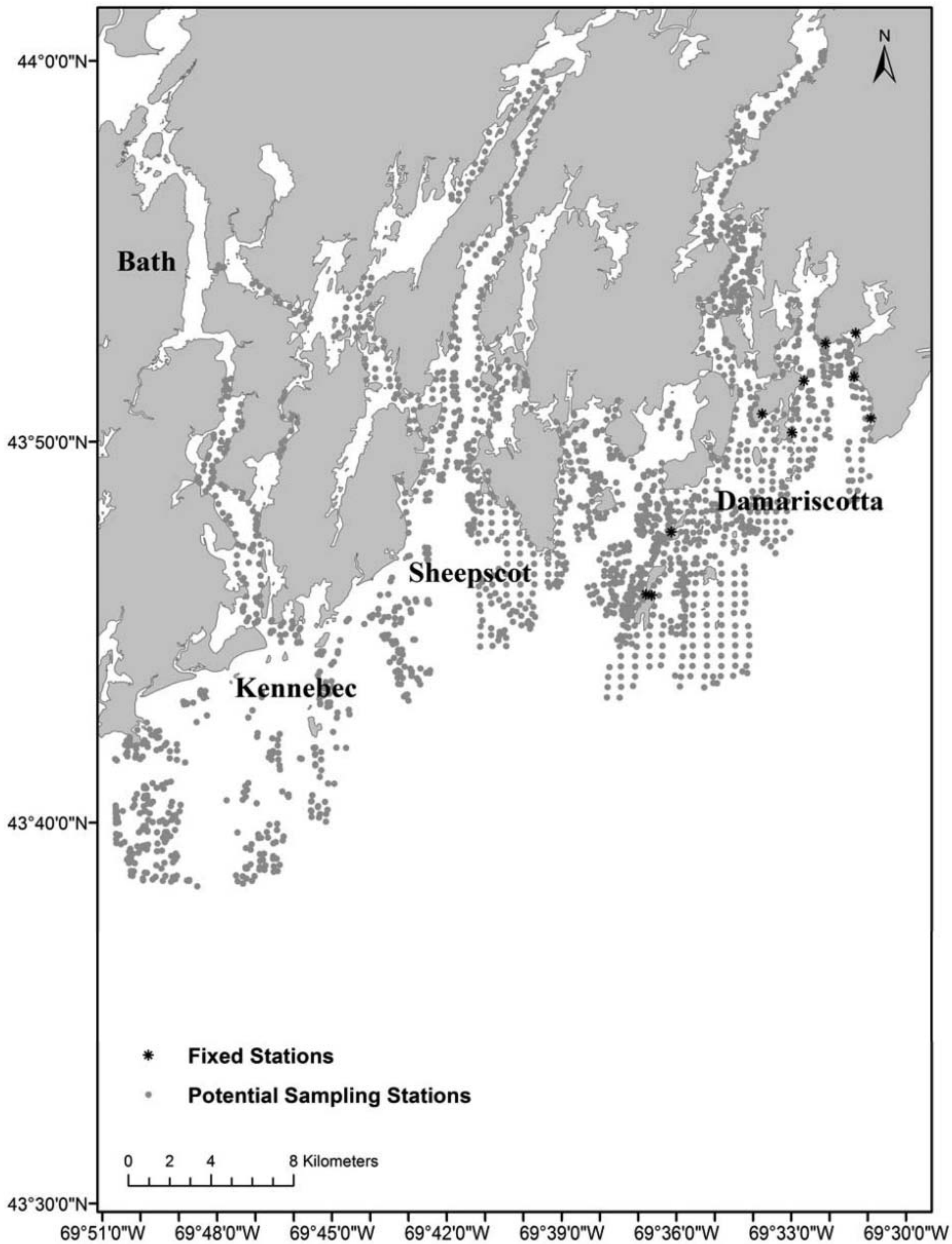

FIGURE 2. Map of mid-coast region of the Gulf of Maine and showing fixed and potential American lobster sampling stations.

GAM to quantify the relationship between lobster survey data and environmental data. Following Chang et al. (2010), the environmental variables built into the model include water temperature (T; °C), salinity (S), settlement type (Se), depth (D; m), distance offshore (DO; decimal degree), distance to the settlement boundary (DS; decimal degree), latitude (La), and longitude (Lo). The first stage GAM estimates the presence of lobsters (p) by using a logit link function with a binomial error distribution,

$$\text{GAM1}: \text{logit}(p) = s(T) + s(S) + s(De) + s(DO) + s(DS) + s(La) + s(Lo) + Se + \varepsilon, \quad (1)$$

where s is spline smoother. The second stage GAM estimates the log-transformed lobster density (d) by using an identity link function with a Gaussian error distribution (Berry and Welsh 2002):

$$\text{GAM2}: \ln(d) = s(T) + s(S) + s(De) + s(DO) + s(DS) + s(La) + s(Lo) + Se + \varepsilon. \quad (2)$$

The comprehensive log-transformed lobster density log(y) (log[number/0.01 km^2]) is estimated by combining the results generated from the first (equation 1) and second (equation 2) stages of the GAM:

$$\ln(y) = \ln(p) + \ln(d) \quad (3)$$

We conducted a preliminary analysis to evaluate the significance of variables in both single and interaction terms. Eight variables were included initially in each stage of the GAM, then the most significant single terms were selected and included as the main effects in the models, based on correlation analysis and chi-square statistical significance ($\alpha = 0.05$; Jensen et al. 2005; Chang et al. 2010). We then evaluated all the possible interaction terms for each stage of the GAM. The most significant interaction term was added to the model as one of the main effects. We compared the model with interaction terms and the model without interaction terms based on the explanatory power. The interaction term was kept if the explanatory power of the model with interaction term was at least 5% greater than the model without the interaction term (Chang et al. 2010).

The performance of the derived model was evaluated using a cross-validation approach (Franklin and Miller 2009). We divided the fall trawl survey and environmental data into training and testing data sets before validating the model. The partitioning of training and testing data sets are random and based on a ratio of 3:1 since the number of predictors was more than five (Franklin and Miller 2009). We compared the predicted lobster density, log(y) (log[number/0.01 km^2]), based on the model developed using training data with the observed lobster density, log(y') (log[number/0.01 km^2]), of the testing data by using the following simple linear regression model:

$$\ln(y') = a + b \times \ln(y) \quad (4)$$

We ran the cross-validation 100 times and averaged the estimated performance measures (Fielding and Bell 1997). The averaged a and b values indicate bias in predicted density. A value of $a = 0$ and a value of $b = 1$ imply that predicted lobster density and observed lobster density (i.e., testing data) have similar spatial patterns and the model has a good predictive performance.

Simulation study.—The density, log(number/0.01 km^2) distributions of early benthic phase lobster and older juveniles in the mid-coast region from 1989 to 2012 were simulated using the GAM model. These distributions were considered as true populations for applying fixed and random sampling schemes. There are 1971 potential sampling stations identified in the mid-coast region of the Gulf of Maine (Figure 2). The GAM model yielded the prediction of lobster density and associated standard deviation for each potential sampling station for each year from 1989 to 2012. For each year, 1,000 realizations of the true population were generated based on the variation in the predicted lobster density among potential sampling stations.

Both fixed and random sampling designs were applied to the 1,000 realizations of the true population each year with a sample size of 10. For the fixed sampling scheme, 10 stations out of the 1971 potential sampling stations that were closest to the 10 fixed stations used in the actual settlement survey were selected. For the random sampling scheme, the sampling process was repeated 100 times with a sampling size of 10 for a given realization of the true population. The 100 replicates were averaged to obtain the true random sampling results for each given realization. As a result, the two sampling schemes each yielded 1,000 sets of estimated mean lobster settler density, log(number/0.01 km^2) for each year. The 1,000 sets of the estimated mean lobster density for each sampling scheme were compared with the mean of true population parameter V^{true} (Yates 1946; Chen 1996; Kimura and Somerton 2006). We calculated relative estimation error (REE) and relative bias (RB) to quantify the comparison result:

$$\text{REE} = \frac{\sqrt{\frac{\sum_{i=1}^{N}(V_i^{estimated} - V^{true})^2}{N}}}{V^{true}} \times 100\%, \quad (5)$$

$$\text{RB} = \frac{\frac{\sum_{i=1}^{N} V_i^{estimated}}{N} - V^{true}}{V^{true}} \times 100\%, \quad (6)$$

where $V_i^{estimated}$ is the estimated mean lobster density of 10 sampling stations in the ith sampling, V^{true} is the mean lobster density of 1971 potential sampling stations for each simulation, and N is the sampling times for a given realization of the true population (i.e., 100 for random station sampling and 1 for fixed station sampling in this study). The REE values reflect the difference between sampling results and true lobster density in an area over time and measure both bias and variation in the evaluation. The RB measures the estimation bias.

A sampling design with smaller REE and RB values indicates better performance (Chen 1996). The fixed-station sampling

TABLE 1. The relationship between degree of persistence (ϖ) values and the probability of fixed-station design being able to estimate interannual change (Warren 1994). The probability value indicates the power of the fixed-station design that can detect the temporal trend of lobster settler density in the mid-coast region of the Gulf of Maine.

ϖ	Probability (%)
0.1	98.1
0.2	91.7
0.3	85.9
0.4	81.4
0.5	77.9
0.6	75.2
0.7	73.0
0.8	71.1
0.9	69.6

design was thought to have biased estimation compared with the random station sampling design and was expected to have a higher value of RB. However, it is unclear if the fixed-station design can yield an abundance index capturing temporal trends of lobster settlers, which is usually a main goal for a monitoring program in fisheries (Hilborn and Walters 1992).

Persistence index analysis.—We estimated stability in American lobster density (number/m^2) by measuring persistence. The measure of degree of persistence (ϖ) was estimated based on lobster density data from the ALSI settlement survey (1989–2013). We did a pairwise comparison of lobster density of all the years and estimated the fixed-station sampling power of detecting temporal trend of the lobster density in mid-coast region of the Gulf of Maine. The value of ϖ (measurement of persistence degree) can be calculated as (Warren 1994)

$$\varpi = \frac{s_y^2/4}{s_s^2 - s_y^2/4}, \quad \text{where} \tag{7}$$

$$s_s^2 = \frac{\sum_{y=1}^{2} \sum_{y=1}^{n_i} (x_{iy} - \bar{x}_y)^2}{(m_1 + m_2 - 2)}, \text{ and} \tag{8}$$

$$s_y^2 = \sum_{i=1}^{m} (d_i - \bar{d})^2/(m-1); \tag{9}$$

s_y^2 = the difference in lobster density of the same site between different years,
s_s^2 = the difference in lobster density between different sites in the same year,
x_{iy} = observed lobster density in site i and year y,
$\bar{x}_y$ = the mean observation of year y,
m_1 = the number of fixed stations in the first years included in the pairwise comparison,
m_2 = the number of fixed stations in the second year included in the pairwise comparison,
d_i = the difference in density between the two years in site i, and
$\bar{d}$ = the mean of the density difference.

A smaller value of ϖ indicates a greater degree of persistence as indicated in Table 1, where values of probability ($\chi^2 < (1 + \varpi)/2\varpi$) for selected ϖ are presented.

RESULTS

Two-Stage GAM Selection and Performance

There were 25 pairs of explanatory variables that had significant correlations among all possible pairs of variables. Latitude and longitude were highly correlated (r = 0.93). Based on a regression tree analysis, we dropped latitude from the main explanatory variables. The two-stage GAM with the remaining seven variables explained 36.5% and 48.8% variances for the first and second stages, respectively. There were five variables in each stage of the GAM after nonsignificant variables (P > 0.05) were removed (Table 2). Salinity (S) and distance to sediment boundary (DS) were found not significant in both stages of GAM. All possible interaction terms for both stages of the GAM did not increase explanatory power. Thus, no interaction terms were included in the final model. The final first stage GAM had a value of 37.7% for deviance and 0.40 for adjusted R^2; and the second stage GAM had 48.8% for explained deviance and an adjusted R^2 of 0.47 (Table 2).

The response curves were presented in Figure 3 for significant variables longitude (*Lo*), bottom water temperature (*T*), depth (*De*), distance offshore (*DO*), and sediment type (*Se*). Lobster presence and density were found to be linearly related to temperature. As temperature increased, presence probability and density of the American lobster also increased. The other environmental variables showed complex relationships with lobster presence and density. The peak presence and density of lobster occurred within depth ranges of 50–75 m. Effects of

TABLE 2. Model selection and performance for the first-stage general additive model (GAMI; presence or absence) and second stage GAM (GAMII; abundance). The significance test results (bold indicates significant, P > 0.05) are given by model and the seven initial variables: temperature (*T*), salinity (*S*), depth (*De*), distance offshore (*DO*), sediment boundary (*DS*), longitude (*Lo*), and sediment type (*SE*). The data size (*N*) and adjusted R^2 were also explained for each model.

Model	***T***	*S*	***De***	***DO***	*DS*	***Lo***	***Se***	*N*	R^2 adj
GAMI	0.001	0.671	<0.001	<0.001	0.271	<0.001	0.02	877	0.40
GAMII	<0.001	0.712	<0.001	<0.001	0.557	<0.001	0.01	658	0.46

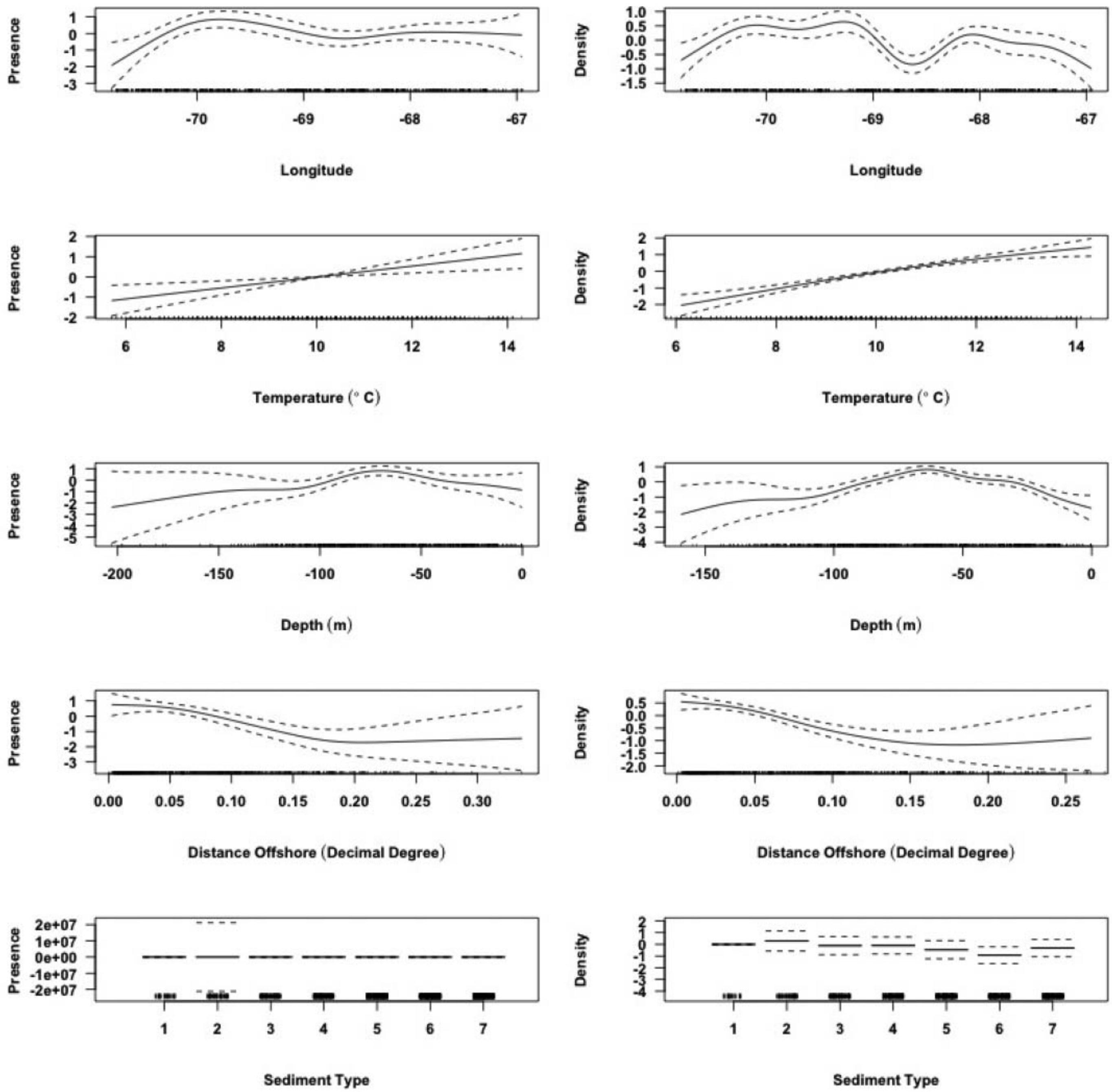

FIGURE 3. Response curves for significant variables of two-stage general additive model (GAM); panels on left are GAMI and those on the right are GAMII. The *y*-axis is the normalized effect of the variables on presence and density component. The *x*-axis is the observed values. Dashed lines give 95% confidence intervals. Sediment type: 1 = gravel, 2 = gravel–sand, 3 = sand, 4 = clay–silt/sand, 5 = sand–clay/silt, 6 = sand–silt/clay, 7 = sand/silt/clay.

distance offshore were significant in both stages of the model. The presence and density of lobster decreased with increased distance offshore. The probability of presence and density of lobster were significantly higher in the gravel sediment and lower in the sand–silt–clay sediment. The response curves from the two-stage GAM support our understanding of lobster ecology.

Model Evaluation

The adjusted R^2 values for the 100 cross-validation runs varied from 0.24 to 0.48. There was a positive relationship between predicted and observed lobster densities (Figure 4). The mean intercept value was 0.86 (SE, 0.27), and the mean slope value was 0.83 (SE, 0.08). The intercept values were significantly larger than 0 ($P < 0.001$), and the slope values were significantly different from 1 ($P < 0.001$). This indicates that the two-stage GAM might have biased predictions for lobster density in the mid-coast region of the Gulf of Maine. However, its predictive performance is sufficient for simulating a reasonable distribution of the true population in this study for evaluating the two sampling designs.

Predicted Distribution of Young Lobsters

The predicted lobster density, log(number/0.01 km^2), varied from 1.38 to 6.29 during 1989–2012 (Figure 5), and the lowest density mean (in 1993) was 1.38 (SE, 0.42). The density increased dramatically in 2012 with a mean of 6.29 (SE, 0.61). The models predicted stable spatial patterns of lobster on sampling stations. The lobster density was higher in the inshore region of Kennebec and Damariscotta Rivers than in the Sheepscot River. There were several hot spots having high lobster density in the mouth of the rivers. The lobster density decreased as distance offshore increased. The spatial patterns were similar for all predicted years.

The mean of 1,000 realizations of the true population for each year was calculated (Figure 6). The mean density of American lobsters was low during the late 1990s but increased dramatically from 2008 to 2012. The mean density of 1,000 simulation runs for each sampling design (i.e., fixed-station

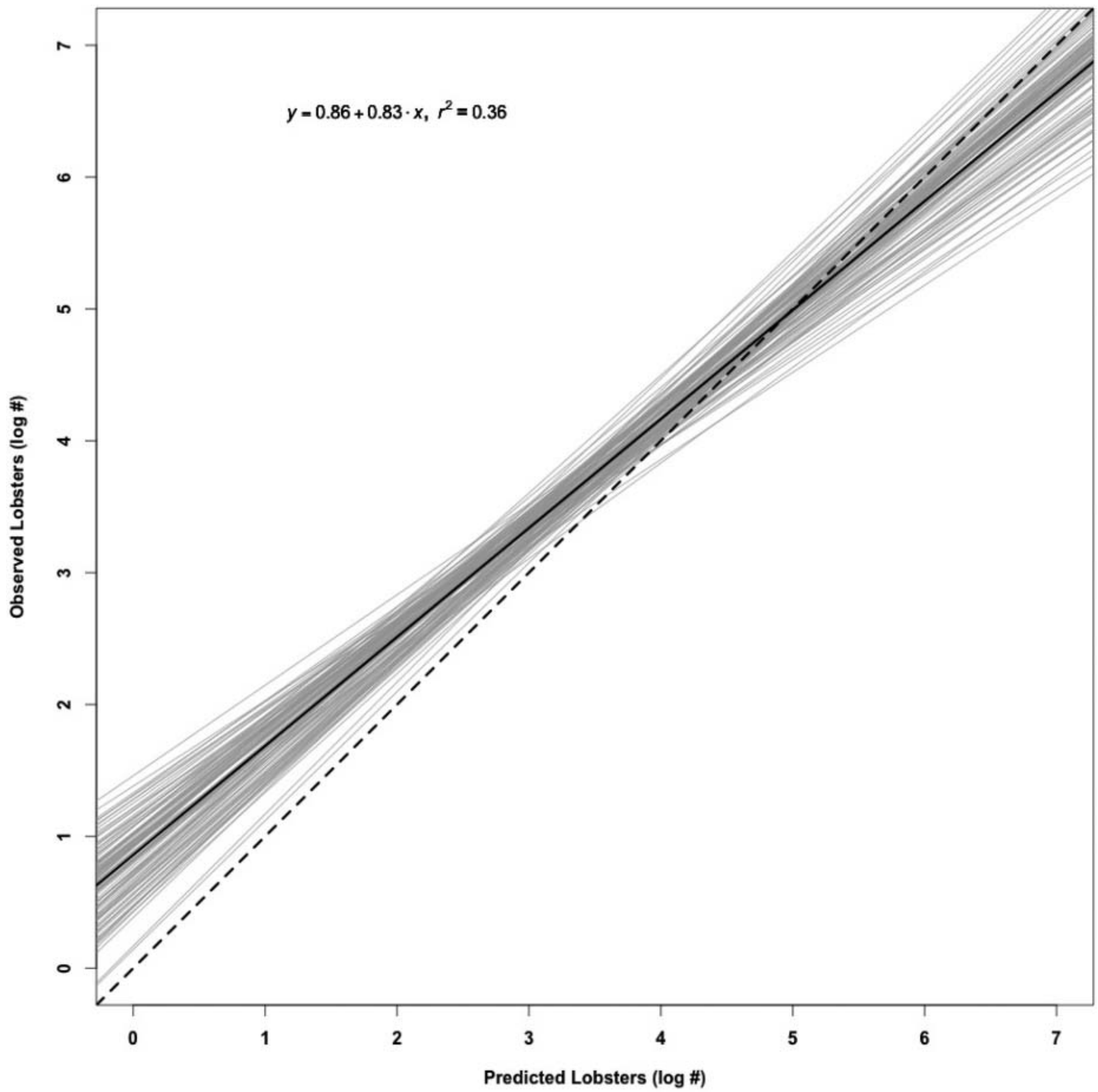

FIGURE 4. Bottom trawl survey data model cross-validation comparing the predicted versus observed lobster density as log(number/0.01 km^2). The light gray solid lines are 100 linear regression lines fit to all of the data. The black solid line is the mean of cross validation results. The dashed line is the 1:1 line.

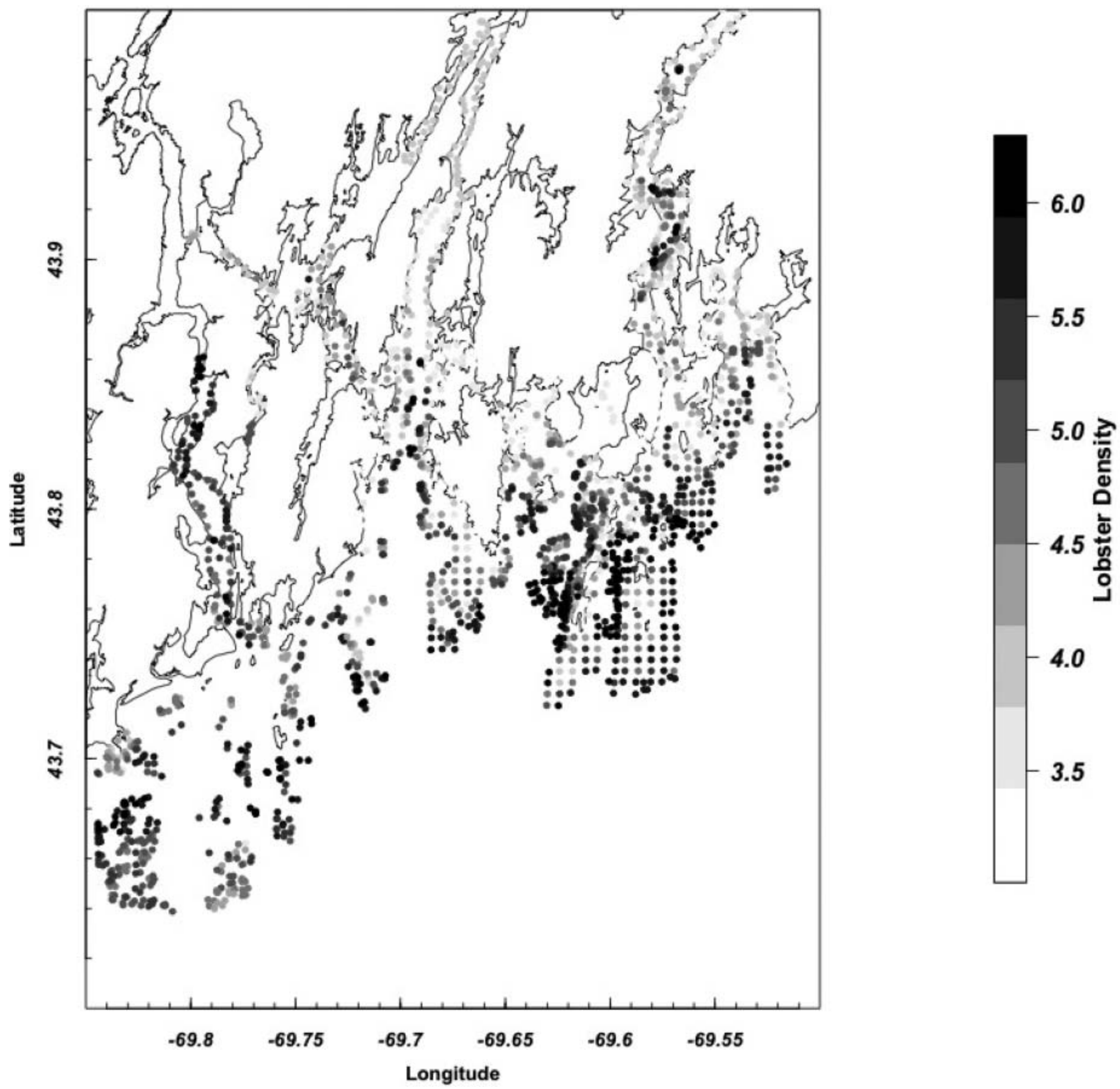

FIGURE 5. Simulated American lobster density, log(number/0.01 km^2), at potential sampling stations in the Gulf of Maine, 2012.

and random design) was calculated, showing temporal trends similar to the true population for both the sampling designs. However, the variability of estimates for the fixed-station sampling was much greater than that for the random-station sampling design. The mean density of random sampling and the mean density of the true population were the same, suggesting that the random design yielded unbiased estimates. The fixed sampling, however, underestimated the true simulated population.

The fixed-station sampling process had a relatively high variation compared with the random station sampling because the variability of random sampling for a given realization of true population was averaged. Random sampling was repeated 100 times for a given realization, and the estimated mean was the average of the 100 sets of sample means. We conducted the fixed-station and random-station sampling once in each year for a given realization of true population, and the random sampling design yielded a larger variance of mean density than the fixed sampling design (Figure 6). The reason we repeated the random station sampling 100 times for each realization was to obtain the true random station sampling result for a given realization. For the same reason, Moffett et al. (2011) also used 100 repetitions of random port removal for error index estimation to evaluate the impact of reducing sampling effort on a northern shrimp port monitoring program.

Relative Estimation Error and Relative Bias

Based on the REE values, the random-station sampling design had better performance than the fixed-station sampling

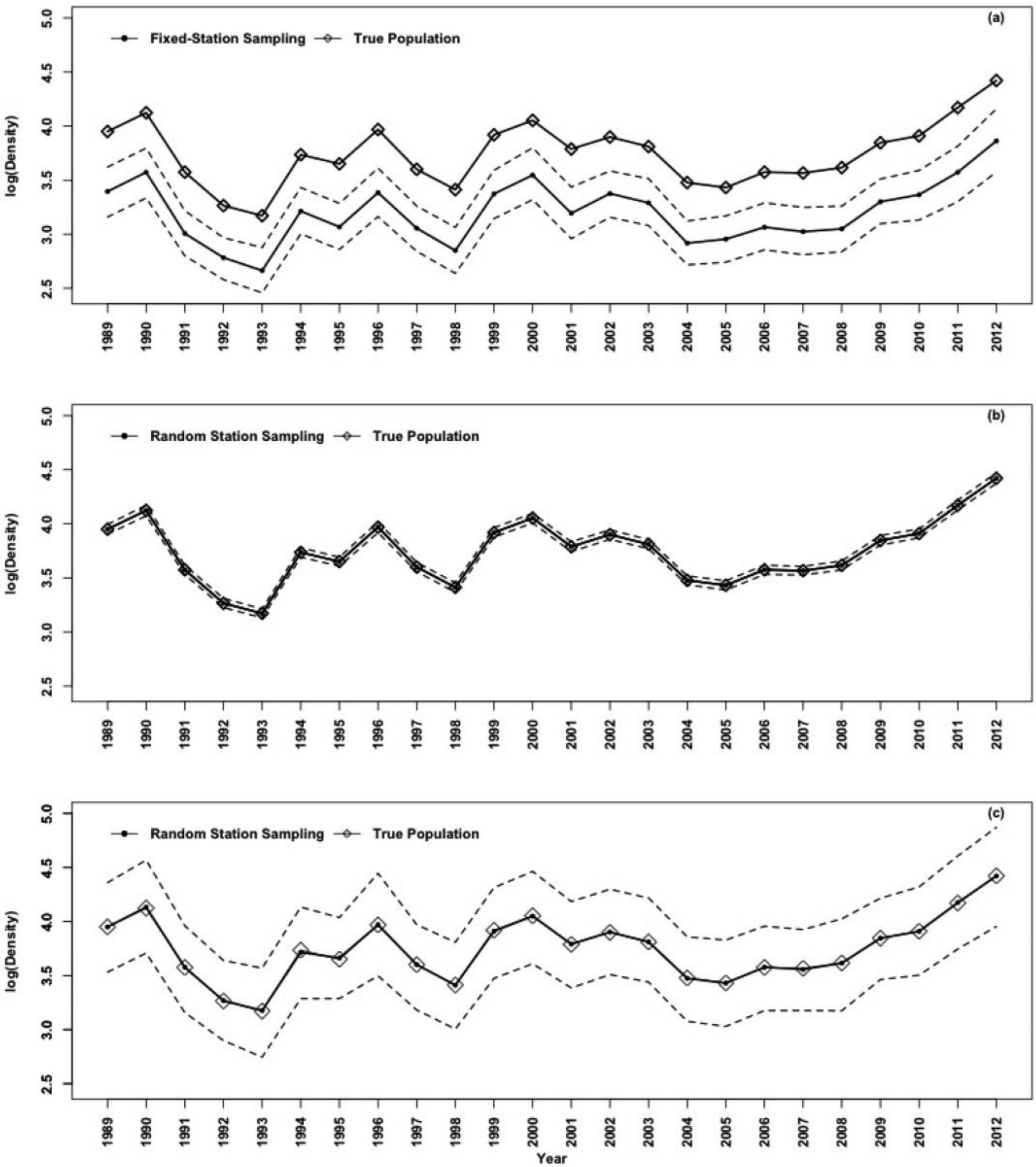

FIGURE 6. Temporal trends of means of American lobster sampling designs and simulated true population from 1989 to 2012. The dashed lines represent the 95% confidence intervals for **(a)** fixed-station sampling, **(b)** random-station sampling with 100 repetitions, and **(c)** random-station sampling without 100 repetitions.

design (Figure 7). The mean REE of the fixed sampling over years ranged from 12.49% (SD, 2.97) to 16.50% (SD, 3.26). The mean REE for the random sampling varied from 5.10% (SD, 0.36) to 6.30% (SD, 0.46). Year 2012 had the smallest REE values for both the sampling designs. Year 1998 had the largest REE values for the fixed sampling, and year 1993 showed the greatest REE value for the random sampling. The REE temporal changes for both the sampling designs showed positive correlations. The fixed-station sampling design was less precise.

The random-station sampling design was unbiased, but the fixed-station sampling design did not have evenly distributed RB values around zero (Figure 8). The annual mean RB of the random sampling ranged from −0.03% (SD, 0.55) to 0.04% (SD, 0.59). The average mean RB of fixed sampling varied from −16.50% (SD, 3.26) to −12.49% (SD, 2.97). For the fixed sampling, the smallest bias was in 2000 and the largest was in 1998. The annual mean RB of 1,000 simulations for random sampling was less than 0.1%. The fixed sampling showed relatively larger variation of RB values than random sampling.

Index of Persistence Between Year Pairs

The mean settlement density (number/m^2) was calculated from settlement survey data in the Gulf of Maine for 25 years

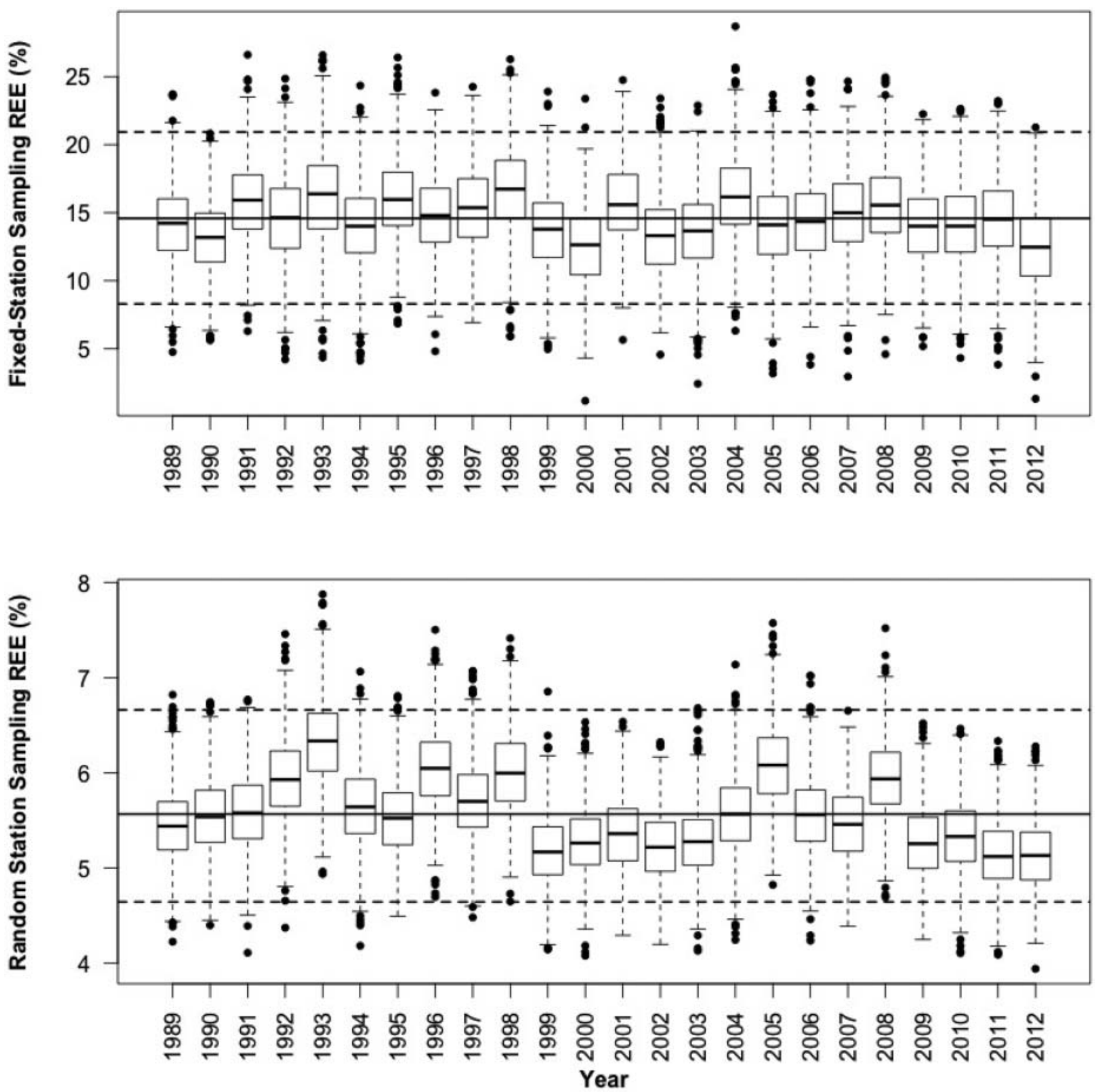

FIGURE 7. Relative estimation error (REE) of two American lobster sampling designs from 1989 to 2012 (Tukey-style boxplots). The solid lines are the mean of REE, and the dashed lines are 95% confidence intervals.

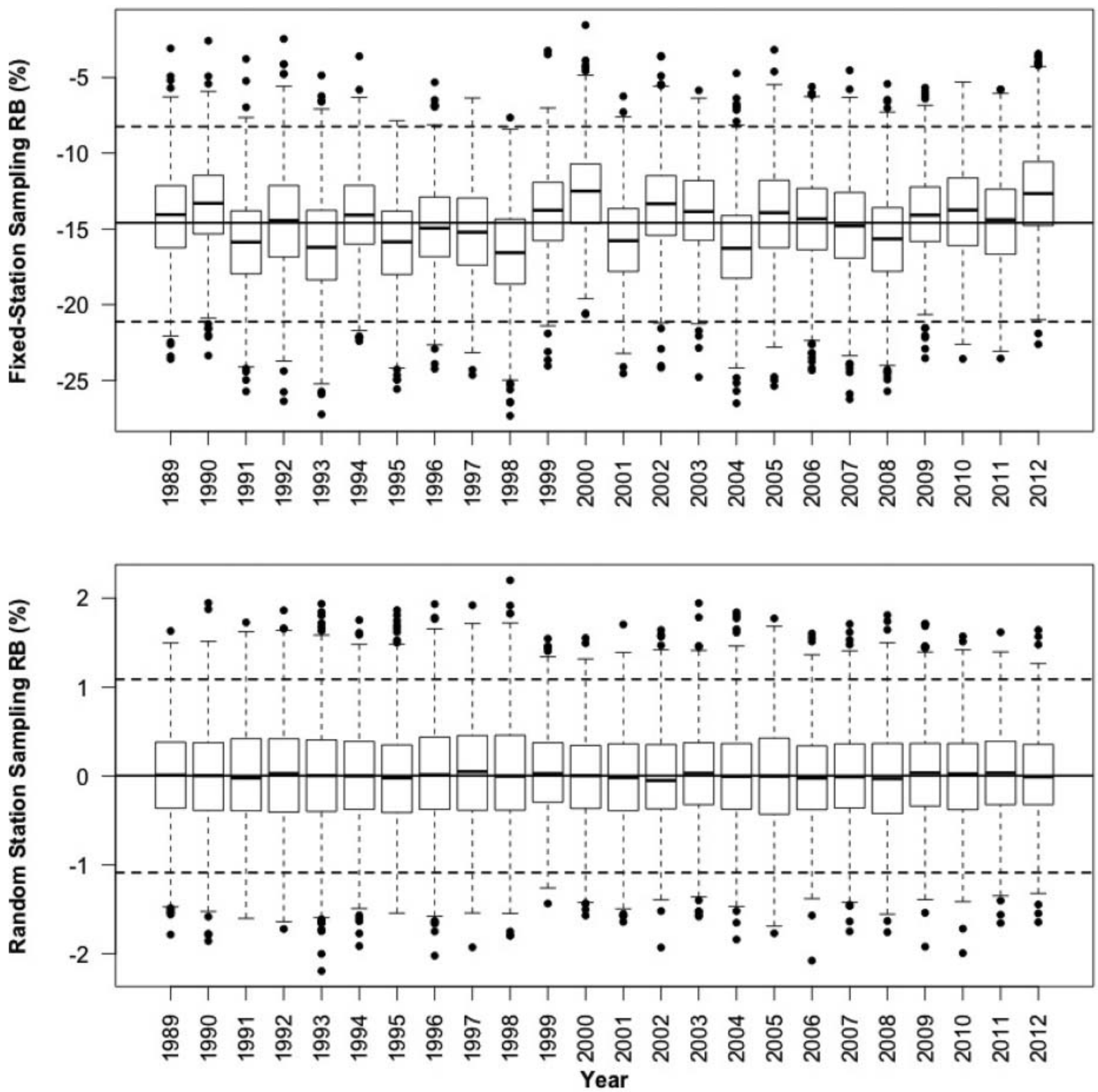

FIGURE 8. Relative bias (RB; %) of two American lobster sampling designs from 1989 to 2012 (Tukey-style boxplot). The solid lines are the mean of the RB, and the dashed lines are 95% confidence intervals.

(1989–2013) and 10 fixed stations. There were 10 fixed stations in this area, and the number of successful sampling sites varied from 8 to 10. There were only 8 sites that had lobster density data during 1989–1994. The stations with no lobster data were dropped from our analysis. The mean lobster density showed considerable interannual variability (Figure 9).

The index of persistence was estimated for each pair of years by using the newly settled lobster density data from the settlement survey. The lower the values of index ϖ, the greater the persistence between two adjacent years. The persistence between two pairs of years was strong during most years (Figure 10). The ϖ value for 1993 and 2008 was the highest with a value of 3.02, which implied the worst degree of persistence. The mean ϖ value for the 24 successive pairs of years was 0.39 (SD, 0.21). The corresponding probability that fixed-station sampling would detect the temporal trend of the lobster density in the mid-coast region of the Gulf of Maine was greater than 81.4% (Table 1). The mean ϖ value for all pairs of years was 0.51 (SD, 0.35). The corresponding probability that fixed-station sampling would detect the temporal trend of the lobster density was around 77.9%.

DISCUSSION

The objectives of a monitoring program need to be clearly identified before designing the program because they may

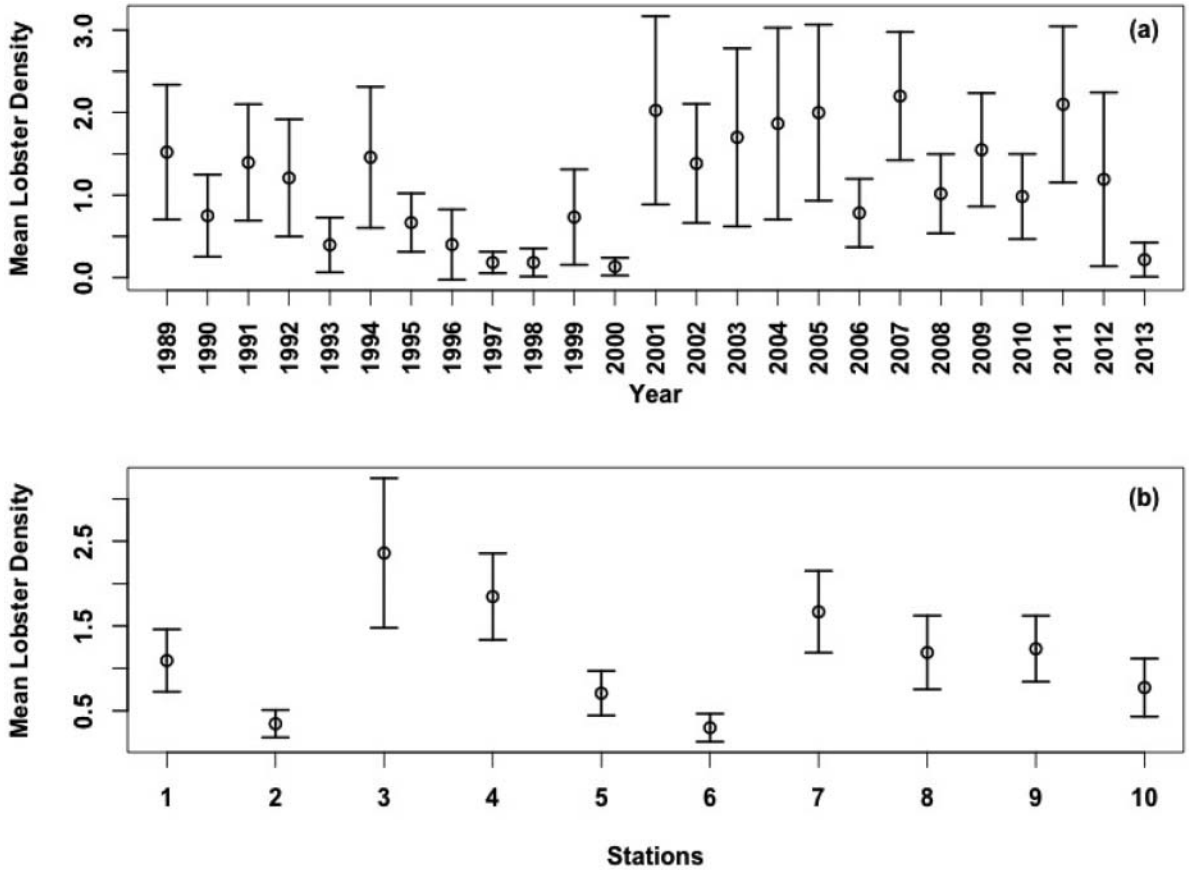

FIGURE 9. Mean lobster density (number/m^2) and 95% confidence intervals from the American lobster settlement survey in the mid-coast region of the Gulf of Maine across **(a)** years, and **(b)** stations.

influence the choice of monitoring designs. An objective of comparing temporal change of species abundance in an area or an objective of observing spatial patterns of a species between two areas can have different optimal sampling designs (Bijleveld et al. 2012). Bijleveld et al. (2012) concluded that none of the sampling designs would fit all the criteria of an objective. For a given objective, sample size can also affect the monitoring results. Smaller sample size reduces estimation precision and even influences the ability to detect temporal changes (Quinn and Keough 2005). The ALSI program is designed to monitor temporal changes of American lobster settlers and juveniles, which can then be used to monitor the dynamics of recruitment (Pershing et al. 2012). Hence, a sampling design that utilizes a small sample size with enough power to detect temporal trend is a cost-effective sampling design.

For historical reasons, a fix-station design is used in the ALSI settlement survey. In our study, we evaluated the ability of fixed-station sampling design to detect the temporal changes in the density of the newly settled lobsters in the mid-coast region of the Gulf of Maine. The results from the simulation study indicate that the fixed-station sampling design underestimated the absolute density of American lobster settlers. The fixed-station sampling sites in this study were distributed along the inshore estuary, where the predicted true density of American Lobster was relatively lower than at other potential sampling sites. This may contribute to the low estimation of the fixed-station sampling design. The random-station sampling, an unbiased sampling design for monitoring newly settled lobster density, captured both the true population values and the temporal trend of settler density. Despite this, the fixed-station sampling yielded temporal patterns of the settler density similar to the true population trend over time.

Although the fixed-station design was thought to be biased, the effectiveness of this sampling design or the power of estimating temporal trend can be evaluated in terms of the probability of detecting temporal change (Millard and Lettenmaier 1986). The power calculation in Van der Meer's (1997) study indicates that the fixed-station sampling yielded a higher power of detecting temporal change than random-station sampling. Warren (1994) also concluded that the fixed-station sampling was able to estimate changes with a relatively good precision. A sudden change between two stations for one given year or two successive years can induce a loss in persistence.

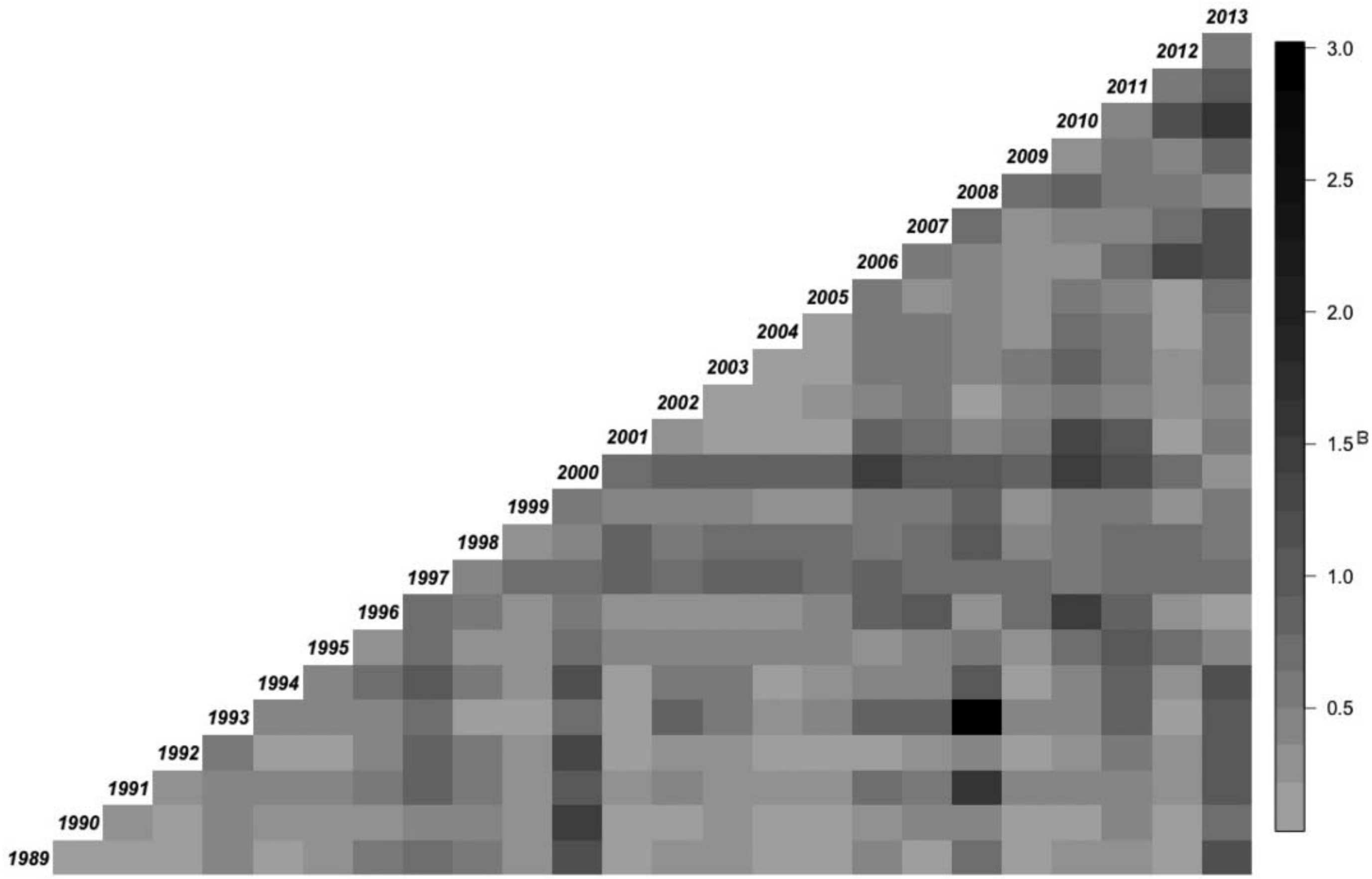

FIGURE 10. American lobster degree of persistence (ϖ) index matrix for paired years (1989–2013). The smaller the ϖ value, the greater the persistence the fixed-station sampling obtains, and the greater the power of differentiating interannual changes in the settler abundance.

We need to understand the change of the habitat characteristics associated with the 10 sampling stations over time. Understanding the effect of environmental changes could help explain the temporal trend of American lobster density in the mid-coast region and fixed-station sampling results. The reduced persistence may cause a loss in precision of the estimated change in the lobster density.

The results of persistence analysis in our study tend to be sensitive to the definition of young of year lobster (i.e., those <10.5 mm CL in our study), which is determined by the size frequency distribution in the benthic collections at the end of the settlement season. So, the upper limit for young of year might change over time, which may affect persistence because the calculated density includes larger lobsters. The persistence increases even when we only increase the upper limit by 0.5 mm. This suggests that the fixed-station sampling design has more power to detect the temporal trend of lobster density when the size range used to define young of year is expanded.

The challenge of our study was to identify the mechanisms that affect the accuracy of the prediction for the density of the American lobster. Statistical modeling provides an effective method for simulating the lobster population (Cao et al. 2014). However, the predictive ability may be affected by the temporal coverage of the data. The model validation from Jensen et al.'s (2005) study indicated that the model had lower discriminatory power if they used 1 year of data to predict the other years. In our study, the bottom trawl survey data were collected from 2000 to 2012, which is short compared with the prediction period of 1989–2012.

The predictive ability of the model could be limited by the environmental data collected from different sources. There were five variables that were included in the two-stage GAM. In addition to bottom water temperature, the other five variables, such as sediment type and depth, were constant for each year. Only bottom water temperature data changed over years. The water temperature data used to fit the model were extracted from the FVCOM model, and highly affected the temporal prediction of the newly settled lobster density. Bottom water temperature is the most important variable correlated with the temporal prediction of the American lobster density from 1989 to 2012. Chang et al. (2010) also indicated that temperature was highly correlated with lobster density and that lobster density increased linearly as water temperature. A strong environmental trend could affect the temporal trend of predicted lobster density, but the temporal trends of REE and RB for the two sampling designs did not show the same pattern as water temperature trend.

We used trawl survey data to build the GAMs and generate the true population. In reality, the trawl survey data used in this study were imbued with considerations of catchability and selectivity. The young of year lobster could be excluded from the trawl survey data because of the mesh size, potentially affecting their population prediction, both in presence and density. Thus, the simulated true population may only explain the distribution of early benthic phase lobster and older juveniles that are greater than 10.5 mm CL. In addition, the two-stage GAM is flexible in adding or dropping predictor variables, but it is difficult to find balance between the development of high explanatory power of a model and the elimination of random noise in the model. The two-stage GAM in our study was used for predicting a reasonable distribution of early benthic phase lobster and older juveniles for comparing the fixed-station and random-station sampling designs. It should be noted that the GAM may not have enough power to predict absolute density of young of year lobster but is sufficient for simulating the spatial structure of the lobster population for this study.

The simulated distribution of American lobster in each year seems reasonable. Although we included different environmental and spatial variables in the final models, the response curves of the same predictor variables had the same trend as the response curves in Chang et al. (2010). The GAM results from Chang et al. (2010) predicted lobster density in the Gulf of Maine well, but with a slight underestimation. This is consistent with our predictions of lobster density. The general spatial pattern of predicted lobster density from our study is consistent with our understanding of lobster ecology. However, the model may not be suitable for predicting lobster density in the mid-coast region of the Gulf of Maine if there are significant changes in oceanic conditions. In this case, a reanalysis may be necessary.

In conclusion, the fixed-station sampling design is biased, underestimating American lobster settler density. The random-station sampling design is not biased. However, the fixed-station sampling has the ability to detect substantial changes in temporal trend of density. This study suggests that the density index from the ALSI program can capture the temporal variability of American lobster settlers and juveniles.

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REFERENCES

ASMFC (Atlantic States Marine Fisheries Commission). 2009. Stock assessment report no. 09-01 (supplement) of the Atlantic States Marine Fisheries Commission: American lobster stock assessment report for peer review. ASMFC, Boston.

Berry, S. C., and A. H. Welsh. 2002. Generalized additive modeling and zero inflated count data. Ecological Modeling 157:179–188.

Bijleveld, A. I., J. A. Van Gils, J. Van der Meer, A. Dekinga, C. Kraan, H. W. Van der Veer, and T. Piersma. 2012. Designing a benthic monitoring programme with multiple conflicting objectives. Methods in Ecology and Evolution 3:526–536.

Bowlby, H. D., J. M. Hanson, and J. A. Hutchings. 2008. Stock structure and seasonal distribution patterns of American lobster, *Homarus americanus*, inferred through movement. Fisheries Research 90:279–288.

Cao, J., Y. Chen, J. H. Chang, and X. Chen. 2014. An evaluation of an inshore bottom trawl survey design for American lobster (*Homarus americanus*) using computer simulations. Journal of Northwest Atlantic Fishery Science 46:27–39.

Chen, C., R. C. Beardsley, and G. Cowles. 2006. An unstructured grid, finite-volume coastal ocean model (FVCOM) system. Oceanography 19:78–79.

Chen, Y. 1996. A Monte Carlo study on impacts of the size of subsample catch on estimation of fish stock parameters. Fisheries Research 26:207–223.

Chang, J. H., Y. Chen, D. Holland, and J. Grabowski. 2010. Estimating spatial distribution of American lobster *Homarus americanus* using habitat variables. Marine Ecology Progress Series 420:145–156.

Chen, Y., S. Sherman, C. Wilson, J. Sowles, and M. Kanaiwa. 2006. A comparison of two fishery-independent survey programs used to define the population structure of American lobster (*Homarus americanus*) in the Gulf of Maine. U.S. National Marine Fisheries Service Fishery Bulletin 104:247–255.

Cooper, R. A., R. A. Clifford, and C. D. Newell. 1975. Seasonal Abundance of the American lobster, *Homarus americanus*, in the Boothbay region of Maine. Transactions of the American Fisheries Society 104:669–674.

Cowan, D. F., A. R. Solow, and A. Beet. 2001. Patterns in abundance and growth of juvenile lobster, *Homarus americanus*. Marine Freshwater Research 52:1095–1102.

Fielding, A. H., and J. F. Bell. 1997. A review of methods for the assessment of prediction errors in conservation presence/absence models. Environmental Conservation 24:38–49.

Franklin, J., and J. A. Miller. 2009. Mapping species distributions: spatial inference and prediction. Cambridge University Press, Cambridge, UK.

Green, B. S., C. Gardner, J. D. Hochmuth, and A. Linnane. 2014. Environmental effects on fished lobsters and crabs. Reviews in Fish Biology and Fisheries 24:613–638.

Hastie, T., and R. Tibshirani. 1990. Generalized additive models. Pages 136–173 *in* D. R. Cox, D. V. Hinkley, D. Rubin, and B. W. Silverman, editors. Monographs on statistics and applied probability. Chapman and Hall, London.

Hilborn, R., and C. J. Walters. 1992. Quantitative fisheries stock assessment: choice, dynamics and uncertainty. Chapman and Hall, New York.

Jensen, O. P., R. Seppelt, T. J. Miller, and L. J. Bauer. 2005. Winter distribution of blue crab *Callinectes sapidus* in Chesapeake Bay: application and cross-validation of a two-stage generalized additive model. Marine and Ecological Progress Series 299:239–255.

Kimura, D. K., and D. A. Somerton. 2006. Review of statistical aspects of survey sampling for marine fisheries. Reviews in Fisheries 14:245–283.

Liu, Y., Y. Chen, and J. Chen. 2009. A comparative study of optimization methods and conventional methods for sampling design in fishery-independent surveys. ICES Journal of Marine Science 66:1873–1882.

Millard, S. P., and D. P. Lettenmaier. 1986. Optimal design of biological sampling programs using the analysis of variance. Estuarine, Coastal and Shelf Science 22:637–656.

Moffett, C. M., Y. Chen, and M. Hunter. 2011. Evaluating port monitoring program: a case study of the northern shrimp fishery in the Gulf of Maine. Fisheries Research 108:321–326.

NRC (National Research Council). 2000. Improving the collection, management, and use of marine fisheries data. National Academies Press, Washington, D.C.

NOAA (National Oceanic and Atmospheric Administration). 2013. Annual commercial landing statistics. Available: http://www.st.nmfs.noaa.gov/commercial-fisheries/commercial-landings/annual-landings/index. (January 2015).

NOAA (National Oceanic and Atmospheric Administration). 1999. U.S. coastal relief model. Available: http://www.ngdc.noaa.gov/mgg/coastal/grddas01/grddas01.htm. (April 2014).

Pershing, A. J., R. A. Wahle, P. C. Meyers, and P. Lawton. 2012. Large-scale coherence in New England lobster (*Homarus americanus*), settlement and associations with regional atmospheric conditions. Fisheries Oceanography 21:348–362.

Poppe, L. J., K. Y. McMullen, S. J. Williams, and V. F. Paskevich. 2005. USGS East Coast sediment analysis: procedures, database, and GIS data. U.S. Geological Survey, Open-File Report 2005-1001, Reston, Virginia.

Quinn, G. P., and M. J. Keough. 2005. Experimental design and data analysis for biologists. 4th edition. Cambridge University Press, Cambridge, UK.

Quist, M. C., K. G. Gerow, M. R. Bower, and W. A. Hubert. 2006. Random versus fixed-site sampling when monitoring relative abundance of fishes in headwater streams of the upper Colorado River basin. North American Journal of Fisheries Management 26:1011–1019.

Selgrath, J. C., K. A. Hovel, and R. A. Wahle. 2007. Effects of habitat edges on American lobster abundance and survival. Journal of Experimental Marine Biology and Ecology 353:253–264.

Seng, Y. P. 1951. History survey of the development of sampling theories and practice. Journal of the Royal Statistical Society 2:214–231.

Steneck, R. S., and R. A. Wahle. 2013. American lobster dynamics in a brave new ocean. Canadian Journal of Fisheries and Aquatic Sciences 70:1612–1624.

Van der Meer, J. 1997. Sampling design of monitoring programmes for marine benthos: a comparison between the use of fixed versus randomly selected stations. Journal of Sea Research 37:167–179.

Wahle, R. A., J. S. Cobb, L. S. Incze, P. Lawton, M. Gibson, R. Glenn, C. Wilson, and J. Tremblay. 2010. The American lobster settlement index at 20 years: looking back - looking ahead. Journal of the Marine Biological Association of India 52:180–188.

Wahle, R. A., L. S. Incze, and M. J. Fogarty. 2004. First projections of American lobster fishery recruitment using a settlement index and variable growth. Bulletin of Marine Science 74:101–114.

Wahle, R. A., and R. S. Steneck. 1992. Habitat restrictions in early benthic life: experiments on habitat selection and in situ predation with the American lobster. Journal of Experimental Marine Biology and Ecology 157:91–114.

Warren, W. G. 1994. The potential of sampling with partial replacement for fisheries survey. ICES Journal of Marine Science 51:315–324.

Xue, H., L. Incze, D. Xu, N. Wolff, and N. Pettigrew. 2008. Connectivity of lobster populations in the coastal Gulf of Maine: part I: circulation and larval transport potential. Ecological Modelling 210:193–211.

Yates, F. 1946. A review of recent statistical developments in sampling and sampling surveys. Journal of the Royal Statistical Society 109:12–30.