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Relating Land Cover Characteristics and Common Loon Mercury Levels Using Geographic Information Systems

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Abstract. This effort models the relationship between mercury (Hg) levels in the common loon (*Gavia immer*) and land cover types as defined by the National Land Cover Database (NLCD). We constructed the model within the framework of a GIS to analyze the spatial relationships between land cover types and blood Hg levels in male common loons. Thiessan polygons were used to generate the territory for each loon. We created 150, 300, and 600-m buffers around the Thiessan polygons and modeled the relationships that existed in each distance class. Within the 150-m buffer, three cover types, crop land, shrub land, and wetland were significantly related to blood Hg levels ($r^2 = 0.552, p < 0.001$), which may indicate that the proximity of these cover types influences Hg availability in loon territories. Cropland exhibited a negative relationship with blood Hg levels and may play a role in reducing the amount of available Hg within the study area while wetlands and shrub lands exhibit a positive relationship. The study area consisted of five major lakes and eleven smaller ponds in northwest Maine, and data included a total of 61 male common loon blood Hg samples.

Keywords: geographic information systems; mercury; common loon; environmental modeling

Introduction

In an effort to understand the fate and transport of mercury (Hg) in aquatic systems researchers have explored the mechanisms that contribute to its bioaccumulation and biomagnification and the associated effect increased Hg can have on higher trophic level piscivores (Thompson, 1996; Wiener et al., 2003). Past studies have addressed the issue through the use of fate and transport algorithms, mass balance equations, and geographic related analysis (Mississippi Department of Environmental Quality, 2000; USEPA, 2001; Delta Tributaries Mercury Council, 2002; Vaidya and Howell, 2002; Rencz et al., 2003). Research has documented that Hg has a significant relationship with certain land cover types such as wetlands as well as with increased dissolved organic carbon (DOC) (Krabbenhoft et al., 1995; Driscoll et al., 1998; Kamman et al., 2003; Peckenham et al., 2003). MeHg export has also been shown to increase in watersheds that

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exhibited higher proportions of forest and wetland cover (Hurley et al., 1995; Kamman et al., 2003).

Zillioux et al. (1993) have suggested that only a small portion of the Hg deposited (between 17% and 25%) through atmospheric deposition makes it to a water body. It follows that Hg deposited closer to the water body, or the contributing streams, is more likely to make it into the hydrologic system. If certain land cover types do influence Hg availability, those found closer to the territory should exhibit a greater influence than those farther away.

We hypothesized that, in the case of the common loon (*Gavia immer*), a high trophic level obligate piscivore, analysis of the land cover variability within certain proximities of the individual territories should lead to more accurate analysis of the variability of Hg within the common loon. This represents a deviation from the commonly chosen method of analyzing relationships at a watershed scale. Our hypothesis is based on known factors that lead to increased availability of Hg such as an increase in the percentage of wetlands within a watershed. Moreover, analysis within the framework of a geographic information system (GIS) can provide additional insight into the factors that lead to elevated Hg levels, the spatial components associated with elevated levels, and can exploit the analytical capabilities for which GIS is so strongly suited. This study presents a method for estimating Hg levels in the common loon within the Rangeley Lakes region of Maine using GIS and statistical methods, and based on the spatial analysis of land cover types in direct proximity to loon territories.

Study area

The study area, located in northwest Maine (Fig. 1), includes five major lakes and over 500 smaller lakes and ponds. Our study focuses on common loons in the five major lakes in the region, all of which have had their levels raised in the past, and eleven smaller ponds. The five major lakes include: Aziscohos, Rangeley, Mooselookmeguntic, Richardson, and Umbagog. All five are characterized as oligotrophic and are reservoirs. Select water chemistry and hydrological parameters are presented in Table 1. Although newly flooded landscapes are well known for the production and release of methylmercury (MeHg) (Gerrard and St. Louis, 2001), the five major reservoirs were created > 90 years ago and the impact of MeHg production from the original flooding is no longer a factor (Schetagne and Verdon, 1999). The current hydrological management varies for each reservoir. Summertime water levels are held steady (i.e., within 1 m) on Mooselookmeguntic, Rangeley and Umbagog, while water level fluctuations on Aziscohos and Richardson Lakes vary over 3 m between May and September. Water level changes and their remobilization of pore

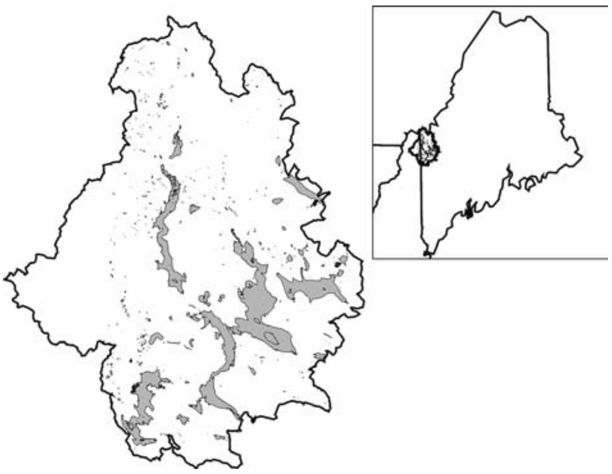

Figure 1. Map of study area in the Rangeley Lakes of western Maine.

Table 1. Chemical properties of the five major lakes and the number of samples per lake that were used to create the "loon territories". Chemistry data are presented in ranges of values from lowest to highest except for pH, which is presented for the last date it was collected. Data were obtained from the PEARL website (http://www.pearl.maine.edu) operated by the George Mitchell Center at the University of Maine, Orono

Lake name	Year flooded	Year range	pH (Year)	Color range	Conductance range	Alkalinity range	Loon samples
Aziscohos	1911	1982–2000	6.64 (1990)	22–32	25–38	6–13	19
Mooselookmeguntic	1853	1981–2001	7.22 (2001)	6–30	26–38	6–9.5	8
Rangeley	1834	1982–2002	7.17 (1997)	4–17	31–38	6–9.5	6
Richardson	1853	1982–2001	7.02 (1991)	14–24	20–34	6–14	9
Umbagog	1853	1983–2001	7.01 (2001)	18–23	23–24	5.5–8	7

water and wetland MeHg loads likely enhances our ability to link shoreline cover characteristics and loon blood Hg levels (D. Evers, pers. com.; Kelley et al., 1997).

We selected the Rangeley Lakes because the Hg levels of the common loon are higher than the national average (Evers et al., 1998, 2003) and because information on common loon territories and blood Hg levels was available (Evers et al., 2004). The area encompasses approximately 246,370 ha and comprises various land cover types including northern hardwood (32.8%), mixed (32.3%), and coniferous forests (20%), and a substantial proportion of the region's wetlands (3.4%), which together account for 88.8% of the total area. We analyzed 61 male common loon blood Hg samples. Individual loon Hg levels exhibited substantial spatial variability both between and within lakes. Samples from the larger lakes represented multiple loon territories within the lakes, while samples from the smaller ponds represented only a single territory.

Methods

Data preparation

We conducted the analysis using ESRI's ArcGIS software package and MiniTab Statistical Software. Initial geo-referenced data were collected in a variety of referencing schemes, and scales varied depending on the data source (Table 2). To provide seamless data sets within the study area, ARC/INFO workstation was used to generate the layers. All vector data were cleaned and built for topology, merged and dissolved, projected into the Maine Stateplane West coordinate system for the North American Datum of 1983, and converted to the ESRI shapefile format. This process insured that all spatially referenced layers used in the analysis were in the same projection and format.

The geo-referenced male common loon blood Hg data (provided by BioDiversity Research Institute) were added as event themes in ArcGIS based on the latitude and longitude of the collection location, converted into shapefile format using ArcGIS, and exported into the Maine Stateplane West coordinate system for the North American Datum of 1983.

After the data were integrated into the GIS, the individual point locations for the loon territories were converted into Thiessan polygons in order to create digital "loon territories". A Thiessan polygon can be described as a polygon created in such a manner that no location within that polygon is closer to any other sample point than the sample point contained within the polygon. This represents an application of nearest neighbor methodology and is an exact spatial predictor, meaning that all predicted polygons equal the value of the data point within that polygon (Burrough and McDonnell, 1998).

The use of Thiessan polygons allowed for segmentation of the lakes in order to explain the within-lake variability of Hg in each of the loon territories. Thiessan polygons also maintained the proportional size of the digitally created loon territories. For example, on the north end of Lake Aziscohos the territories are very small and close together and on the south end the territories are larger and further apart. The use of Thiessan polygons maintained this relationship between territories on the same lakes.

Table 2. The type, scale, and source of the data sets

Data sets	Data type	Data scale	Source
Precipitation rates	Raster	1:250,000	http://www.wcc.nrcs.usda.gov/climate/prism.html
Wetland type	Raster	30-m Resolution	http://seamless.usgs.gov
Forest cover	Raster	30-m Resolution	http://seamless.usgs.gov
Land use	Polygon	30-m Resolution	http://seamless.usgs.gov
Slope/Topography	Raster	30-m Resolution	http://seamless.usgs.gov
Hydrography	Line	1:24,000	http://apollo.ogis.state.me.us/catalog
Hydrography	Polygon	1:24,000	Maine office of GIS/Granite
Loon samples	Point/tabular	Autonomous GPS	Biodiversity Research Institute
Territory	Point/tabular	Autonomous GPS	Biodiversity Research Institute

We implemented a spatial join between the male loon samples and the Thiessan polygons to provide Hg values per territory (Fig. 2). If there were multiple loon blood Hg samples in the same territory from repeated captures, the values were averaged. This process has the effect of segmenting the lakes into smaller components, each of which can be analyzed. A total of 61 territories were created accounting for 65.5% of the total number of territories with 49 of the polygons distributed across the five major lakes and 12 of the polygons distributed across the smaller single territory ponds. Of the 61 territories, five were removed either due to error in the NLCD (3) data or because elevated loon mercury levels (2) were believed to be influenced by factors other than atmospheric deposition. Once the Thiessan polygons were generated and the sample Hg levels incorporated, the individual territories were buffered at three intervals: 150, 300, and 600 m.

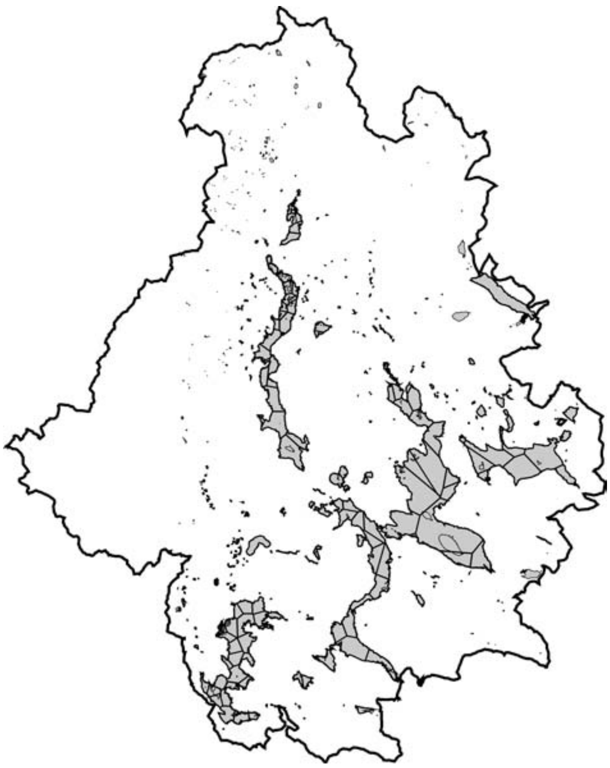

Figure 2. Theissan polygons generated within the GIS to produce loon territories.

Buffering of the Thiessan polygons created areas around each territory that encompassed the territory in question as well as the land area within the specified buffer distance and allowed for analysis of inter-lake variability of loon Hg levels. Individual land cover characteristics from each of the buffered zones were then incorporated into the territory shapefile.

Analysis methods

The percent land cover of each class considered (wetland, shrub land, mixed forest, deciduous forest, cultivated land, coniferous forest, and barren land) was recorded and spatially joined into the buffered territory table using a zonal statistics function. The USGS describes barren land as composed of three individual types of cover: bare rock, mines and gravel pits, and clear-cut/transitional areas. Within our buffered zones, barren areas were rare. Most of the barren areas were bare rock or gravel pits, rather than clear-cuts, particularly within the 150-m buffer.

The buffered territory table was exported from ArcMap as a dbase file and then imported into Minitab for statistical analysis. As noted earlier, blood Hg levels were log-transformed to meet normality requirements of least squares regression. Pearson's Product Moment Correlation Coefficient was used to determine the relationship between the percent of each land cover type within the buffer and the transformed loon Hg level. After the individual relationships were determined, we used ordinary least squares regression to create the regression models based on the predictor variables. Once completed, the resulting residuals were analyzed to further insure that the assumptions of ordinary least squares regression were met. This process was repeated for all three of the buffered areas (150, 300, and 600 m) surrounding the loon territories. Modeled loon territory risk levels were then implemented geographically in the GIS for all territories by use of the Raster Calculator available in ESRI's Spatial Analyst extension for ArcGIS.

Regression model

The regression model was developed using MiniTab statistical software. We used ordinary least squares regression, implementing multiple independent variables. Coefficients and their associated *p*-values from the regression model were analyzed to determine those variables that exhibited little influence on the predictive ability of the model and were removed to prevent over-fitting and to simplify the number of explanatory variables. Residuals from the regression model were analyzed to insure that they met the assumptions of least squares regression in distribution and randomness. The Durbin-Watson statistic was calculated to determine if autocorrelation existed in the residuals. In addition, the r^2 value, the predicted r^2 value, and the adjusted r^2 value were compared to assess whether or not the model was over-fit based on the number of predictors. Variance inflation factors (VIF's) were used to determine if multicollinearity existed between independent variables in the model. Generally a value less than 5.0 can be considered acceptable (MiniTab, 2003).

We then tested the fitted values against the measured values to determine if there was equal variance around the means using an *F*-test. Finally, a two-tailed *t*-test was used to determine if there was any significant difference between the fitted values and the measured values.

Use of GIS to predict loon risk across the study area

Incorporation of the resulting fitted values back into the GIS required several steps. To restrict the results of the regression model to the extent of the Thiessan polygons (e.g., the "loon territories"), the percent value of each land cover class was converted into its own raster layer based on the extent of the loon territories created. The resulting raster layers were then incorporated into the regression model using the raster calculator available in ArcGIS Spatial Analyst. Results from the final output were back-transformed for display purposes and to allow for ranking based on Hg categories developed by Evers et al. (2004). This process also allowed comparison between the fitted values and the measured values (residuals) as a function of lake size, and comparisons to determine how well the fitted values estimate risk levels. The mapping of these differences from a spatial context helped us to identify and investigate lakes in which the model did not perform well.

Results

Correlation

Three variables were significantly correlated with blood Hg levels in male common loons within the 150-m buffer ($p < 0.05$). Some relationships existed between the independent variables but the variables did not exhibit signs of multicollinearity within the regression model. Two of the independent variables had positive relationships and one exhibited a negative relationship with blood Hg levels (Table 3).

Regression

The model for the 300-m buffer was not nearly as robust as the 150-m buffer, failing at least one of the assumptions of least squares regression. Within the 300-m buffer, the residuals were not normally distributed ($n = 56$, $p = 0.016$, AD = 0.941). The F-test used to determine if the variance between the fitted values and the measured values was significant ($F = 1.69$, $p = 0.053$) and the t-test was significant ($t = 0.57$, $p = 0.571$, $df = 110$). The assumptions were met within the 600-m buffer, however the overlap between territories, which may contain significant independent variables that do not directly influence the territory itself, may reduce the validity of the model. The r^2, adjusted r^2, and predicted r^2 for both the 300 m and the 600-m buffers were considerably lower than the 150-m buffer indicating a less robust model (Table 4).

The ANOVA of the regression for the 150-m buffer ($r^2 = 55.2\%$, $F = 15.71$, $p < 0.0001$, $df = 55$) indicates that at least one coefficient is different than zero and that the model is significant at the 95% confidence interval. The p-values of the estimated coefficients (Table 5) show that all but one of the independent variables is significant at the 95% confidence interval. The one independent variable not significant at that level is wetlands, but it was included because its p-value (0.052) is only slightly higher, and because the Pearson's Product Moment test indicated the variable is significantly correlated to blood Hg levels in the male common loon.

The variance-inflation factors (VIF) (Table 5) provide insight to the amount of multicollinearity that exists between the independent variables. The independent variables shrub and barren exhibit moderate signs of multicollinearity, but are still

Table 4. r^2 values for the 150, 300, and 600 m buffered areas

	150 m	300 m	600 m
r^2	55.2	44.6	46
Adjusted r^2	51.7	40.3	41.7
Predicted r^2	49.51	36.33	36.83

Table 3. Correlation coefficients and p-values for initial variables tested in the model with 150-m buffer. Those significant at the 95% confidence interval are noted in bold type

	Hg_Log10	Wetland	Shrub	Mixed	Deciduous	Cultivated	Coniferous
Wetland	**0.492**						
	0.000						
Shrub	**0.550**	**0.333**					
	0.000	**0.011**					
Mixed	0.115	0.051	0.201				
	0.392	0.708	0.133				
Deciduous	0.018	0.021	0.075	**0.723**			
	0.891	0.876	0.577	**0.000**			
Cultivated	**−0.300**	−0.199	−0.073	0.022	0.015		
	0.023	0.137	0.59	0.872	0.910		
Coniferous	0.200	0.249	0.131	0.177	0.263	**0.293**	
	0.135	0.061	0.333	0.188	0.048	**0.027**	
Barren	0.164	0.056	**0.721**	0.242	0.099	−0.044	−0.090
	0.223	0.679	**0.000**	0.070	0.462	0.743	0.506
Precipitation	0.155	0.098	0.257	**0.597**	0.668	0.079	0.099
	0.25	0.469	0.053	**0**	0	0.557	0.465

Table 5. Coefficients, *p*-values, and variance inflation factors (VIF) from the regression model

Predictor	Coef	SE Coef	*T*	*P*	VIF
Constant	0.29028	0.03048	9.52	0	
Wetlands	1.8854	0.9474	1.99	0.052	1.3
Shrub	54.98	10.32	5.33	0	2.6
Cultivated	−7.049	3.177	−2.22	0.031	1
Barren	−3.0262	0.9708	−3.12	0.003	2.3

considered acceptable because the VIF's are less than 5.0.

The residuals (Fig. 3) did not exhibit signs of autocorrelation (Durbin-Watson statistic, $d = 1.16$), indicating that the model is stable across its predictive range. Assumptions of homoscedasticity were met (F-test, $p > 0.05$) and no significant difference existed between the distribution of the observed and modeled values (two-tailed t-test, $p > 0.05$).

The model developed for the 150-m buffer had the best predictive capabilities; the regression model after removal of the insignificant variables is as follows:

$$\begin{aligned} \text{HG\_Log} &= 0.290 + 1.89\ \text{WT} \\ &\quad + 55.0\ \text{SB} - 7.05\ \text{CT} - 3.03\ \text{BN} \end{aligned}$$

where

Hg_Log = the log-transformed mercury levels in the common loon blood samples;

WT = the percent of wetlands within the 150-m buffer;

SB = the percent of shrub land within the 150-m buffer;

CT = the percent of cultivated land within the 150-m buffer;

BN = the percent of barren land within the 150-m buffer.

Discussion

Overall, the model based on the 150-m buffer best predicted blood Hg levels for male common loons.

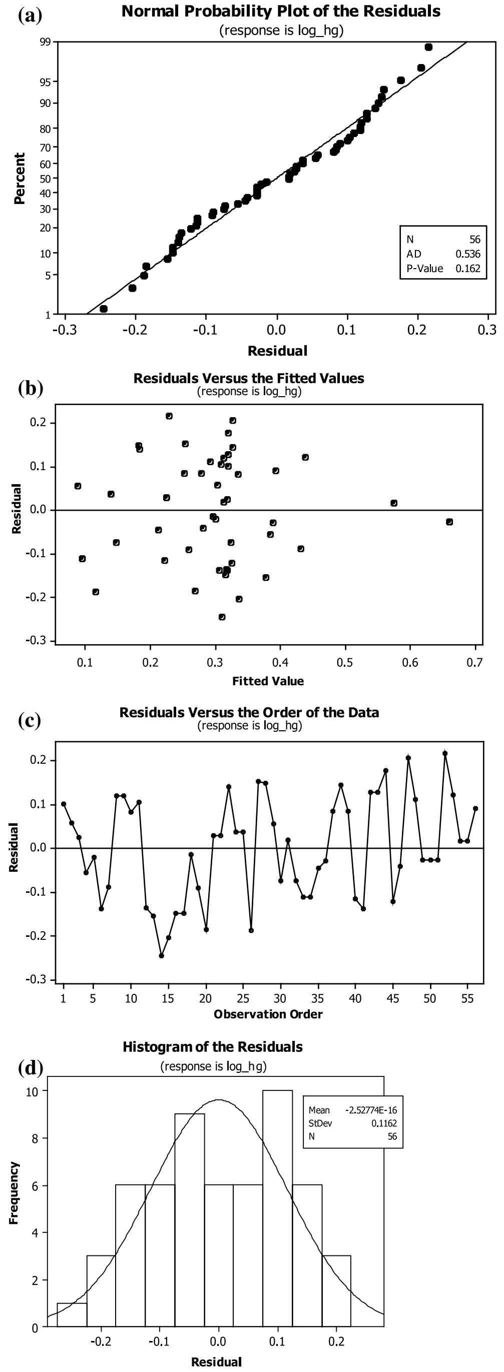

Figure 3. (a) Residual Plots Plot displaying normal distribution of the residuals from the regression model. (b) Graph of residuals versus the fitted values. Note the random distribution of residuals around 0. (c) Residuals versus the order of the data. (d) Histogram of the residuals showing an almost normal distribution.

The r^2 value of 0.55 demonstrates that the model is capable of explaining over half of the variance using the four independent variables. The adjusted r^2 value and predicted r^2 value, 0.52 and 0.50 are close, which suggests that the model is not over fit. At greater distances from the loon territories (300 and 600 m) accuracy and acceptability of the model declined. The marked decrease in accuracy indicates that the land cover characteristics correlated with loon blood Hg are most important in areas proximal to the target territory.

Within the 150-m buffer, the largest difference between the predicted and measured Hg levels were in the northern end of Aziscohos Lake and in the smaller single territory ponds. The average error between the fitted and known risk categories was generally an overestimate in the model. For Aziscohos Lake, loon mercury levels are likely influenced by waterborne point sources unrelated to shoreline methylation dynamics. We believe that underestimates in the smaller ponds may be attributed to a smaller combined (buffered area + total lake area) area restricting the potential for variation between the independent variables, and in effect closing the data set. Figures 4 and 5 present the results of the regression model in the context of the "loon territories" for the 150-m buffer as implemented in the GIS and as Hg categories based on the Hg blood levels.

The relationships found between wetlands, cultivated lands, and Hg are documented in other studies (Krabbenhoft et al., 1995; Driscoll et al., 1998; Mississippi Department of Environmental Quality, 2000; Kamman et al., 2003). Wetlands in

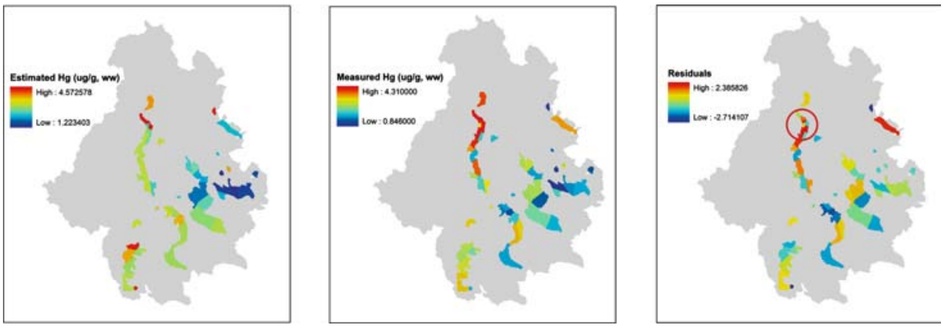

Figure 4. Results implemented in the GIS. From Left to Right: Estimated values of Hg from the loon sample locations displayed as a function of territory, measured values based on the regression equation, implemented in the GIS, and residuals from the analysis implemented to provide information on error variance.

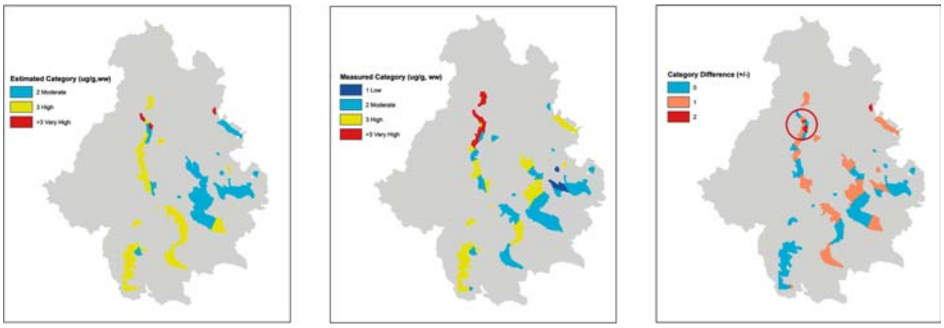

Figure 5. From Left to Right: Estimated blood Hg categories calculated from the loon samples displayed as a function of territory, Observed blood Hg categories, implemented in the GIS, and the difference between the ranked groups. Note the red value in the upper center portion of the third map. This represents the area on Lake Aziscohos with elevated loon mercury levels we believe to be influenced by factors other than atmospheric deposition.

particular are important because they increase methylation rates (Mierle and Ingram, 1991; Miskimmin, 1991; Driscoll et al., 1994; Shanley et al., 2005). The factors contributing to the MeHg transport from wetlands, water flow (Shanely et al., 2005), plankton diversity (Chen et al., 2005), and invertebrate density (Tremblay et al., 1998), will all have a greater influence the closer the wetland is to a water body. Therefore, wetlands closer to a water body will exhibit greater influence over the bioavailibilty of Hg to loons. The strong relationship between loon Hg levels with shrub lands in close proximity to the water body likely represents shrub-scrub wetland communities such as alder (*Alnus* spp.) thickets incorrectly classified as shrub land. An examination of the land cover data compared to aerial photographs showed that this was in fact the case in a number of areas.

The negative relationship with agricultural land can likely be explained by a combination of factors. Although there may be a considerable increase in the export of allocthonous DOC from agricultural lands, it may not be of the type commonly known to contribute to an increase in MeHg in a system (Kamman pers. com.), and the lack of favorable environments, such as wetlands, may further limit methylation rates (Babiarz et al., 1998). Agricultural lands may also create a bloom dilution effect (e.g., eutrophication) within the loon territory (Pickhardt, et al., 2002; Chen et al., 2005).

Future research targeting the relationships between Hg levels in aquatic biota and land cover characteristics while accounting for spatiotemporal factors may further improve predictive abilities of such modeling efforts.

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