Habitat Vulnerability Assessment in the Hudson River Valley

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Introduction

The Hudson River Valley (HRV), extending from Albany to New York City, provides habitat for hundreds of migratory and resident species of wildlife while supporting approximately half of New York State's human population. Recent data developed by the New York Gap Analysis Project (NY-GAP, Smith et al. 2001) shows that over 80 percent of the terrestrial vertebrate species within New York State can be found in the Hudson River Valley. A subsequent, regional gap analysis project (Smith et al. 2002) focused on the Hudson River Valley (HRV-GAP).

To date, HRV-GAP has identified the extent to which the HRV contributes to statewide diversity of terrestrial vertebrates (fine-filter biodiversity elements). Currently in New York, 69 percent (25 species) of all amphibian species, 58 percent (28 species) of all reptile species, 87 percent (214 species) of all breeding bird species, and 90 percent (57 species) of all total mammal species can be found in the HRV. Among terrestrial vertebrates, 75 percent have all or a significant portion of their entire range within the HRV study area (Smith et al. 2002).

This concentration of biodiversity occurs in a region that is under constant development pressure, largely emanating from New York City. Additionally, the HRV may well be facing a period of reindustrialization and concomitant residential development, which will continue to threaten the overall ecological health of the ecosystem and the community (Smith et al. 2004). The ability to accurately predict the loci of human development and subsequently identify the ecologically and culturally sensitive areas susceptible to the resulting impacts could empower decision makers. Possessing knowledge about potential conflict areas could enable decision makers to take actions to minimize adverse effects and maintain wildlife and fish habitat, biological diversity, and regionally significant historical/cultural sites.

The adverse effect of sprawling urbanization on ecologically sensitive areas has prompted a growing effort to understand spatial patterns of residential development (Birch 1971). In the Habitat Vulnerability Assessment for the HRV project, our goal was to develop a census-based model that would show local officials where residential development was likely to occur in the near future and to highlight locations where such development would affect vulnerable habitats and animal species. A census-based model allows one to consider explicitly both social and economic factors that can affect regional biodiversity. Such an approach can be used to integrate both biological and human demographic elements into the planning process. The Habitat Vulnerability Assessment Project area covers ten counties (Albany, Columbia, Dutchess, Greene, Orange, Putnam, Rensselaer, Rockland, Ulster, and Westchester) in the HRV of New York State.

Methods

Determination of Residential Development Hot Spots

To obtain the finest spatial resolution possible in our predictions of areas with high potential for residential development, we used census block groups as our geographical units of analysis. Block groups are used in the decennial censuses of U.S. population and housing for the collection and tabulation of responses to the census questionnaires. These areas contain approximately 1,000 persons and 400 housing units and may vary in size and location of boundaries from one census to another. For Census 2000, the ten counties of the HRV contained 2,212 block groups with a minimum, maximum, and mean area of 0.02, 544.16, and 7.37 square kilometers, respectively. As reported in Census 2000, the number of housing units in block groups in the HRV varies from a minimum of 0 to a maximum of 2,602, with a mean of 396 (Census 2002). Block groups are statistical units of census geography, rather than political units, such as counties, cities, towns, and villages. Data from the census long-form questionnaires administered to a sample of households are tabulated for block groups and summarized by the U.S. Census Bureau (U.S. Census Bureau 1994, 1999, 2002).

To determine the level of residential development within block groups, we used data from the Census 2000 on the year that housing units were built. We defined new housing units as those built over the interval 1990 to 2000. For small areas, such as the block groups used in this analysis, a ten-year interval as presented by the decennial census data is advantageous for a number of reasons. First, the data are measured in a consistent and uniform manner across all types of housing units and for all political and administrative jurisdictions. Second, the ten-year interval is longer than a typical business cycle and therefore the net change over the decade—net of new construction, conversion of existing units, and demolitions—is more representative of longer-term trends than a shorter time frame, which might overemphasize a boom or bust period.

We used other variables from the previous census, Census 1990, to explain variations in the amount of residential development among block groups. We found that the best model for explaining variations in residential development had five independent variables: (1) the neighborhood stage of development (cf. Birch 1971); (2) the number of housing units built in the prior decade; (3) the regional labor market area; (4) the density of the local road network; and (5) the proximity to centers of population. An explanation of these variables follows.

Independent Variable: Neighborhood Stage of Development
Using 1990 census data, we identified the growth stage for each block group. Neighborhood development and housing characteristics were modeled as stages, from single-family subdivision, to buildup, to structure-type conversion, to downgrading, and finally renewal (Hoover and Vernon 1959, 190–207). We adapted Birch's (1971) method of identifying neighborhood growth stages for our project. The six stages of neighborhood development are rural, suburbanization, infill, packing, thinning, and recapture. Table 1 provides a description for each of these six stages of neighborhood growth.

According to the theory, as a neighborhood moves from one growth stage to another, it experiences changes in its level of construction activities, housing prices, and population density. Figure 1 diagrams these trends. New housing construction is the

Table 1. Description of neighborhood growth stages (adapted from Birch 1971 and Bourne 1981).

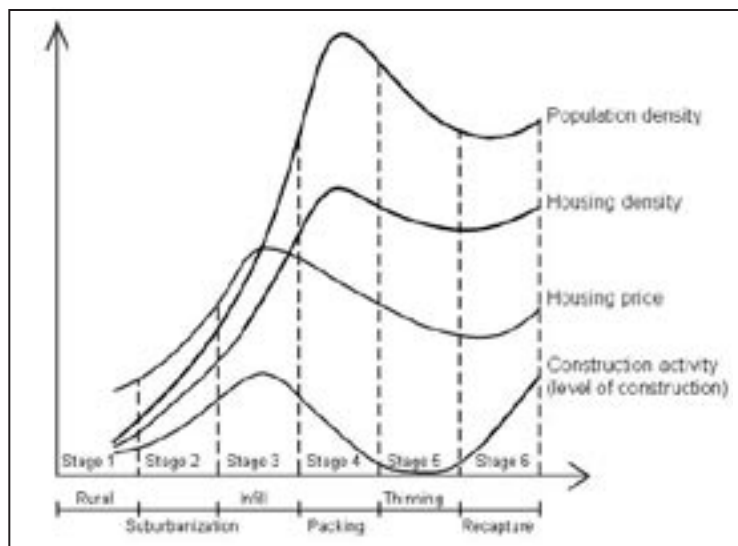| Stage	Major Neighborhood Characteristics
Stage 1. Rural	Low population density, a predominance of single family units and absence of multi-unit structures, very little housing construction
Stage 2. Suburbanization	Increasing population density, high rates of new construction of mainly single family units, and absence of multi-unit structures
Stage 3. Infill	Increasing proportion of multi-unit structures, high property values and rents, moderate population density, low and decreasing rates of housing construction
Stage 4. Packing	Maximum population densities, aging housing stock, overcrowded living condition, low rates of housing construction
Stage 5. Thinning	Continuing deterioration of housing units, absolute population decline, little or no housing construction
Stage 6. Recapture	More profitable use of properties, high density, a predominance of renter-occupied housing units

Figure 1. Neighborhood changes in one life cycle. Units of the Y-axis are modifiable according to the labeling on the graph (right side) and are not scaled to reflect the real units (Yang 2001; adapted from Birch 1971).

most active when a neighborhood is at stage 2 or 3. The level of new construction declines in stage 4, reaches the lowest by stage 5, and may resume in stage 6.

Characterizing neighborhood change by "stages" may falsely imply that this is an evolutionary process and that all neighborhoods have passed and will pass through each stage; that is not the case. However, these stages can help us classify block groups in terms of their present level of development and suggest possible transitions.

Independent Variable: New Housing Units in Prior Decade
A simpler approach than neighborhood life stage is one of development inertia. Simply stated, those block groups with little or no residential development are likely to continue to have little or no development. On the other hand, block groups that experienced high levels of residential development in the prior decade are likely to continue to be areas attractive to development. The prior level of new housing construction is already captured in the variable for neighborhood stage of development; however, it is combined with other characteristics to arrive at a stage score. By including these data as a simple variable, we are giving development momentum greater weight in suburbanizing areas.

Independent Variable: Regional Labor Market Area
The ten counties of the study area do not represent a single economic region, but rather they fall into four regions based on commuting patterns. We have used the economic grouping of counties developed for the U.S. Department of Agriculture (Tolbert and Killian 1987; Tolbert and Sizer 1996) and defined as labor market areas (LMAs). The counties of the United States were grouped into 394 LMAs, and the ten counties bordering the Hudson River were part of four such LMAs.

We used the LMAs to classify block groups by stage of neighborhood development. Indicators such as population density and housing value were evaluated relative to the other block groups within the LMA.

LMAs were also used as independent variables to see if there was a regional effect on residential development. Regional labor markets were used to calibrate the neighborhood housing characteristics to regional (multicounty) levels. How high is high? High housing values and high levels of housing density are different for the counties in the New York City labor market area than for the labor market area covering the mid-Hudson and upper-Hudson regions. The relationship was significant and LMA was kept in the model.

Independent Variable: Density of Local Road Network
The purpose of the road density layer was to identify block groups possessing a substantial transportation network, which might provide the necessary access for development. Land area

that can be accessed by an existing road is apt to have a lower development cost and thereby is more likely to be developed.

Independent Variable: Proximity to Centers of Population
To capture the proximity of each block group to the centers of population (Edmonston 1975) within the region, we used a measure of "population potential." Population potential measures the proximity of a place or point to concentrations of population. Places with a population of greater than 25,000 were used as "centers of population." The advantage of using population potential is that it summarizes the potential influence of all centers of population, relative to their distance from the block group.

Determination of Expected Species Biodiversity Hot Spots
In this approach, we are assuming that it is desirable to at least maintain the terrestrial vertebrate species richness associated with a given block group. If local planners want to incorporate the conservation of biodiversity into the planning process, it could be desirable to direct development activities away from clusters of block groups that have higher species richness.

We developed data sets of total expected vertebrate class distributions for amphibians, reptiles, mammals, breeding birds, and a total aggregation of all vertebrate classes using the HRV-GAP (Smith et al. 2002) predicted species distribution data, available as a raster (grid cell) data set with a 30 x 30 meter cell resolution. Expected or predicted species were those likely to occur in a block group on the basis of species habitat association models developed for NY-GAP (Smith et al. 2001) and applied to the HRV (Smith et al. 2002).

These expected species distribution data contained an identifier for each unique combination of species. All grid cells with that unique combination were assigned to a single class. For each of these unique combinations, a total species count for all species in each vertebrate group was calculated. This was also done for species that are threatened, endangered, or of special concern, as identified by the New York State Department of Environmental Conservation (NYDEC 1999), for each vertebrate group.

To assign a species count number to a specific block group, each unique species count is weighted by the area of the block group involved (species count area). A weighted species count is computed for each table cell entry using the following formula: (species count area/block group area) ∗ number of species.

These weighted species counts were then tallied for all unique species counts in the block group to arrive at the final weighted species count for each block group. This weighted species count was ineffective for understanding the relative concentrations of mammals, amphibians, reptiles, or breeding birds. The weighted species counts were converted into percentages of total species expected for each vertebrate class. Using the percentage of total

species enabled comparisons of relative concentrations between vertebrate classes. This same process was used to develop data and maps for species that are threatened, endangered, and of special concern.

The methodology described above resulted in an underestimation of species expected within any block group. This underestimation arises from the fact that species counts from any one 30 x 30 meter grid cell to another did not adjust for species composition changes. In other words, the ten species contributing to the species count for "Cell A" may not be the same ten species contributing to the species count for "Cell B."

This integrated error was deemed acceptable for three reasons. First, the 30 x 30 meter resolution of the species richness grid was determined by the satellite imagery used to map the plant community types, and does not reflect the resolution of the species data collected (most species data exists at a township or similar scale). Second, since relative species distributions were desired to rank the block groups and the identification of individual species was not required, the discrepancies introduced by not accounting for different species across grid cells within a block group were not important. Third, a separate analysis for species already identified as endangered, threatened, or of special concern allows for explicit consideration of the potential effects of development on those sensitive species. Subsequent field studies or a substantially more complicated analysis could refine these estimates of species richness.

Results

We have identified 77 block groups out of a total of 2,212 in the ten counties of the HRV that are prime candidates for a major share of the new housing to be built between 2000 and 2010 (Figure 2). These are the predicted "hottest" spots for high levels of residential development. To associate these hot spots with counts of new housing units, we refer to the new housing experience of the previous decade, 1990–2000. The Census 2000 reported that over the previous decade, 89,648 new housing units were built in the HRV. If the same level of residential development occurs in this decade, it is probable that, on average, each of the "hottest" block groups will receive 135 or more new housing units.
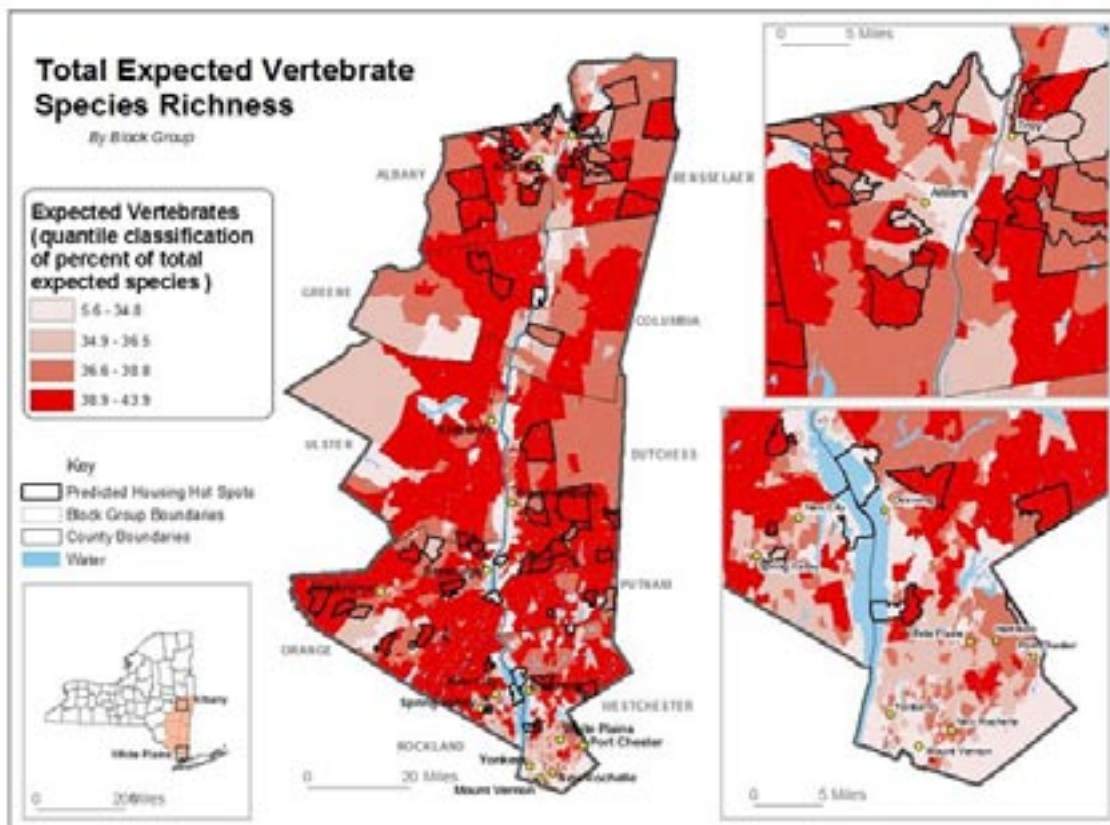

Figure 2. Total expected terrestrial vertebrate species richness, based on wildlife habitat association models for block groups in the Hudson River Valley study area. Because block groups are of different sizes and the total number of expected species varies by vertebrate group, a quantile classification is used. Species richness is expressed as a relative density of all species expected. Areas of greatest potential conflict are represented by those block groups with the greatest potential for new housing by 2010, outlined in black on the map. Areas of potential conflict merit more detailed study to verify species occurrences within their boundaries.

Species richness values for all block groups were calculated as a ratio of all species expected in the block group and all species expected within the study area. These ratios provide a relative concentration rating for each of the species groups, permitting comparison across groups.

For all terrestrial vertebrates (Figure 2), the regions of greatest potential future conflict lie at the north and south ends of the HRV, influenced by the spread of development outward from New York City and Albany. Effects are not limited to block groups in proximity to the Hudson River; in both regions, potential conflicts span the width of the HRV. Secondary centers of more local potential conflicts are associated with the cities of Kingston, Middletown, and Poughkeepsie.

Table 2 shows percentages of each species group found within the residential development hot spot block groups. A large number of the 77 block groups identified as residential development hot spots contain species concentrations that place them in the upper distribution quartile (Table 2). Total vertebrates, amphibians, reptiles, and mammals are heavily represented in the 77 block groups each having more than 48 percent of the block groups in their fourth quartile of species richness. Breeding bird species richness is more heavily concentrated in the second quartile, which comprises more than 57 percent of the hot spot block groups. When reviewing the threatened and endangered species (TES) species by species group, again, total vertebrates, reptiles, and mammals are heavily concentrated, with more than 41 percent of the hot spot block groups being in the fourth quartile of richness. What is surprising is that TES breeding bird species are similarly concentrated, with 44 percent of the hot spot block groups being in the fourth quartile of richness. Also surprising is that expected TES amphibian species richness does not follow the same distribution. More than 63 percent of the 77 block groups rank in the lowest quartile of TES amphibian species richness, and this percentage expands to 75 percent when the second quartile is included.

Discussion

This process should be seen as a coarse-filter approach for identifying block groups likely to receive residential growth within the next decade. This model integrates social and economic variables with the biological variables typically associated with the conventional coarse-filter approach. As stated earlier, the model was specifically designed not to rely on or incorporate local or site-specific data. For this reason, application of the results to site-specific areas without implementing further filtering processes is not recommended. The purpose of this analytical process is to identify block groups of potential concern. These block groups require further investigation of the zoning restrictions, the presence of public land holdings, or other site-specific limitations to determine to what extent these localized conditions will affect the likelihood of the prediction being fulfilled.

Specifically, this model is viewed as a method to assist town, county, and regional planners in the identification of block groups that may need additional development planning or control efforts. HRV-GAP (Smith et al. 2002) now provides a baseline of data against which future planners will be able to review the impacts of their land-use decisions on species distribution and biodiversity in general. This biodiversity data, coupled with the residential growth predictions, can provide planners with an opportunity to direct growth and control efforts to maximize species protection.

The identification of the 77 high-growth-probability block groups will enable conservation efforts to be focused on these more vulnerable areas, and thereby increase the effectiveness of those efforts. With such limited funds for conservation efforts, the ability to target vulnerable areas or vulnerable species would be highly beneficial. In situations where intense development pressures exist, conservation efforts targeted toward large-scale land preservation are likely to face legal challenges and may fail

Table 2. Distribution of vertebrate species predicted to occur within the 77 predicted residential development hot spots in the Hudson River Valley, New York.

Vertebrate Group	Species Richness Quartile Based on All Block Groups			
	1st Quartile	2nd Quartile	3rd Quartile	4th Quartile
Total Expected Vertebrates	7.8	13.0	26.0	53.2
Expected Amphibians	3.9	5.2	42.9	48.1
Expected Reptiles	9.1	2.6	39.0	49.4
Expected Mammals	3.9	10.4	24.7	61.0
Expected Breeding Birds	24.7	57.1	11.7	6.5
Total Expected TES Vertebrates	2.6	3.9	51.9	41.6
Expected TES Amphibians	63.6	14.3	1.3	20.8
Expected TES Reptiles	0.0	10.4	41.6	48.1
Expected TES Mammals	3.9	2.6	28.6	64.9
Expected TES Breeding Birds	2.6	2.6	50.6	44.2

unless sufficient scientific data can be amassed to support such actions. The acquisition of such empirical data can be very costly and time consuming. The identification of probable development areas will enable the focusing of monitoring efforts that will, over time, acquire the scientific data required to assess and demonstrate cause-and-effect relationships between habitat use or change and species viability

The growth allocation model can also be used to identify block groups where predicted development will have minimal effects on species and biodiversity. Identification of these block groups could help direct development toward less sensitive areas that are still desirable sites from the perspective of housing stages, road density, and population potential. Such proactive use of the model has the advantage of being less confrontational and thereby less controversial.

As was our goal, all of these data were acquired or derived from readily available public sources. Restricting ourselves to these data perhaps reduces our predictive power relative to specific block groups, but it greatly increases the applicability of this model to other regions in the state or in other states. Additionally, a model not relying on detailed digital local data is likely more realistic for regional studies. At the present time, complete detailed digital local data do not exist for much of the state and country. Used as an enhanced coarse filter to identify areas of concern, the model is effective and potentially a useful tool for county and regional planning.

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