IDENTIFYING MOLE SALAMANDER MIGRATION PATHS

to and from woodland vernal pools in Ulster County, New York.

Jay Locke

INTRODUCTION.



Photo: migrating spotted salamander (A. maculatum) in Ulster County, NY. Photographed by Jay Locke.

Mole salamanders (so named for their subterranean habitat during most of the year), such as *Ambystoma maculatum*, *A. laterale*, *A. jeffersonianum*, and *A. opacum*, inhabit woodlands in the northeastern United States and migrate each year to seasonal pools ("vernal pools") of water to breed. These migrations tend to happen at night, under sustained wet conditions, and at temperatures just above 40 degrees Fahrenheit. The presence of these conditions will trigger migrations in the Spring or Autumn, depending on the species. For example, mole salamanders that breed in the Spring (e.g. *A. maculatum* and *A. jeffersonianum*) will often start migrating on rainy nights as soon as temperatures rise sufficiently from Winter levels, sometimes en masse. As vernal pools are only temporarily filled with water during the year (e.g. due to Spring snowmelt), they present an ideal meeting place for salamander courtship and breeding that is free from the predation risk in permanent water bodies.

Per a review of the current literature, mole salamander migration paths tend to start from 30 m to around 1000 m (depending on the individual and species) away from breeding pools.[1] These paths are most likely to cross through unfragmented forest, although different types of fragmentation (e.g. roads, rivers, mowed grass, or concrete) vary in their deterring effect salamander migration.[2] The migration paths are also more likely to cross through forested areas with 1) greater canopy cover, 2) a high density of leaf litter and coarse woody debris, and 3) well-drained soils with small mammal burrows,[3] though they are less influenced by change in elevation.[4] Mole salamanders have also been found to alter their migration paths over time,[5] and their paths to breeding pools may zig-zag within a lateral range of 40 m or less.[6] They are also more likely to be found in places with a higher density of vernal pools.[7]

Knowledge of mole salamander migration paths tends to be local and anecdotal, due to the specific and limited timing of their migration (i.e. only a few nights per year with suitable conditions), uncertainty around their hidden habitats and temporary breeding pool locations, and the relatively small scale of each individual's range. Migration paths (and any associated conservation threats) are therefore difficult to systematically predict, identify, and assess on a larger scale. At the same time, the analysis power of geographic information systems (GIS) has increased, as has the range and quantity of publicly available geographic data. However, it remains a challenge to accurately predict migration paths using GIS analysis due to the uncertainty and scale problems mentioned above.

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[1] Compton, 2007; Gamble, 2006; Homan, 2008; Regosin, 2005; Scott, 2013; Van Drunen, 2020; Veysey, 2009

[2] Gamble, 2006; Gibbs, 2005; Homan, 2008; Regosin, 2005; Rittenhouse, 2006; Veysey, 2009

[3] Gamble, 2006; Homan, 2008; Jenkins, 2006

[4] Shoop, 1965

[5] Jenkins, 2006

[6] Coster, 2015

[7] Compton, 2007

This project proposed to explore the potential of publicly available data on wetlands, forest and soil characteristics, and biodiversity for better understanding the migration of mole salamanders in New York State. Specifically, **this project hypothesized that likely mole salamander migration paths in Ulster County could be accurately identified using GIS suitability analysis and publicly available data.** If the hypothesis held, a map could then be produced of likely migration paths in the county, possibly differentiated by relative likelihood. This could be useful for researchers in locating and monitoring mole salamander migration and any associated threats (e.g. the effects of new roads or development) at a local or larger scale. It could also be useful to conservationists in prioritizing the protection of areas with high levels of migration.

For this analysis I selected data sources that describe wetlands (particularly woodland vernal pools), forest characteristics, soil characteristics, biodiversity, and the locations of mole salamander observations.

To identify the correct wetlands, I selected the following data set:

- National Wetlands Inventory: inventory of wetlands by type, specifically those with attribute PFO1E: "Non-tidal, forested wetland (deciduous), seasonally flooded."

To identify the suitable conditions for amphibian habitat and migration around those wetlands, I selected the following data sets:

- Hudson Valley Forest Index: forest condition index for forest patches >100m in counties in Hudson River Estuary watershed (Source: NYSDEC, 2020)
- Significant Biodiversity Areas (SBAs): 22 landscape areas with a high concentration of biological diversity in the Hudson River Valley (Source: NYSDEC/Cornell, 2006)
- NRCS Soil Survey: soil survey units and corresponding data tables containing drainage classes (Source: USDA NRCS, 2021)
- Landsat 8 Orthoimagery: satellite images of Ulster County taken in 2017, 2019, and 2021, obtained from the Earth Explorer portal provided by the U.S. Geological Survey.

To confirm the results of my models, I selected the following observation data:

- iNaturalist citizen science observations: geotagged observations of mole salamanders (genus *Amybstoma*) with photos and coordinates uploaded by iNaturalist app users.
- Mohonk Preserve monitoring observations: geotagged observations of mole salamanders (genus *Ambystoma*) in the Mohonk Preserve identified as part of a long-term scientific monitoring project and obtained through the iNaturalist portal.

To set the scope of my analysis, I selected the following data set:

- NYS Civil Boundaries: boundaries for counties, cities, towns, and villages in New York State (Source: NYS GPO, 2021)

METHODS.

Overview. My purpose was to identify places in which mole salamanders are more likely to migrate in Ulster County each Spring and Autumn. To accomplish this, I developed a suitability analysis model that uses positive indicators of migration paths drawn from the available literature on mole salamanders. My model produced a score for greater or lower migration likelihood in areas of Ulster County which are near woodland vernal pools and forested. I then tested the results of this model with empirical ground-truth observations.

Analysis Steps. My model includes two initial conditions for an area to be under consideration: 1) sufficient proximity to a vernal pool (where mole salamanders may breed), and 2) forest cover. To address proximity to woodland vernal pools, I merged five National Wetlands Inventory HUC8 watershed datasets (U.S. Fish and Wildlife Service, 2020) which together covered the entire extent of Ulster County, and then used zoning data to clip the merged wetlands data to the county's boundaries. I then selected and copied a subset of wetlands containing an attribute beginning with "PFO1E," which described seasonal non-coastal wetlands and which I identified as most likely to be woodland vernal pools. Finally, I calculated 100 m, 500 m, and 1000 m buffers from these wetlands to account for the migration distances of mole salamanders (100 m being most likely, and 1000 m being least likely).

Next, to ensure that areas under consideration were forested as well as proximal to vernal pools, I clipped Hudson Valley forest fragmentation data (NYSDEC, 2020) to the boundaries of Ulster County, dissolved the forest fragments into one polygon, and then created three new layers from the intersection of forest fragments and each of the three buffers (100 m, 500 m, and 1000 m). Additionally, I removed any intersection fragments that did not directly border vernal pools by transforming the new layers into singlepart polygons, making them feature layers, and selecting by location and copying only fragments within 1 meter of a vernal pool into a final set of three layers. Only areas within these resulting layers would be under consideration for analysis.

To determine which areas were more or less likely to contain migration paths, my model featured a score for the confluence of positive indicators of mole salamander migration. These positive indicators (also detailed in Table 2 below) include *proximity to woodland vernal pools*, *continuity of forest cover*, *density of canopy cover*, *aggregation of leaf litter*, *aggregation of coarse woody debris (CWD)*, *well-drained soils*, *and presence of small mammal burrows.* A greater score represents a greater number of positive indicators, and therefore a greater likelihood that an area includes migration paths. To produce and test this score, I 1) created layers for each of the positive indicators, 2) calculated the count of overlapping layers, and 3) tested the score with publicly available ground-truth observations.

1) *Building the possible score by creating layers for positive indicators.*

Proximity and forest cover: One positive indicator was the proximity to vernal pools, already captured in the three forested buffer layers extending 100 m, 500 m, and 1000 m from vernal pools. Another positive indicator was continuous, unbroken forest cover, also captured in these layers. Because 500 m and 1000 m buffers still extended to the edge of the vernal pool, all three layers (100 m, 500 m, and 1000 m) would overlap at a forested area within 100 m of a vernal pool, while only two (500 m and 1000 m) would overlap at an area between 100 m and 500 m, and one (1000 m) would overlap at an area between 500 m and 1000 m. (*Possible score increase: 3*)

Canopy density: As a proxy for canopy density, I calculated the average Normalized Difference Vegetation Index (NDVI), with the rationale that greater forest vegetation would include denser tree canopies. I obtained Landsat 8 images of the Ulster County region (with minimal cloud cover) taken on July 30, 2017, August 5, 2019, and June 7, 2021 (summer months to measure maximum NDVI), and using a separate model and data frame, I calculated an NDVI raster for each date using the red and near infrared bands. I then calculated an average NDVI raster from the values for these three dates. It was then necessary to reproject the average NDVI data (from the WGS 1984 UTM Zone 18N coordinate system to NAD 1983 UTM Zone 18N, using bilinear resampling) to incorporate it into my original model and data frame. Next, I set any NDVI values ≤ 0 as null for the reprojected raster, as they described minimal vegetation and were out of scope. I extracted a subset of the raster using the 1000 m buffer as a mask to confine it to my area of analysis, and reclassified the remaining average NDVI values (> 0) into categories of 1-3 using Jenks' natural breaks (Table 1 below). Finally, I transformed the raster data into polygons defined by their categories (1-3), and then created three layers by selecting and copying category 3 only, selecting categories 2 and 3 and dissolving them, and dissolving categories

1-3. The result was a layer of category 3 only, a layer of category 2 and 3, and a layer of categories 1-3. (*Possible score increase: 3*)

Table 1: *Reclassification of average NDVI to three categories.*

Old Values	New Values
0.00 – 0.37	1
0.37 – 0.43	2
0.43 – 0.58	3
NoData	NoData

Leaf litter and CWD: Two additional positive indicators were aggregation of leaf litter and CWD. As a proxy for both indicators, I used "oldforest_prop" from the Hudson Valley Forest Index data (NYSDEC, 2020). This was a measurement of the percentage of old forest (i.e. undeveloped in 1974) for individual Hudson Valley forest fragments, and this proxy required an assumption that older forest would have a greater timespan of continuous succession and therefore a greater accumulation of leaf litter and CWD. I first clipped the Forest Index data to Ulster County's boundaries. I then selected forest fragments with certain percentages of old forest and clipped them to the 1000 m buffer (as the maximum area of analysis) to create three new layers: forest fragments with greater than 50% old forest, those with greater than 70%, and those with greater than 90%. All three layers (50%, 70%, and 90%) would overlap at an area with greater than 90% old forest, but only one layer (50%) would be present at an area with between 50% and 70% old forest. Thus, if an area had 91% old forest, its score would increase by three, or if it had 51% old forest, its score would increase by one. (*Possible score increase: 3*)

Soil drainage: Another positive indicator of migration paths was well drained soils. As a measurement of well drained soils I used the "well drained soils" and "moderately well drained soils" drainage classes from the U.S. Soils Survey (other drainage classes indicated too much or insufficient saturation). I joined a table of NRCS drainage classes to a feature class of soil survey units (i.e. areas of measurement for the soil survey). I then selected soil survey units with the "well drained soils" class and clipped them to the 1000 m forest buffer created earlier. I repeated this step for the "moderately well drained soils" class. This resulted in a layer for well drained soils, and a layer for moderately well drained soils, which did not overlap each other. There was not enough justification from the literature to assign an increased score to well drained over moderately well drained soils, or vice versa. Thus, if an area had either well drained soils or moderately well drained soils, its score would still increase by one. (*Possible score increase: 1*)

Small mammal burrows: A final positive indicator of migration paths was the presence of small mammal burrows (which may be used by mole salamanders for shelter). One proxy for the presence of small mammal burrows might be soil drainage, in which well drained soils would be more likely to have small mammal burrows. Measurement of well drained soils is already captured above. Another possible proxy for the presence of small mammal burrows is the designation of a "Significant Biodiversity Area" (SBA) in the Hudson Valley area, with the rationale that a forested area with significant biodiversity would be more likely to have small burrowing mammals included in that biodiversity. While this is a rough proxy measurement, it is likely correlated with other measurements above (e.g. average NDVI, proportion old forest) and the presence of mole salamanders themselves, so it was included in the possible score. The Hudson Valley SBAs (NYSDEC/Cornell, 2006) were first clipped to the Ulster County boundaries, and then clipped to the 1000 m forest buffer, resulting in one layer. (*Possible score increase: 1*)

Table 2: *Summary of migration path indicators, measurements used, and methods.*

Migration Path Indicator	Actual Indicator or Proxy Measured	Data Source	Data Preparation

Proximity to vernal pool	100 m, 500 m, and 1000 m buffers from wetlands with attribute PFO1E: "Non-tidal, forested wetland (deciduous), seasonally flooded."	National Wetlands Survey (2021)	Three buffer area layers created from selected wetland areas: ▶ 100 m - 1 ▶ 500 m – 0.75 ▶ 1000 m – 0.5 >1000 m excluded from analysis
Forest continuity	Forest as designated land-use type	Hudson Valley Forest Fragments (2020)	Non-forest excluded from analysis, buffer layers only include continuous forest extending to edge of vernal pool
Degree of canopy cover	Average NDVI from 3 consecutive years as a proxy for canopy cover, where a higher NDVI indicates greater canopy cover	Landsat 8 ortho-imagery (2017, 2019, and 2021)	Average NDVI calculated and reprojected, average NDVI < 0 excluded, average NDVI > 0 reclassed using Natural Breaks to categories of 1-3, three new layers created: ▶ NDVI Category 3 ▶ NDVI Category 2-3 ▶ NDVI Category 1-3
Mass of leaf litter	Old forest proportion as a proxy for leaf litter, assuming greater forest age indicates a greater mass per area of leaf litter	Hudson Valley Forest Index (2020)	Three layers created for proportions of old forest ▶ > 50% old forest ▶ > 70% old forest ▶ > 90% old forest
Frequency of coarse woody debris (CWD)	Old forest proportion as a proxy for CWD, assuming greater forest age indicates a greater mass per area of CWD	Hudson Valley Forest Index (2020)	Three layers created for proportions of old forest ▶ > 50% old forest ▶ > 70% old forest ▶ > 90% old forest
Soil drainage and temperature	Soil drainage class of either "well drained" or "moderately well drained" as a proxy for sufficient but not excessive soil drainage	NRCS Soil Survey Geographic Database (2021)	Created a new layer for well drained soils and another non-overlapping layer for moderately well drained soils, treating both equally
Frequency of small mammal burrows	Soil drainage class of either "well drained" or "moderately well drained" as a proxy for small mammal burrows, and additionally, the occurrence of a Significant Biodiversity Area (SBA) as a proxy for the likelihood of small burrowing mammals.	NRCS Soil Survey Geographic Database (2021), Hudson Valley SBAs (2006)	Created a layer for well drained soils and another non-overlapping layer for moderately well drained soils, treating both equally, and created a layer for SBAs

2) *Calculating a score by counting overlapping layers.*

After creating a series of layers for positive indicators of migration paths (11 in total), the next task was to create a feature class with a count of overlapping layers (1-11), which would serve as the model's scoring system. At a minimum, a score of 1 would indicate that an area was within 1000 m of a vernal

pool and connected to the vernal pool by continuous forest. At maximum, a score of 11 would indicate that an area was within 100 m of a vernal pool, connected to the vernal pool by continuous forest, with an average NDVI of greater than 0.43, greater than 90% old forest, well drained or moderately well drained soils, and a Significant Biodiversity Area designation.

To create a feature class with a count of overlapping layers, I used the "spaghetti" method. I first merged the 11 layers above into a single feature class, and then transformed features into polygons so that each area of overlap was represented as a unique polygon and no more overlaps existed. I then spatially joined (one to one) the fields of the merged feature class and the new polygon layer, creating a new feature class with a join count (i.e. a count of overlaps). I then joined the new join count field created in the spatial join back onto the polygon layer, resulting in a final layer of polygons distinguished by their overlap count. The last step was to select any polygons with a join count of zero (by making them a feature layer) and delete them, as artifacts created by the process rather than actual data points.

3) *Testing the score with publicly available ground-truth observations.*

I obtained a Darwin Core Archive (a packaged dataset, through the Global Biodiversity Information Facility or GBIF) of individual observations of salamanders of the *Ambystoma* genus (i.e. mole salamanders) in Ulster County from 2015 to 2022. This data set included observations collected through citizen science (the iNaturalist app) and another research project (Mohonk Preserve Vernal Pool Amphibian Breeding Ecology Monitoring).

From this archive, I loaded a text file of occurrence data into a file geodatabase as a table. I transformed the table into an event layer in order to plot points for observations, using decimal degrees data in the table. I then reprojected the observations (from WGS 1984 to NAD 1983) to match the projection of my data frame. Next, I selected and copied the iNaturalist and Mohonk Preserve observations separately, to create two layers of observations. Finally, I loaded another text file of multimedia links from the archive to a file geodatabase, and joined it to the iNaturalist observations (so that these observations would include links to photos of the observed salamanders). I overlaid these two observation layers over the layer of polygons with overlap counts.

RESULTS.

The original hypothesis of this project was that likely mole salamander migration paths could be identified using publicly available geographic data. Using the method and model above, I was able to identify areas of likely salamander migration in Ulster County with a precision of around 30 m. After identifying, obtaining, testing, and transforming relevant public data sets, I was able to use GIS analysis to first identify a scope of areas most likely to contain migration paths (i.e. areas of continuous forest extending 1000 m from vernal pools) and then differentiate between areas within this scope based on their relative likelihoods.

This analysis produced a polygon feature class that described areas with likely migration paths, grouped by 11 successive categories of relative likelihood. When compared to publicly available ground-truth observations from iNaturalist and the Mohonk Preserve monitoring project, the accuracy of this feature class varied. 8 of 26 iNaturalist observations, and 81 of 206 Mohonk Preserve observations, were located well outside this feature class and the scope of analysis (i.e. beyond 1000 continuously forested meters from identified vernal pools).

The resulting feature class and comparison with ground-truth observations can be found in the map documents included below. Images of the two ArcMap models created (one for calculating average

NDVI, and one for identifying migration areas and overlaying ground-truth observations) are also included below.

DISCUSSION.

My results seemed to support the hypothesis for this project, at least partially. I was able to identify specific areas in Ulster County where mole salamander migration paths were likely to occur, using publicly available data and a model for systematically combining it. However, one limitation to the precision of identified migration areas was their error of ± 30 m (30 m was the minimum pixel area for satellite image raster data used), which itself accounts for a significant portion of estimated migration path distances of 30 m to 1000 m. It might therefore be possible for migration areas to extend 30 m beyond where they were mapped by this project.

The accuracy of identified migration areas was additionally limited when compared with ground-truth observations from iNaturalist and the Mohonk Preserve monitoring project. While some ground-truth observations did fall within likely migration areas as predicted, there were a significant number that fell outside of identified migration areas. My workflow sequence was to first develop a model and map potential migration areas, before any comparison with ground-truth observations, so there may likely be improvements to the original model that would result in greater consistency with ground-truth observations. Anecdotally, my personal ground-truth observations of migration paths in Ulster County did fall within likely migration areas identified by this project.

One possible reason for inconsistency with ground-truth observations might be incompleteness in the National Wetlands Survey data. While it captures significant wetlands in detail, there may be smaller or more remote vernal pools with active salamander breeding that are unknown or not yet considered by the National Wetlands Survey. The temporary, small-scale, and sometimes remote nature of these vernal pools likely makes them difficult to verify,[8] including at the extensive (though detailed) scale of the wetlands survey. As an example, my own observation of a small roadside vernal pool in Ulster County with active salamander breeding was not included in the wetlands survey data. Therefore, many ground-truth observations that fell outside of the identified migration areas may still have met the model's conditions (e.g. for forest cover, soil drainage, etc.), but were instead proximal to unidentified and unknown vernal pools.

Another possible reason for this inconsistency is that ground-truth observations may occur at places where a forest is fragmented, whereas this model prioritizes continuous forest as the most likely migration area. Some forms of fragmentation (e.g. narrow low-traffic roads or small streams) are relatively more permeable to migration than others,[9] and my results may underpredict actual migration paths across roads, streams, or fields. Migration across roads or fields is also much more likely to be noticed by humans, and it is therefore more likely that ground-truth observations collected from citizen scientists via iNaturalist will be at fragmentation points. This may be a reason why some citizen science iNaturalist observations fell just outside of migration areas identified by this project. On the other hand, the Mohonk Preserve monitoring project was a systematic study focused on specific vernal pools rather than opportunistic sightings at fragmentation points, so inconsistent Mohonk Preserve observations would not be explained by fragmentation.

My model included a differentiation of potential migration areas by their relative likelihood. Of the ground-truth observations that did fall within the identified migration areas, the majority fell within areas with a score of 8 (out of 11) or greater. While the sample is limited, this seems to support the

[8] Compton, 2007
[9] Compton, 2007

model's overarching assumption that some areas (within 1000 m from vernal pools) are more likely than others to contain migration paths based on the presence of suitable conditions.

There are many possibilities for improvement in my model, and my hope is that it would be useful to others as a starting point or an inspiration. One possible area for improvement is the proxies and assumptions I used to apply available data to ideal migration conditions. For instance, I used forest age as a proxy indicator for density of leaf litter and coarse woody debris, NDVI as a proxy for canopy cover, and significant biodiversity areas as a proxy for the presence of small mammal burrows. These proxies relied on assumptions described in the methods section, and their value to the model could be better investigated. Another area for improvement might be my assumptions around the relative correlations between positive indicators and migration path likelihood. For example, my model assumed equal correlations of canopy cover and soil drainage to migration likelihood (whereas one of these may be a much more powerful predictor), and assumed that 90% old growth forest was significantly different than 70% old growth forest in its predictive power. In terms of the score itself, the relative difference between 10 and 11 has less meaning than the difference between 6 and 11, but an improved score could potentially be constructed with a more systematic meaning for each incremental difference.

It is also my hope that these results may be useful for conservation aims, to ensure that mole salamanders and their migration paths are protected in Ulster County and elsewhere. Knowledge of likely migration areas could help with informing research or policy, and ultimately mitigating human effects on mole salamanders, so that we can better support and appreciate these beautiful creatures and their nightly journeys.

LITERATURE SOURCES.

Compton, Bradley W, et al. "A Resistant-Kernel Model of Connectivity for Amphibians That Breed in Vernal Pools." Conservation Biology, vol. 21, no. 3, 2007, pp. 788–799.

Coster, Stephanie S, et al. "Characterizing the Width of Amphibian Movements During Postbreeding Migration." Conservation Biology, vol. 28, no. 3, 2014, pp. 756–762.

Gamble, Lloyd R, et al. "LIMITATIONS OF REGULATED 'BUFFER ZONES' FOR THE CONSERVATION OF MARBLED SALAMANDERS." Wetlands, vol. 26, no. 2, 2006, pp. 298–306.

Gibbs, James P, and W Gregory Shriver. "Can Road Mortality Limit Populations of Pool-Breeding Amphibians?" Wetlands Ecology and Management, vol. 13, no. 3, 2005, pp. 281–289.

Homan, Rebecca N., et al. "Multiyear Study of the Migration Orientation of Ambystoma Maculatum (Spotted Salamanders) among Varying Terrestrial Habitats." Journal of Herpetology, vol. 42, no. 4, 2008, pp. 600–607.

Jenkins, Christopher L, et al. "Orientation of Movements and Habitat Selection in a Spatially Structured Population of Marbled Salamanders (Ambystoma Opacum)." Journal of Herpetology, vol. 40, no. 2, 2006, pp. 240–248.

Regosin, Jonathan V, et al. "VARIATION IN TERRESTRIAL HABITAT USE BY FOUR POOL-BREEDING AMPHIBIAN SPECIES." The Journal of Wildlife Management, vol. 69, no. 4, 2005, pp. 1481–1493.

Rittenhouse, Tracy A.G, and Raymond D Semlitsch. "Grasslands as Movement Barriers for a Forest-Associated Salamander: Migration Behavior of Adult and Juvenile Salamanders at a Distinct Habitat Edge." Biological Conservation, vol. 131, no. 1, 2006, pp. 14–22.

Scott, David E, et al. "Terrestrial Distribution of Pond-Breeding Salamanders around an Isolated Wetland." Ecology (Durham), vol. 94, no. 11, 2013, pp. 2537–2546.

Shoop, C R. "Orientation of Ambystoma Maculatum: Movements to and from Breeding Ponds." Science (American Association for the Advancement of Science), vol. 149, no. 3683, 1965, pp. 558–559.

Van Drunen, S.G, et al. "Estimating Critical Habitat Based on Year-Round Movements of the Endangered Jefferson Salamander (Ambystoma Jeffersonianum) and Their Unisexual Dependents." Canadian Journal of Zoology, vol. 98, no. 2, 2020, pp. 117–126.

Veysey, Jessica S, et al. "An Experimental Assessment of Buffer Width: Implications for Salamander Migratory Behavior." Biological Conservation, vol. 142, no. 10, 2009, pp. 2227–2239.

GEOGRAPHIC DATA SOURCES.

Amy Conley, NYNHP, Spatial Ecologist. Hudson Valley Forest Fragmentation. New York Natural Heritage Program: Albany, NY. 2020.

Landsat 8. L2SP_014031. Band 4. U.S. Geological Survey, July 30, 2017.

Landsat 8. L2SP_014031. Band 5. U.S. Geological Survey, July 30, 2017.

Landsat 8. L2SP_014031. Band 4. U.S. Geological Survey, August 5, 2019.

Landsat 8. L2SP_014031. Band 5. U.S. Geological Survey, August 5, 2019.

Landsat 8. L2SP_014031. Band 4. U.S. Geological Survey, June 7, 2021.

Landsat 8. L2SP_014031. Band 5. U.S. Geological Survey, June 7, 2021.

New York State Natural Heritage Program. Hudson Valley Forest Index. New York Natural Heritage Program, NYSDEC Hudson River Estuary Program, and Cornell University: Albany, NY. 2020.

NYSDEC Hudson River Estuary Program working with the New York Cooperative Fish & Wildlife Research Unit at Cornell University and the NY Natural Heritage Program. Hudson River Significant Biodiversity Areas. NYSDEC Hudson River Estuary Program: New Paltz, NY. 2006.

NYS Office of Information Technology Services GIS Program Office (GPO). New York State county boundaries. NYS GIS Program Office. 2021.

Soil Survey Staff, Natural Resources Conservation Service, United States Department of Agriculture. Web Soil Survey. Available online at the following link: http://websoilsurvey.sc.egov.usda.gov/. Accessed December 6, 2021.

U.S. Fish and Wildlife Service. USFWS National Wetlands Inventory. U.S. Fish and Wildlife Service: Washington, DC. 2021.

MAPS AND FURTHER INFORMATION.

A full map document of the results of this project was produced from ArcGIS 10.8.1 and included below. A companion web map was also created on ArcGIS Online, and is available for the public to view and explore at https://arcg.is/1TOffu0. Due to size limitations for data uploads to ArcGIS Online, only results data for the town boundaries of New Paltz, NY and Esopus, NY was uploaded to the web map as an illustrative example.

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Author: Jay Locke

Date Saved: 7/22/2022

▲ *iNaturalist Observations*

▲ *Mohonk Preserve Observations*

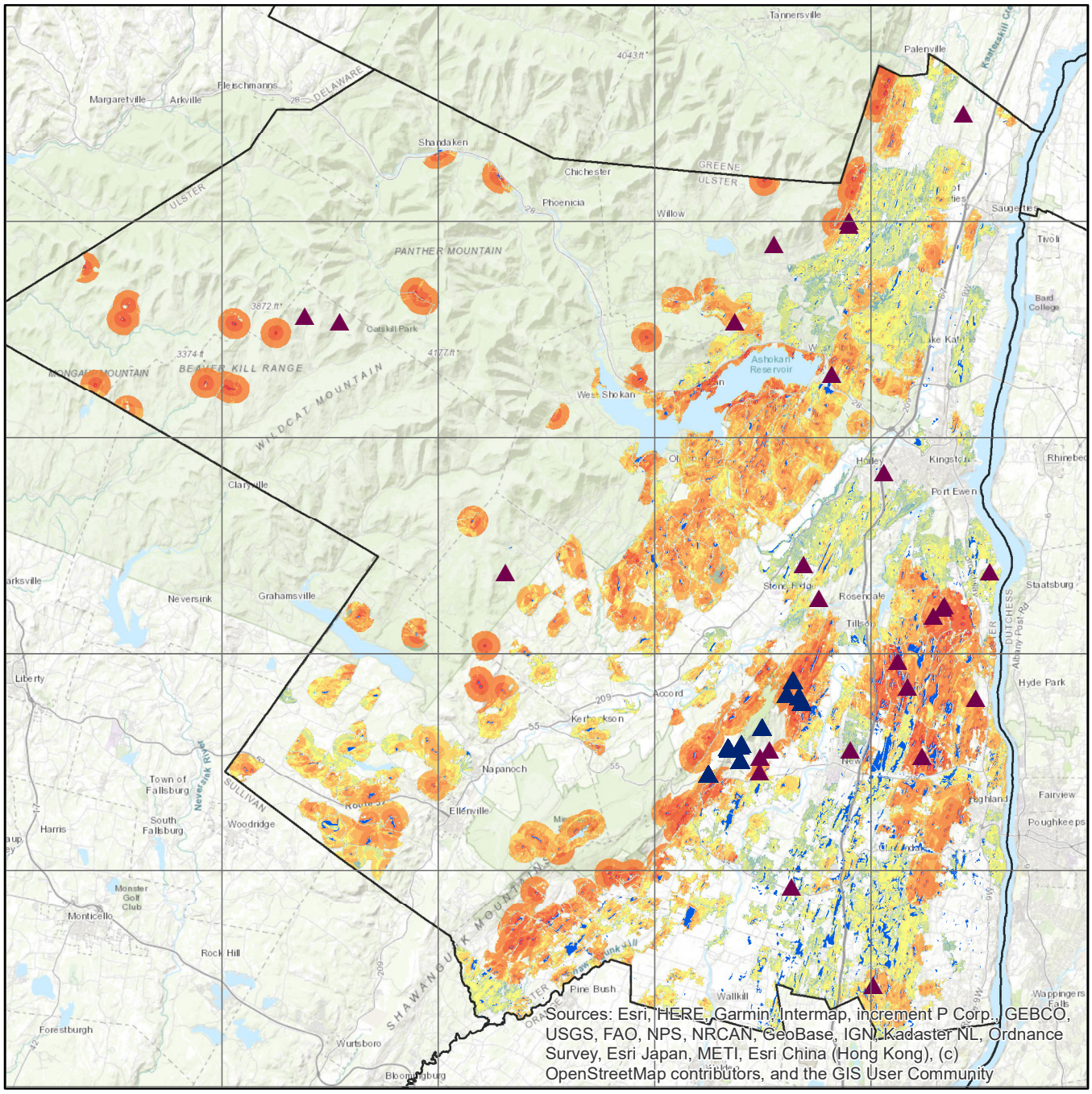
Migration Areas Score 1 2 3 4 5 6 7 8 9 10 11

Coordinate System: GCS North American 1983 UTM Zone 18T (Calculated)
Projection: Transverse Mercator

0 3 6 12 18 24 Kilometers

N

Sources:
GBIF.org (16 July 2022) GBIF Occurrence Download https://doi.org/10.15468/dl.nftp6n
Hudson Valley Forest Fragmentation. New York Natural Heritage Program: Albany, NY. 2020.
Hudson Valley Forest Index. New York Natural Heritage Program, NYSDEC Hudson River Estuary Program, and Cornell University: Albany, NY. 2020.
Hudson River Significant Biodiversity Areas. NYSDEC Hudson River Estuary Program: New Paltz, NY. 2006.
Landsat 8. L2SP_014031. Bands 4 and 5. U.S. Geological Survey, July 30, 2017, August 5, 2019, and June 7, 2021
New York State county boundaries. NYS GIS Program Office. 2021.
Web Soil Survey. Soil Survey Staff, Natural Resources Conservation Service, USDA. Accessed December 6, 2021.
USFWS National Wetlands Inventory. U.S. Fish and Wildlife



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iNaturalist Observations

Mohonk Preserve Observations

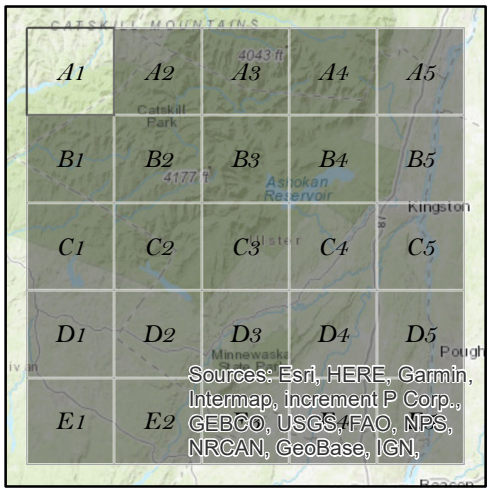
Migration Areas Score 1 2 3 4 5 6 7 8 9 10 11

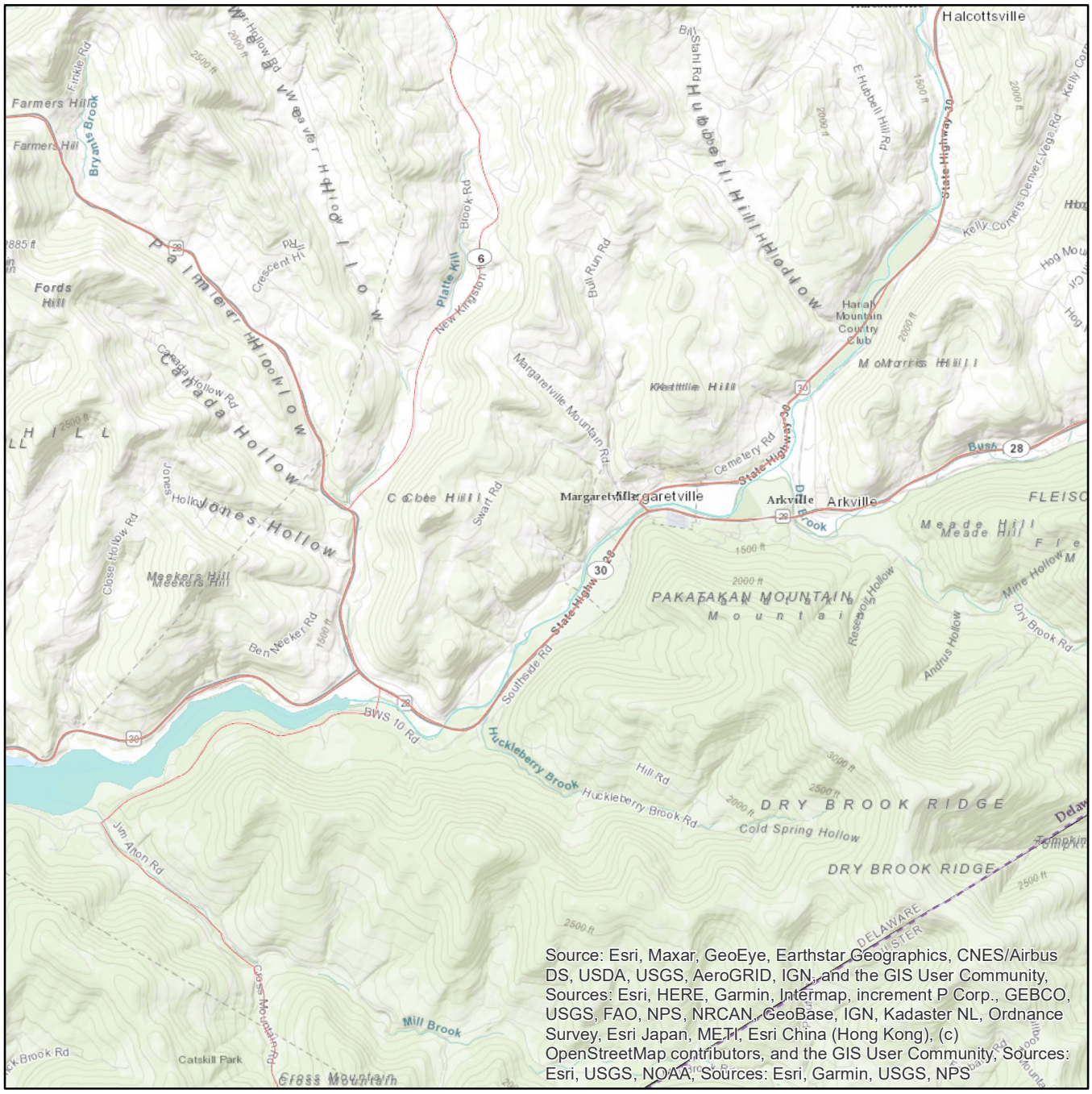
Coordinate System: GCS North American 1983 UTM Zone 18T (Calculated)
Projection: Transverse Mercator

A1

0 10 20 40 60 80 Kilometers

N





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iNaturalist Observations

Mohonk Preserve Observations

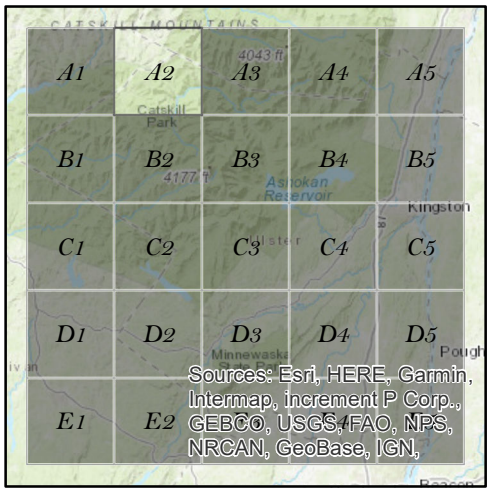
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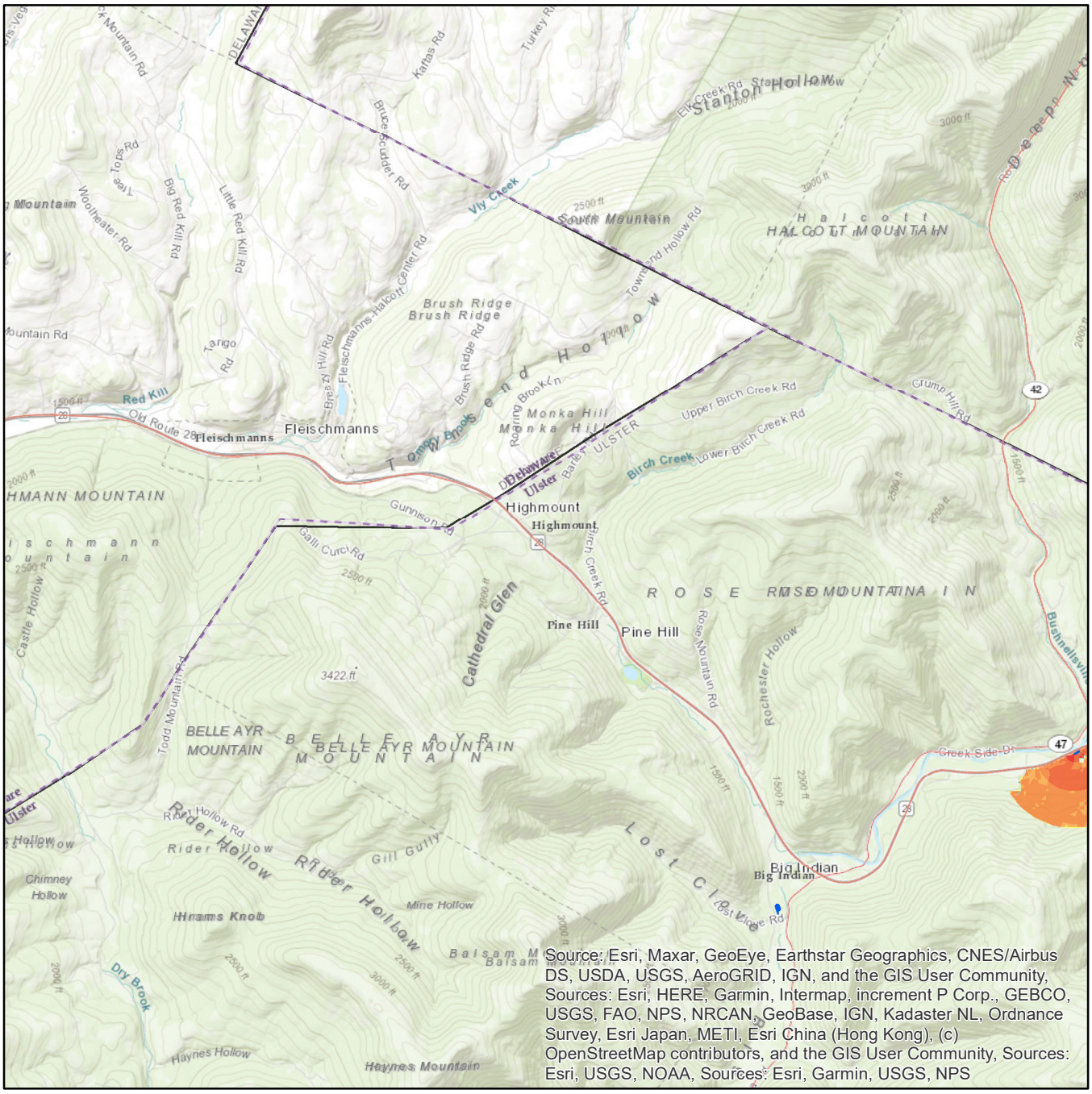
Coordinate System: GCS North American 1983 UTM Zone 18T (Calculated)
Projection: Transverse Mercator

A2

0 10 20 40 60 80 Kilometers

N





Identifying Suitable Mole Salamander Migration Paths in Ulster County, NY

Author: Jay Locke *Date Saved: 7/22/2022*

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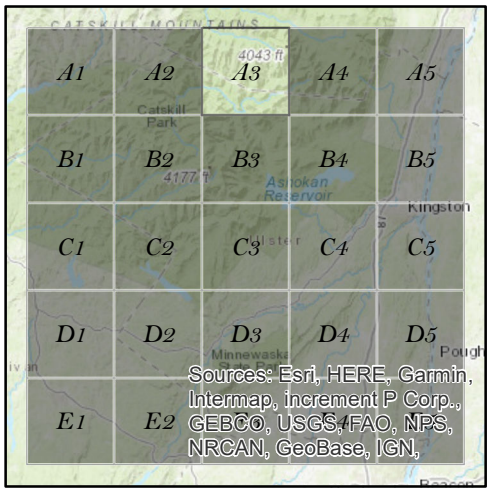
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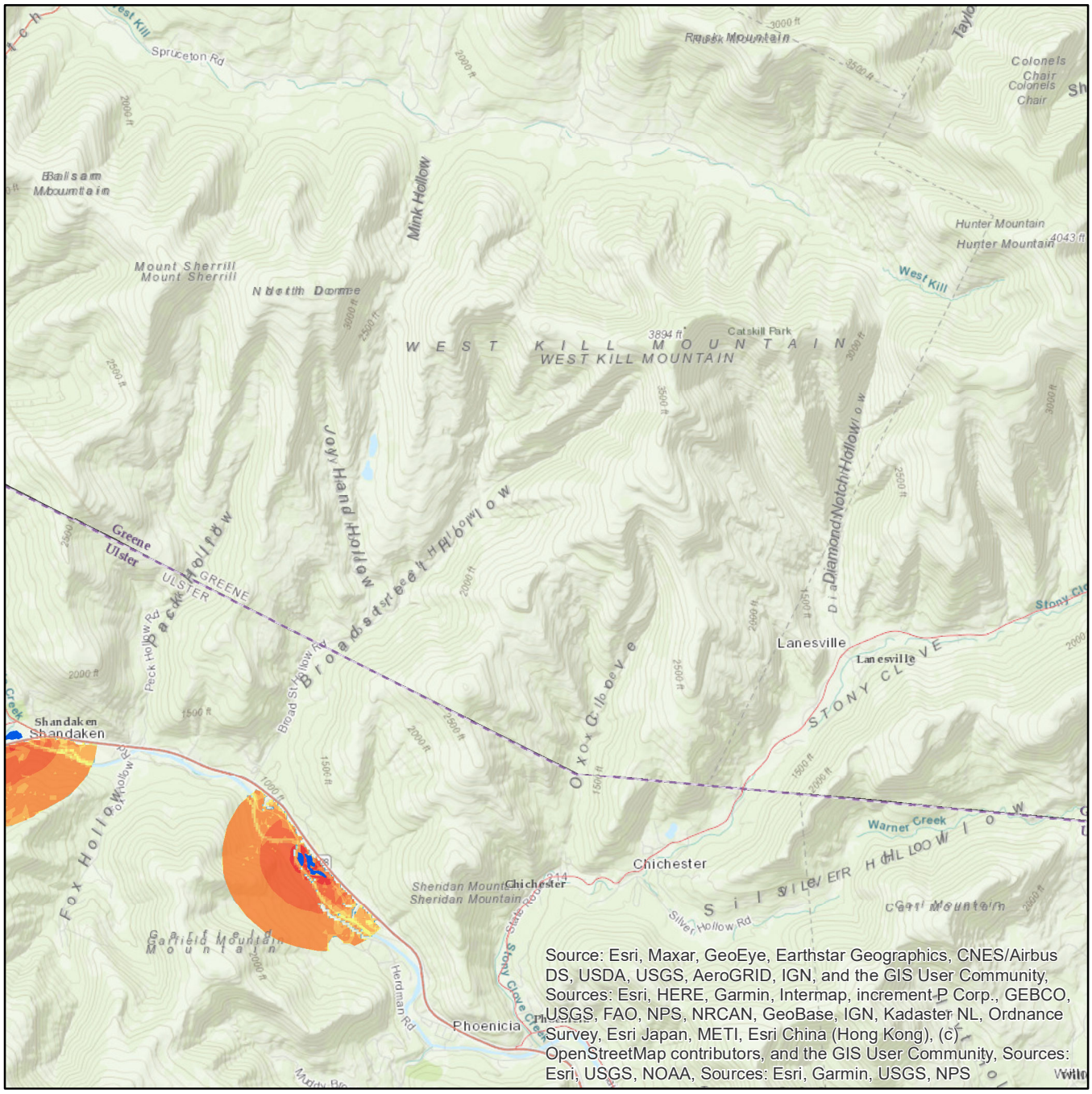
Coordinate System: GCS North American 1983 UTM Zone 18T (Calculated)
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A3

0 10 20 40 60 80 Kilometers

N





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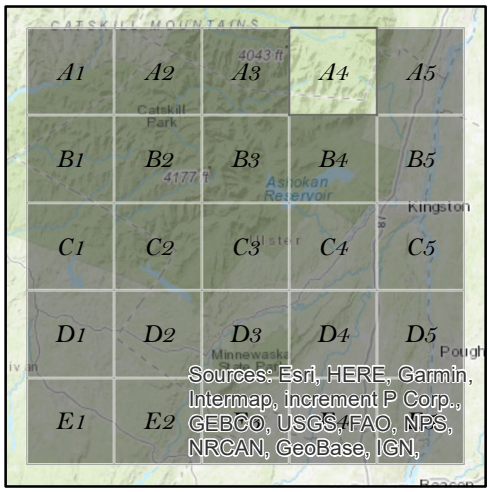
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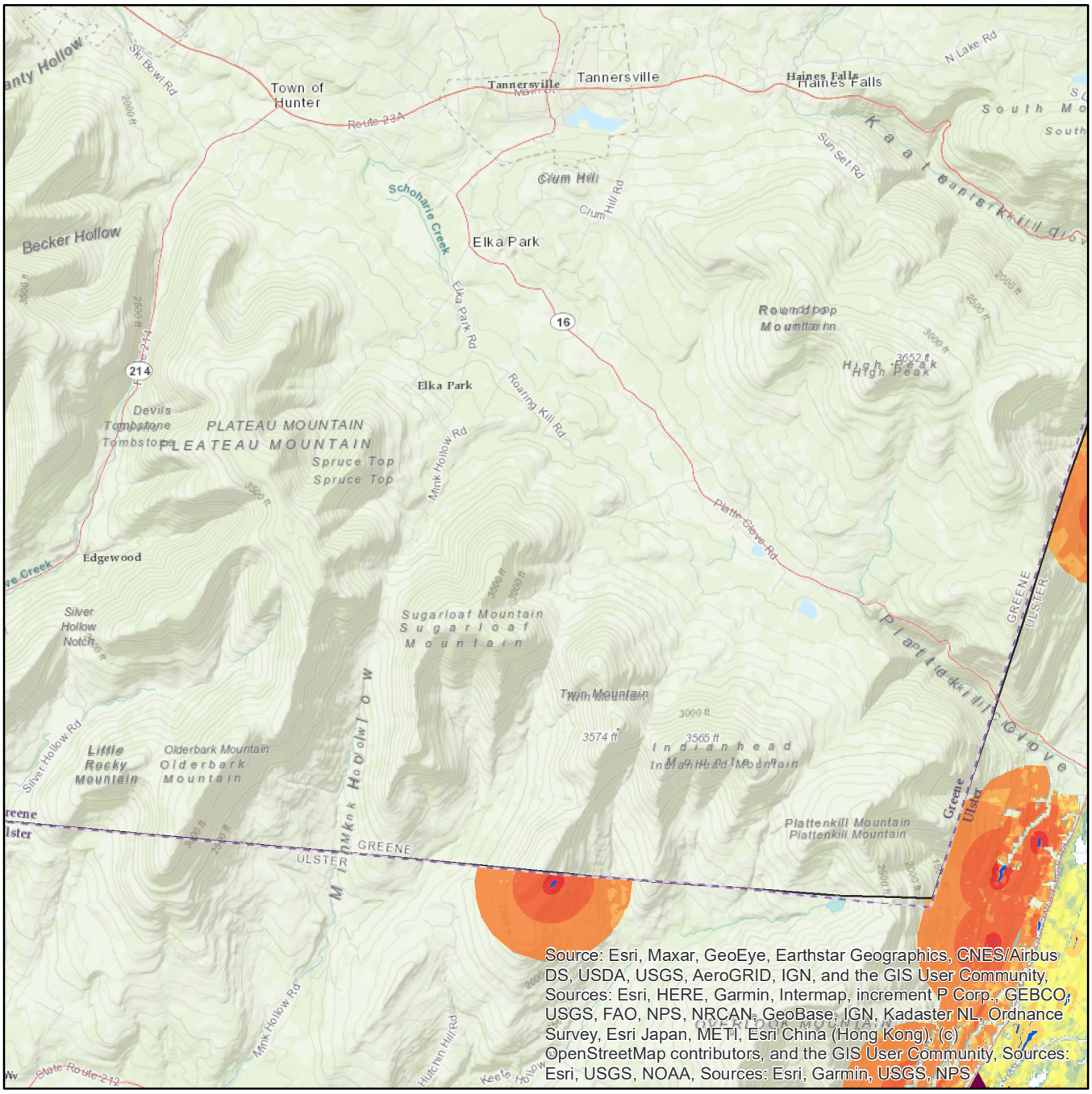
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Projection: Transverse Mercator

A4

0 10 20 40 60 80 Kilometers

N





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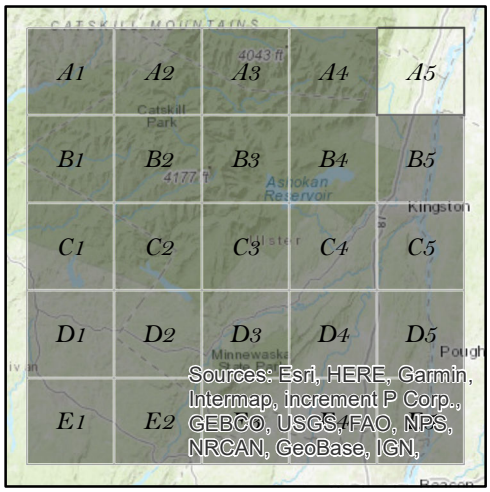
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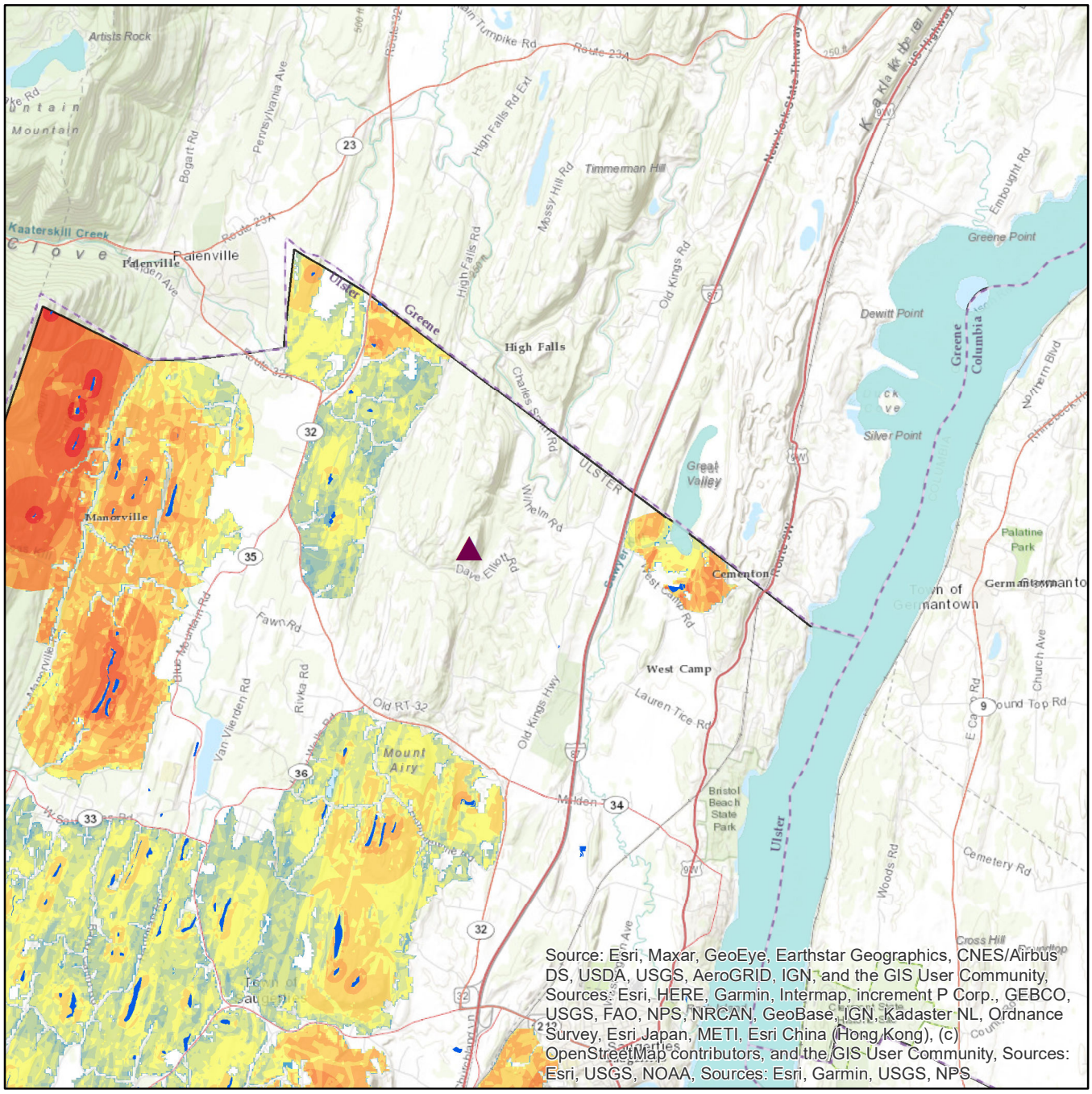
Coordinate System: GCS North American 1983 UTM Zone 18T (Calculated)
Projection: Transverse Mercator

A5

0 10 20 40 60 80 Kilometers

N





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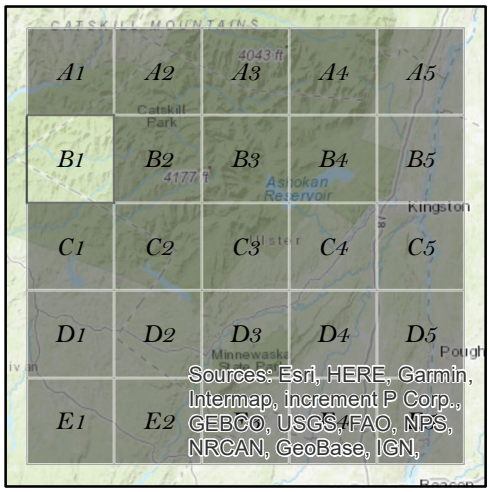
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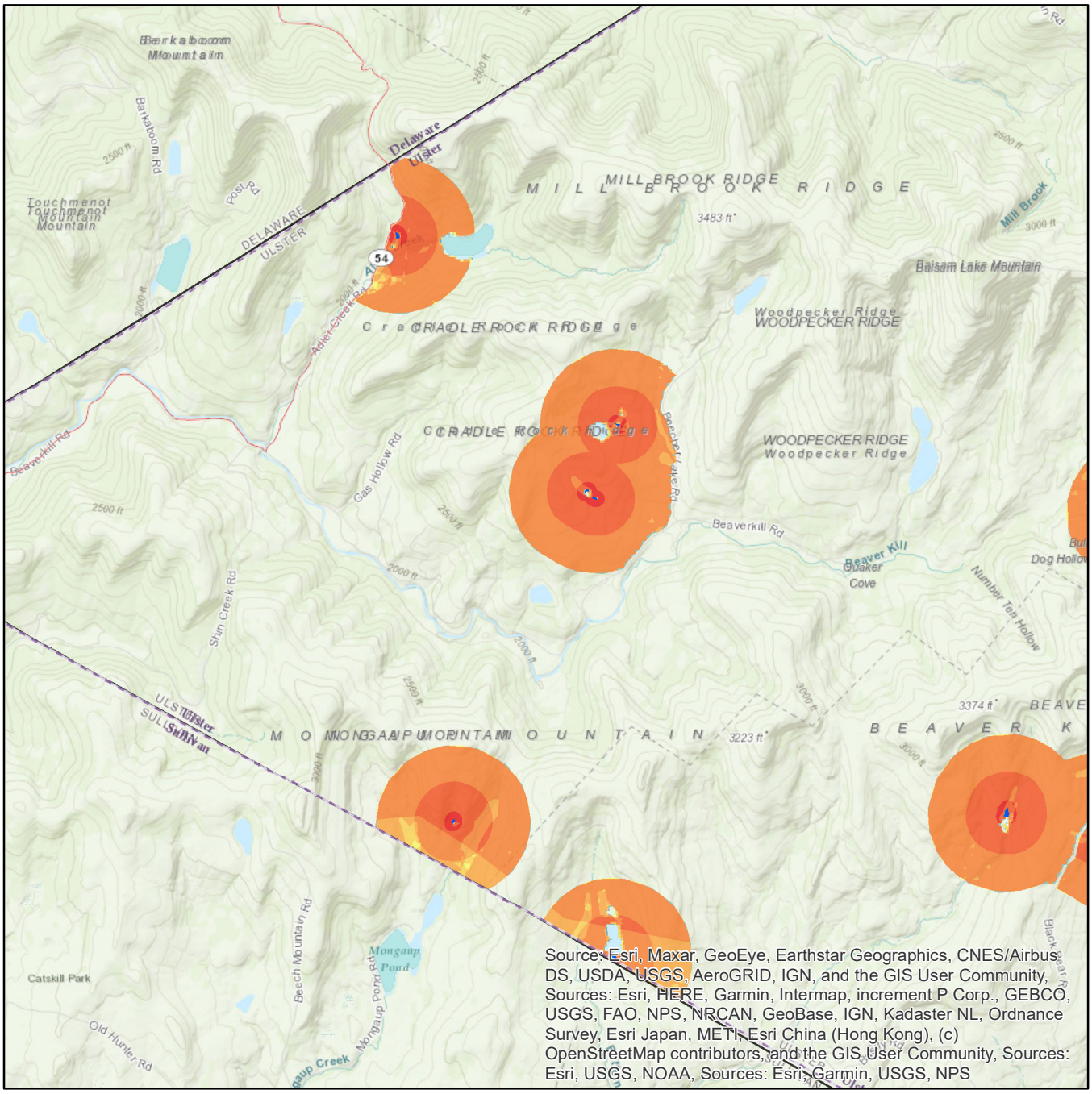
Coordinate System: GCS North American 1983 UTM Zone 18T (Calculated)
Projection: Transverse Mercator

B1

0 10 20 40 60 80 Kilometers

N





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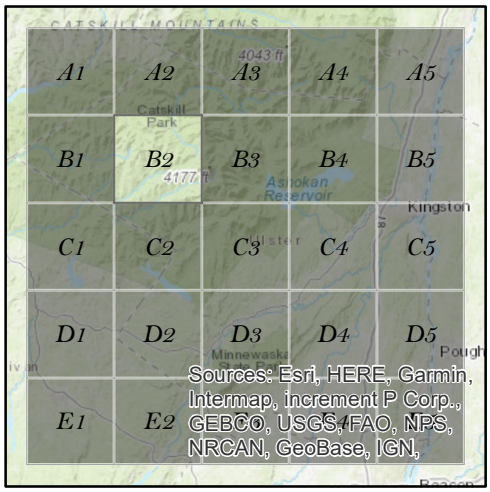
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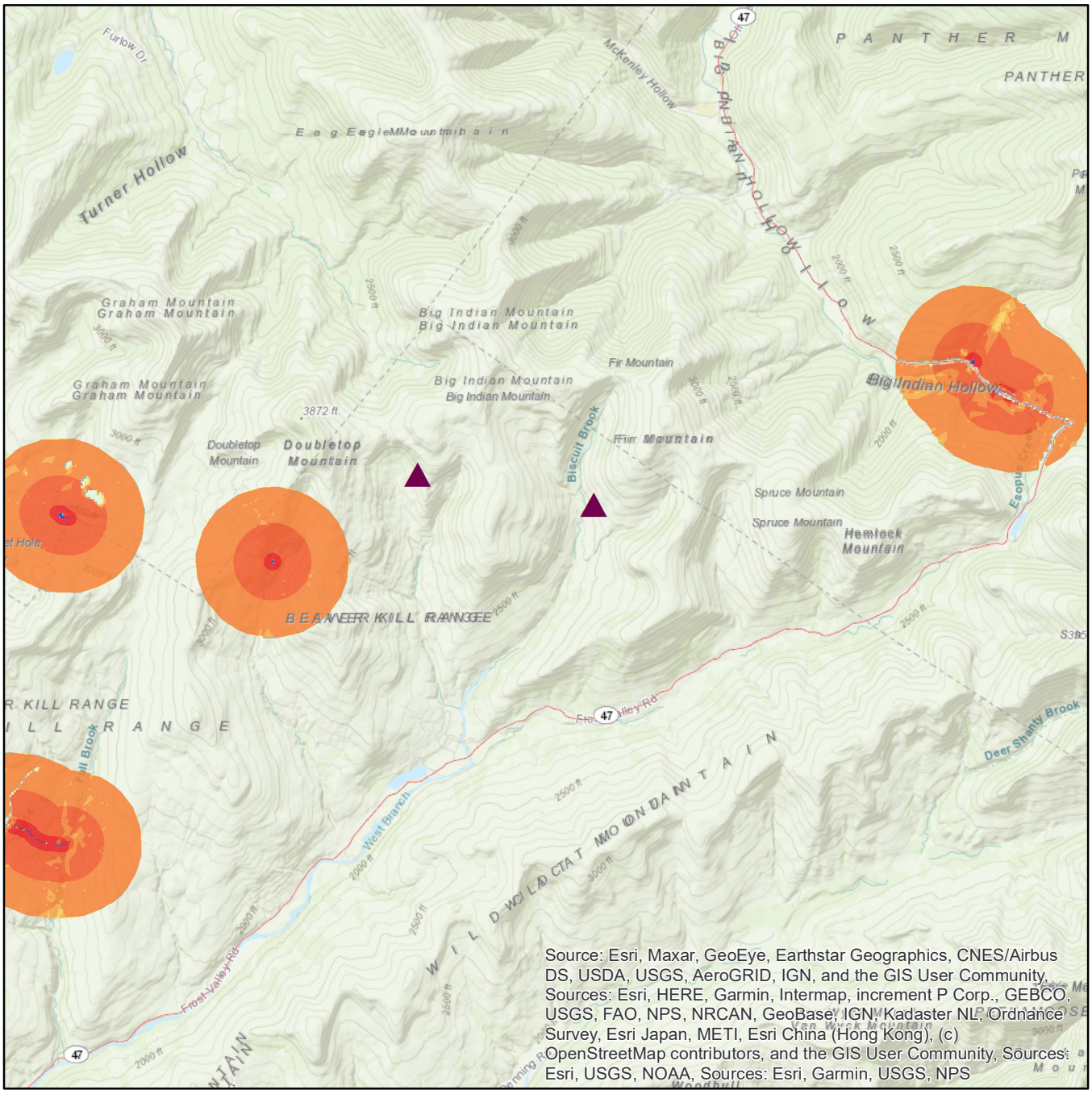
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B2

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N





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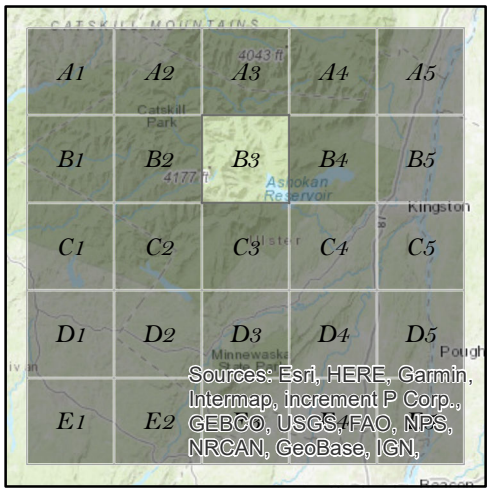
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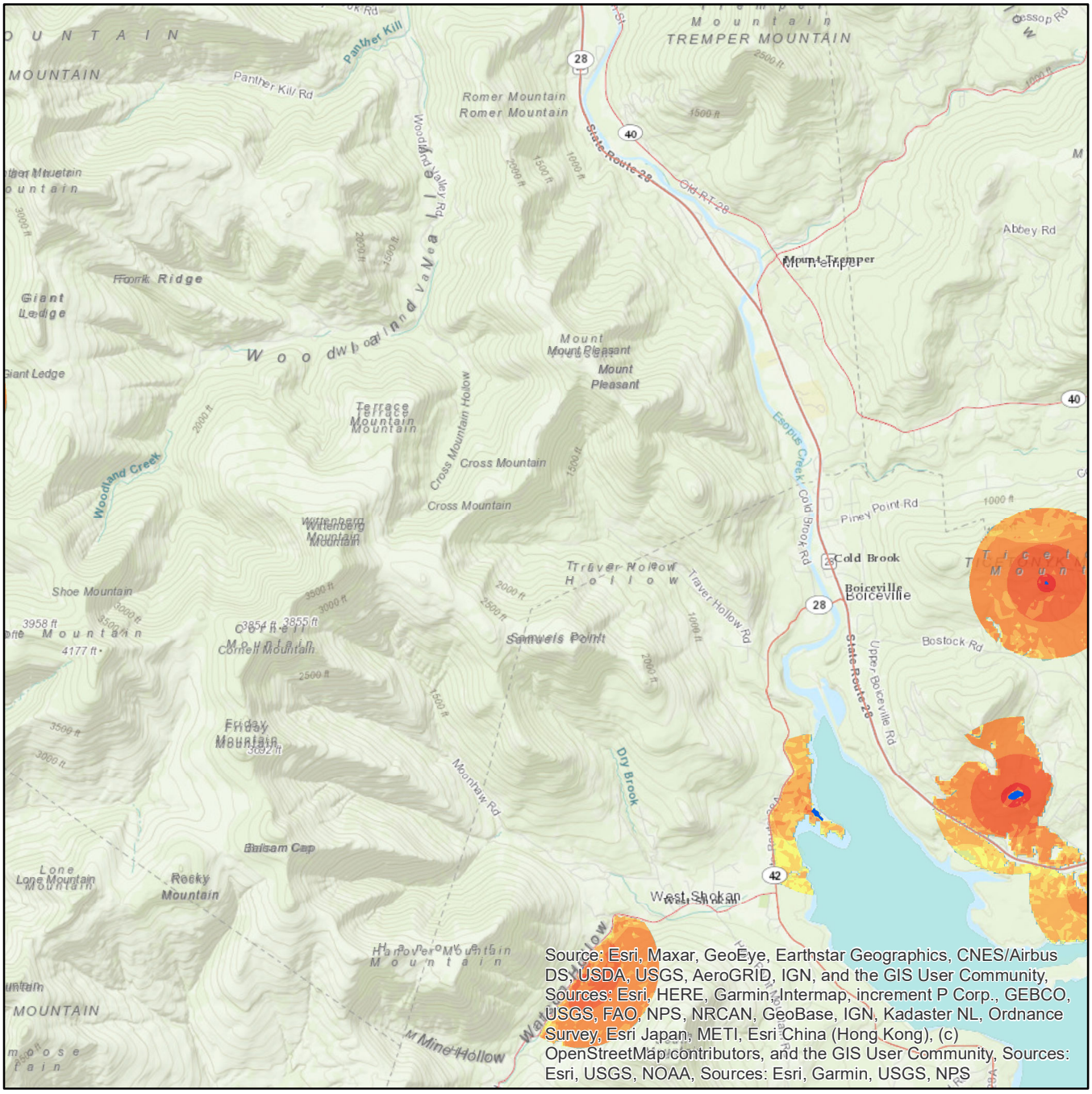
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B3

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N





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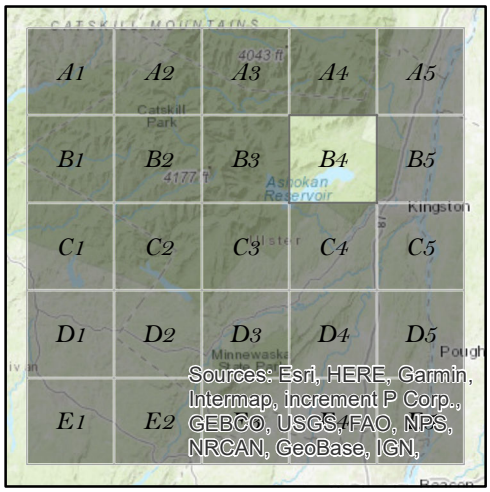
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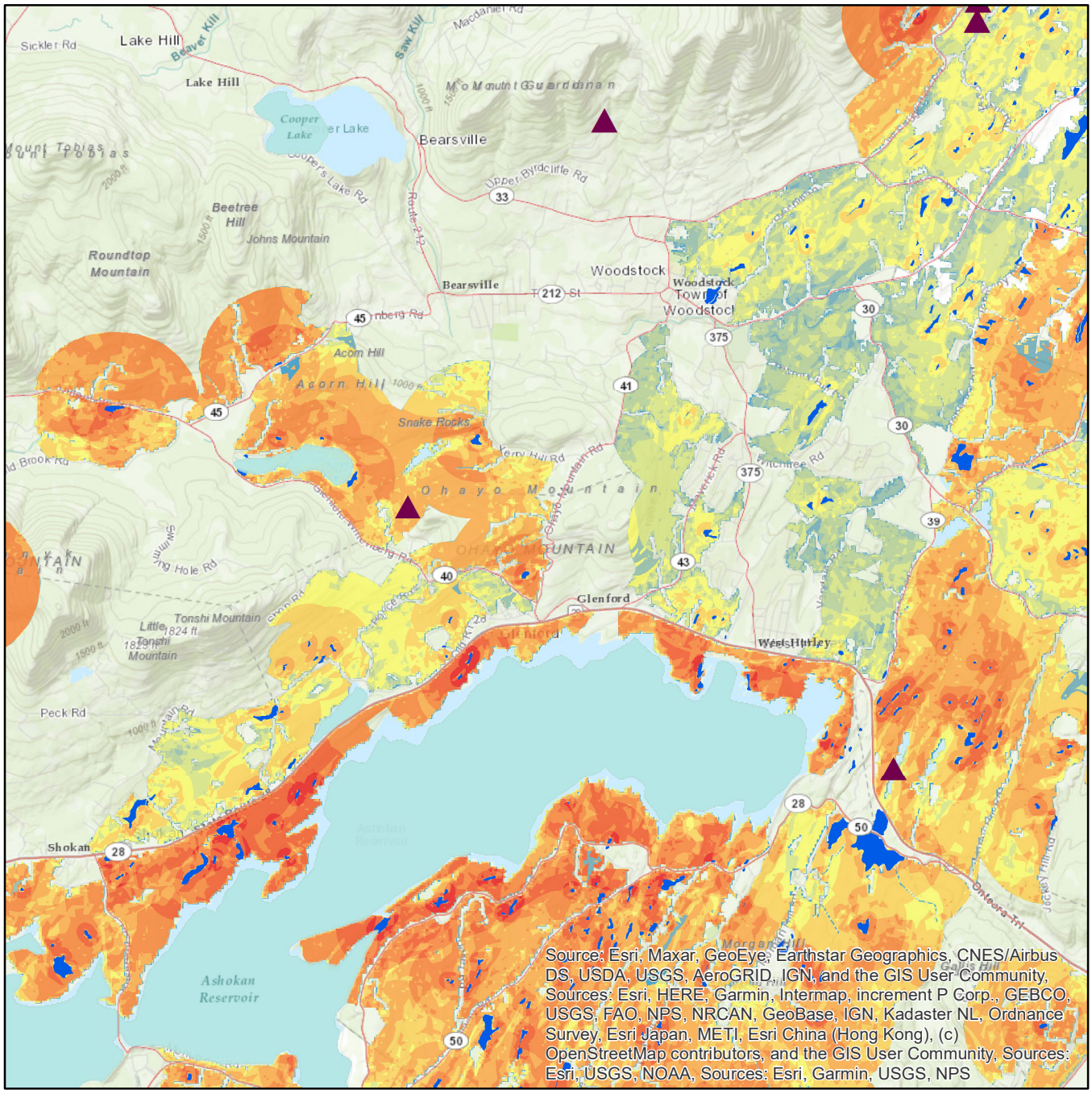
Coordinate System: GCS North American 1983 UTM Zone 18T (Calculated)
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B4

0 10 20 40 60 80 Kilometers

N





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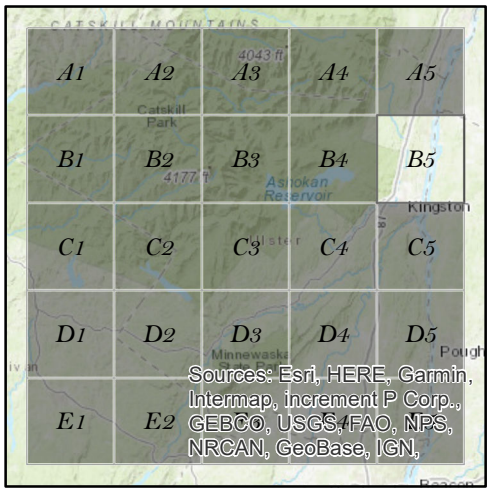
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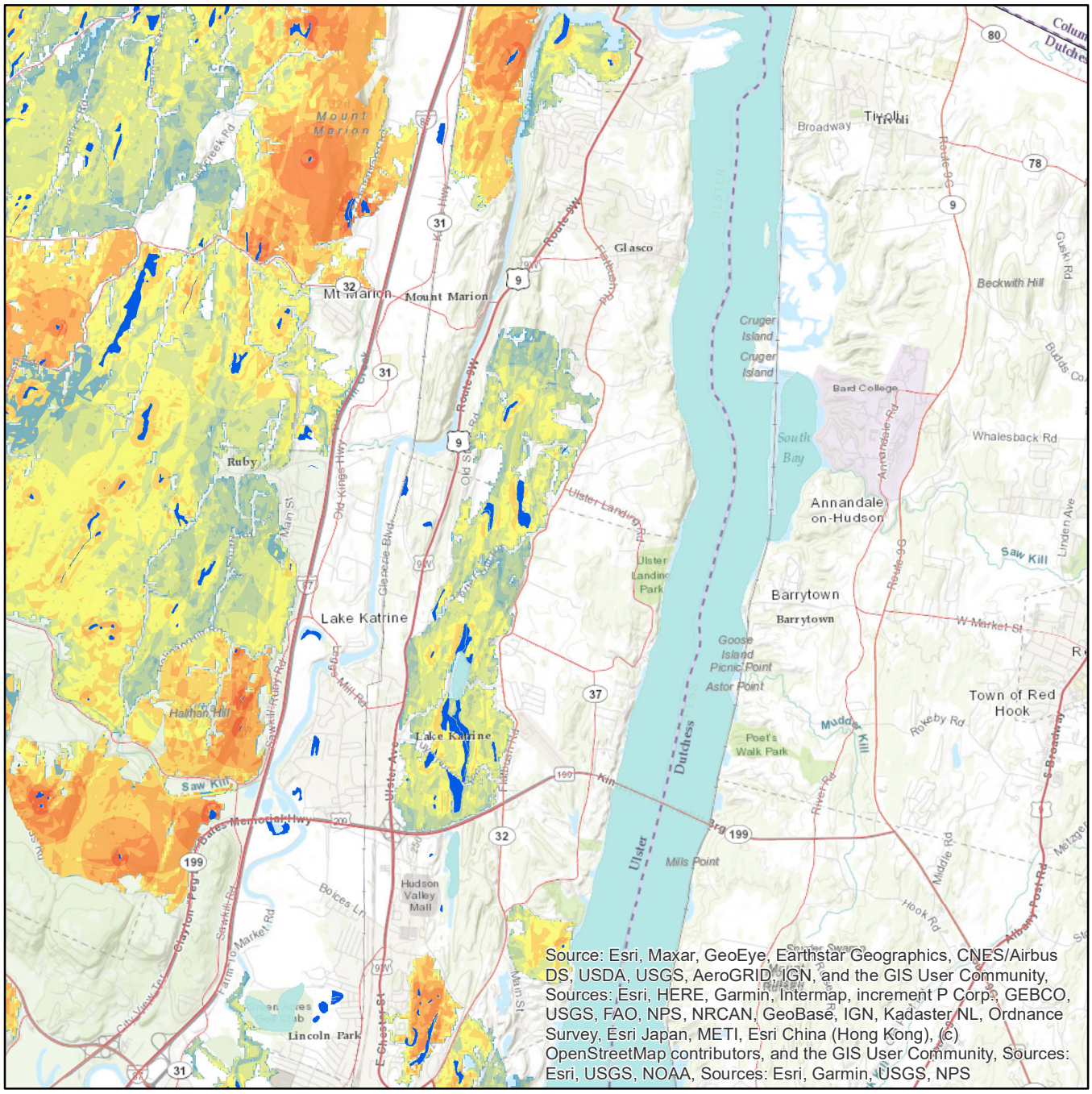
Coordinate System: GCS North American 1983 UTM Zone 18T (Calculated)
Projection: Transverse Mercator

B5

0 10 20 40 60 80 Kilometers

N





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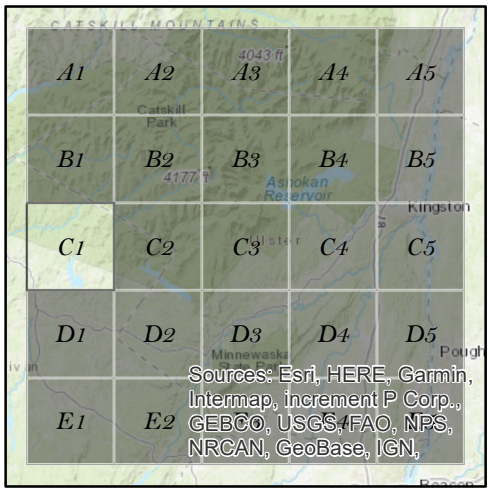
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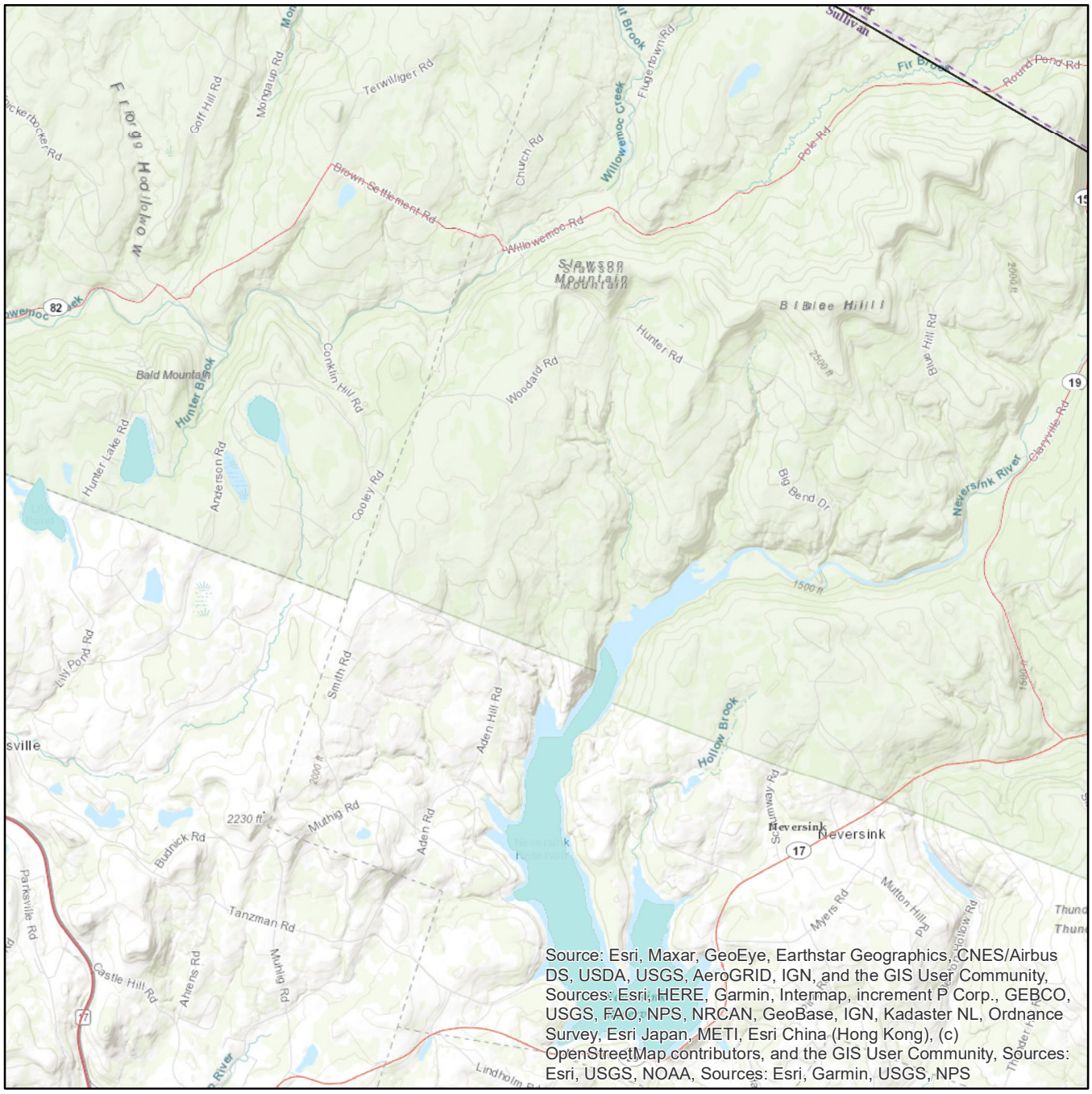
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Projection: Transverse Mercator

C1

0 10 20 40 60 80 Kilometers

N





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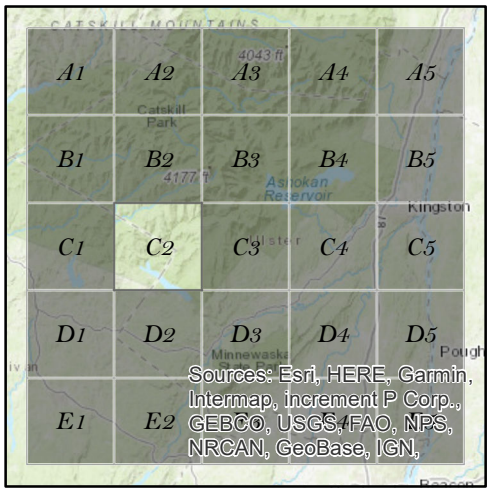
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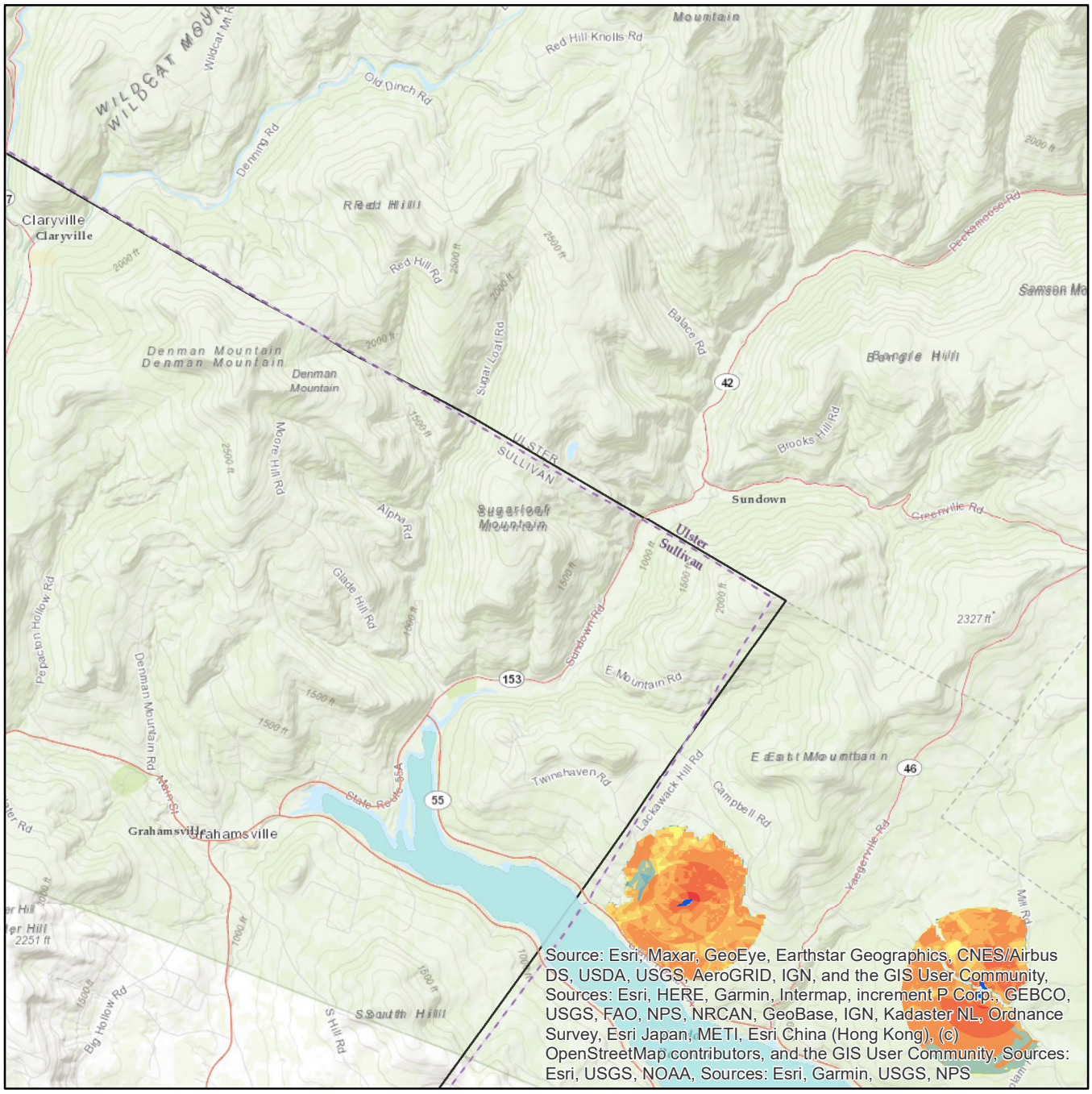
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Projection: Transverse Mercator

C2

0 10 20 40 60 80 Kilometers

N





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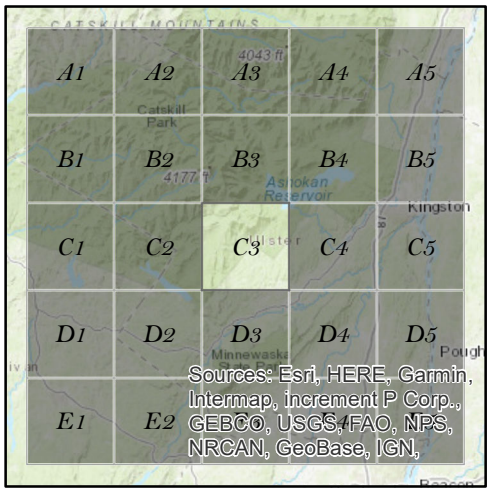
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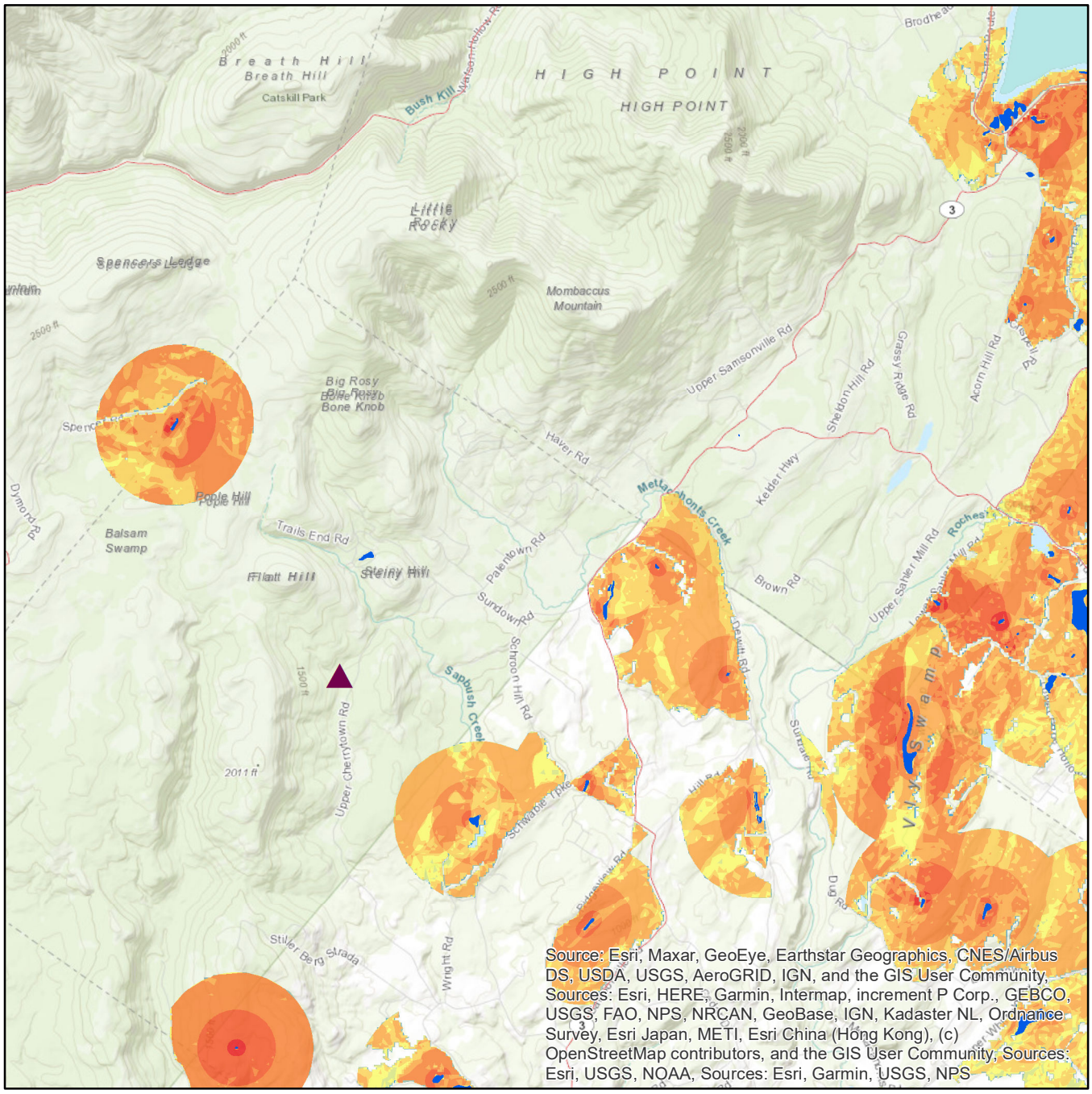
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Projection: Transverse Mercator

C3

0 10 20 40 60 80 Kilometers

N





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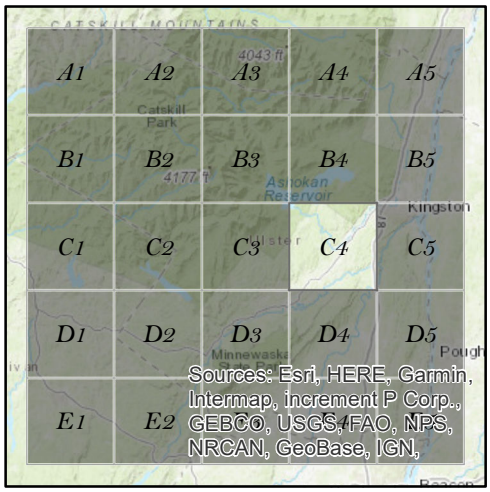
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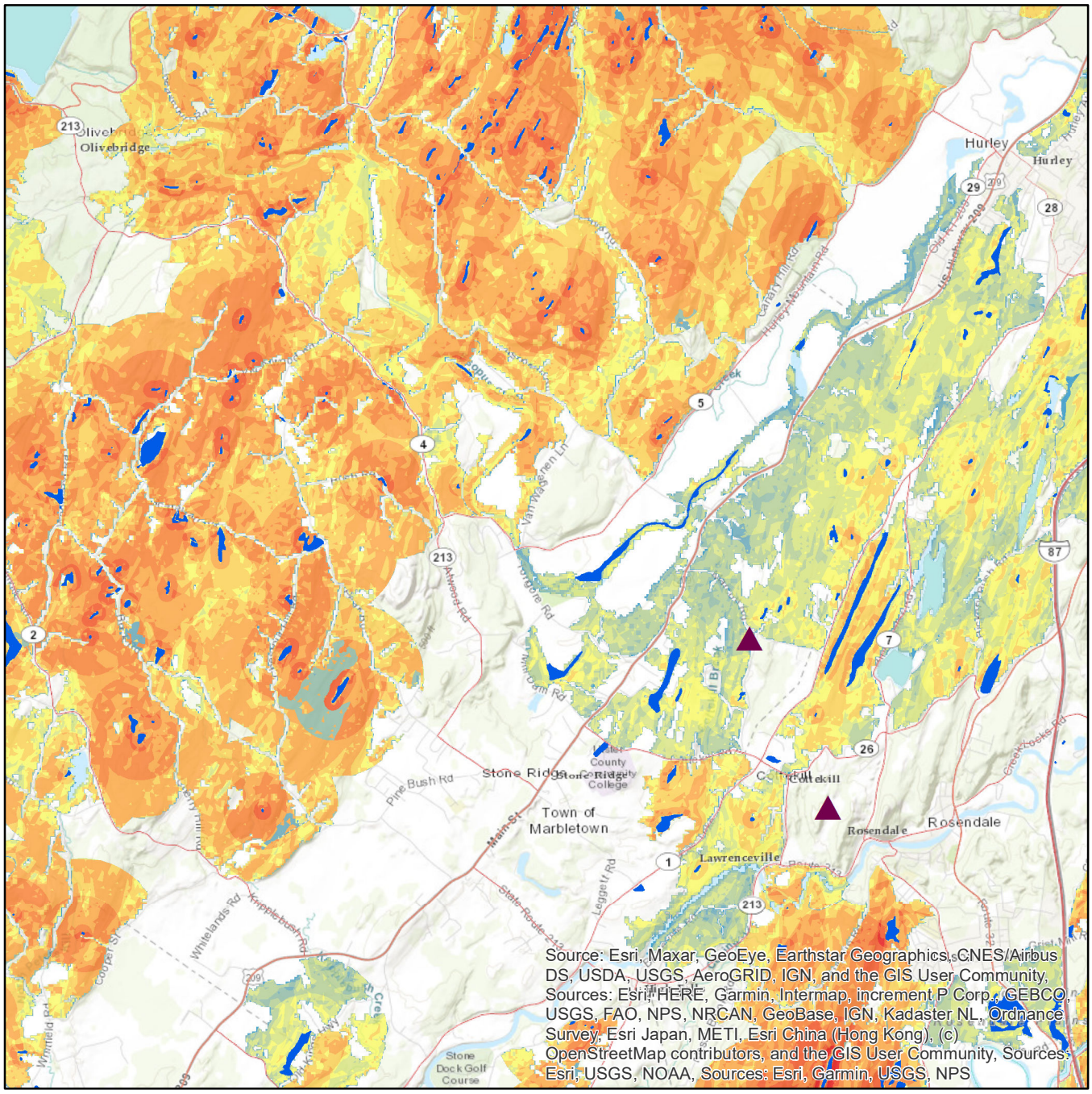
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Projection: Transverse Mercator

C4

0 10 20 40 60 80 Kilometers

N





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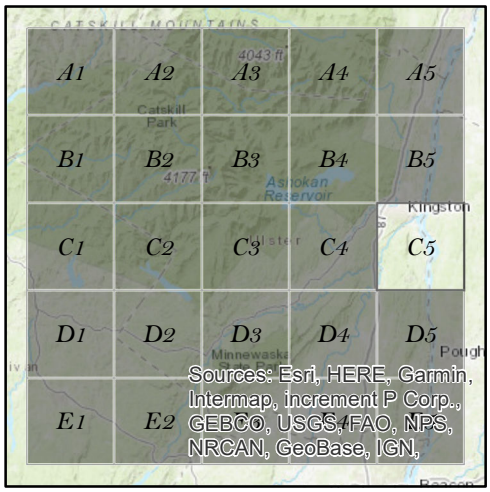
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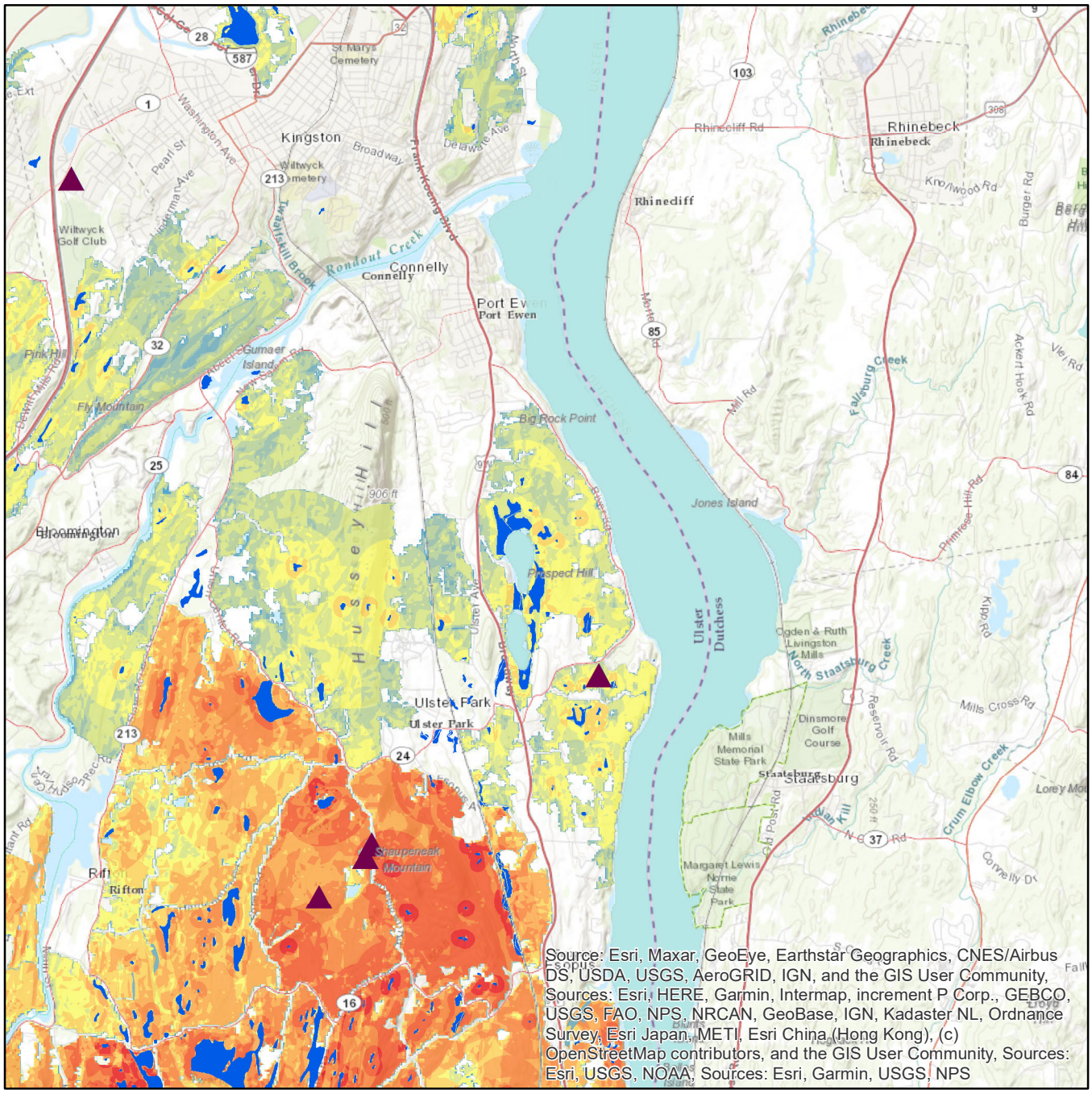
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Projection: Transverse Mercator

C5

0 10 20 40 60 80 Kilometers

N





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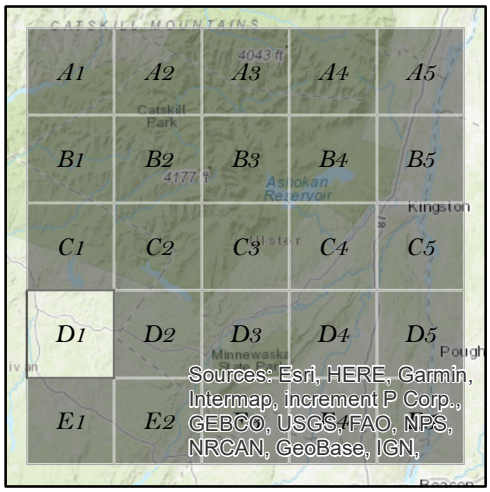
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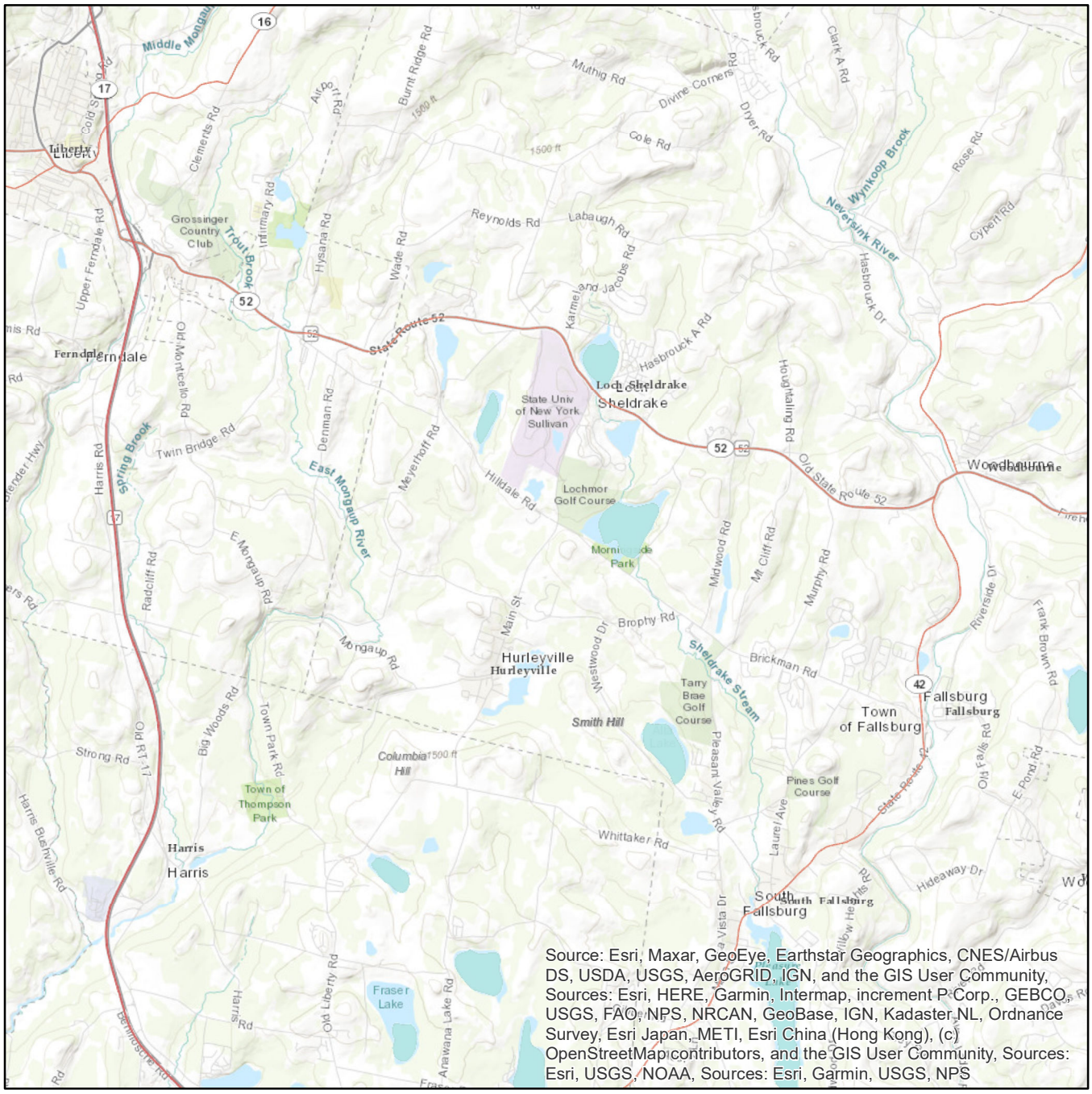
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Projection: Transverse Mercator

D1

0 10 20 40 60 80 Kilometers

N





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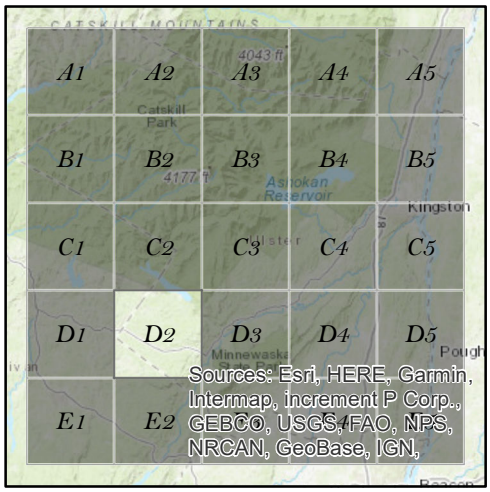
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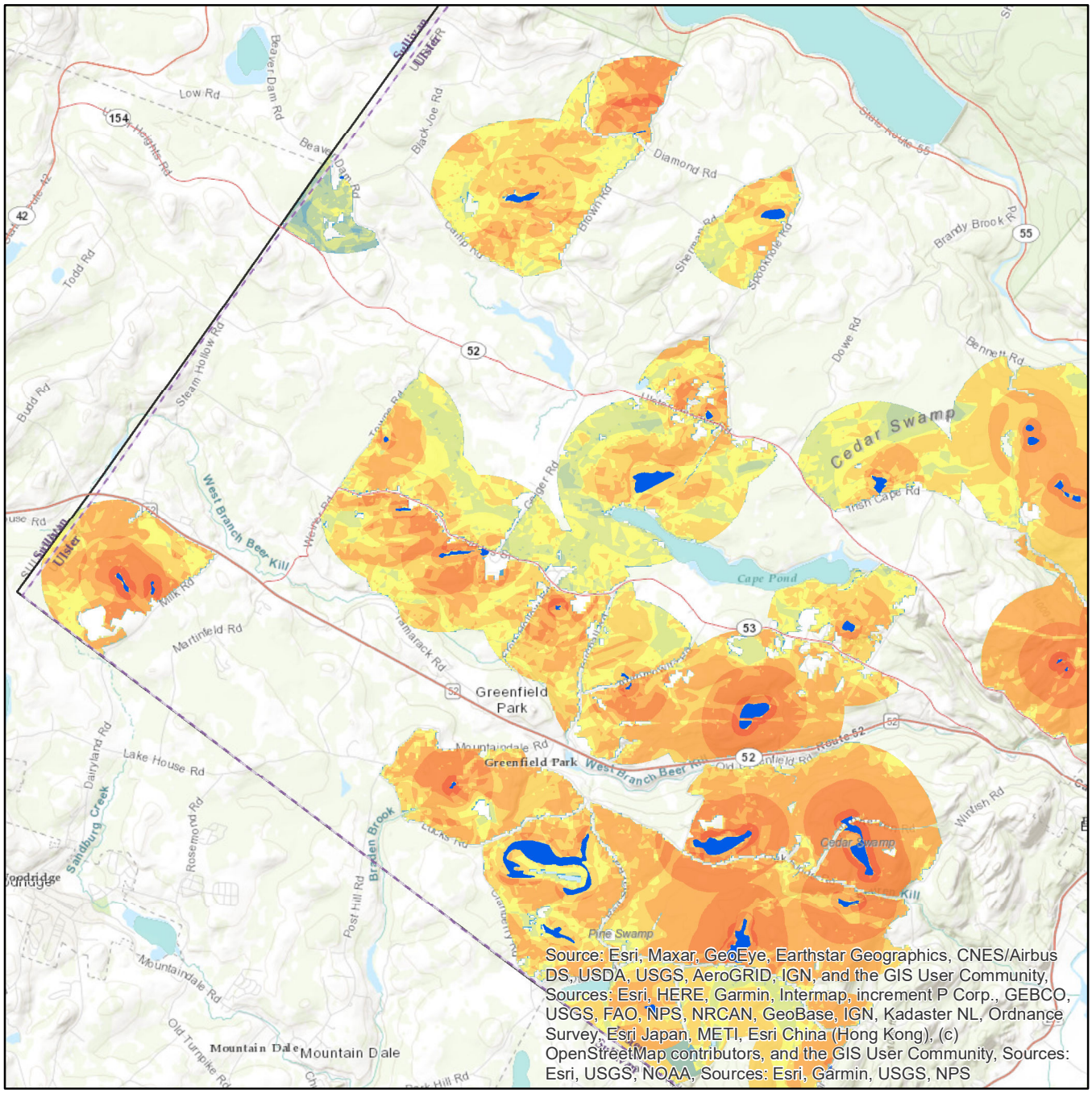
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Projection: Transverse Mercator

D2

0 10 20 40 60 80 Kilometers

N





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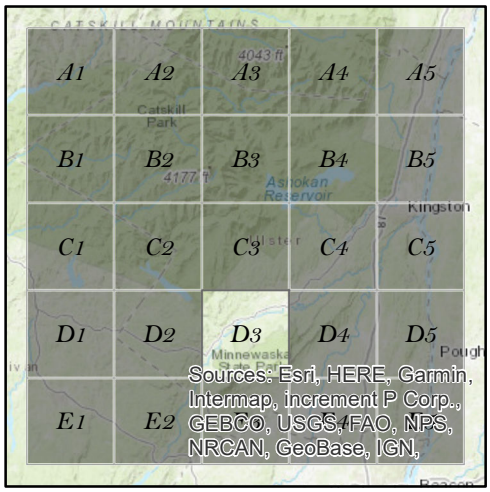
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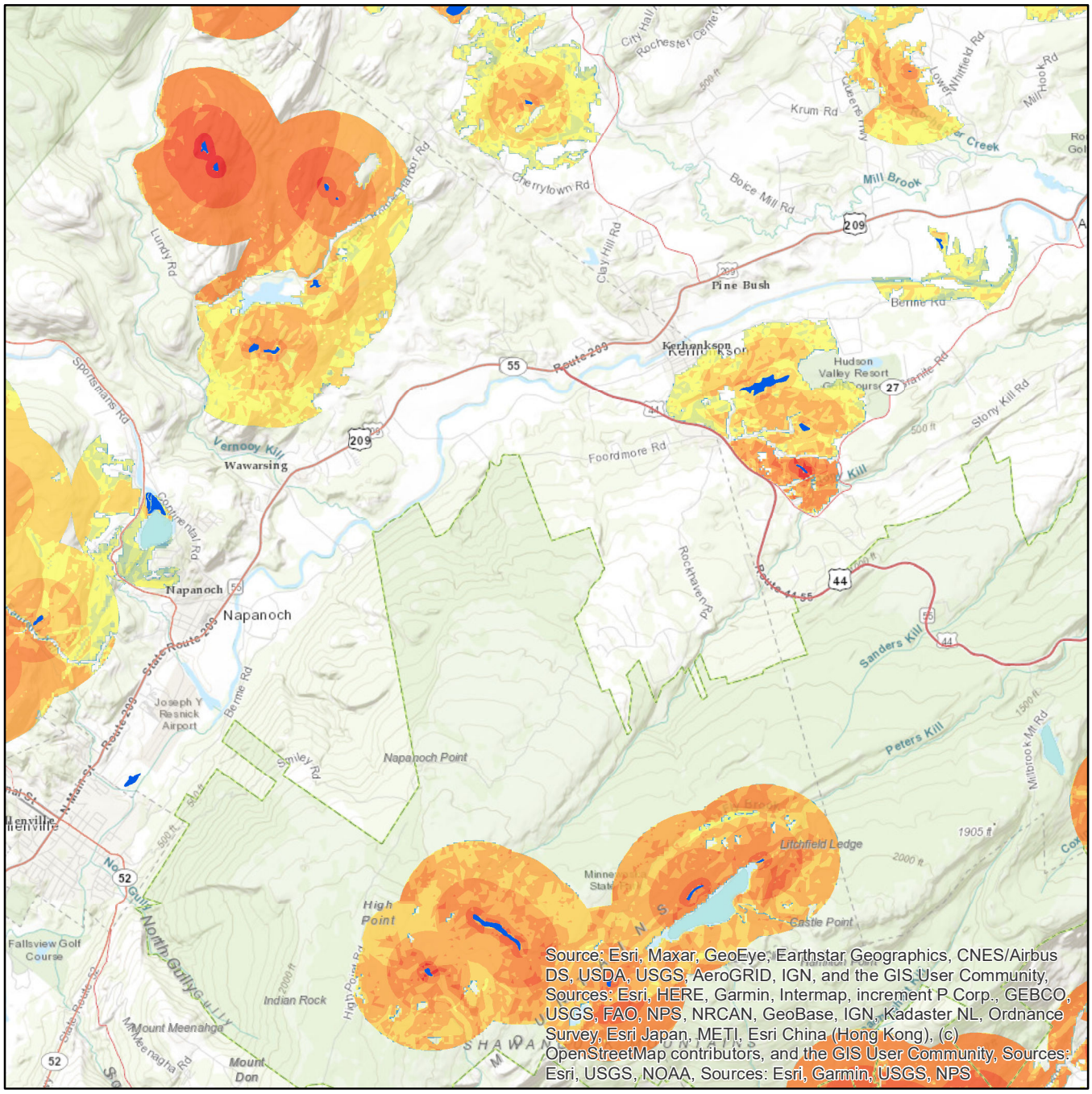
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Projection: Transverse Mercator

D3

0 10 20 40 60 80 Kilometers

N





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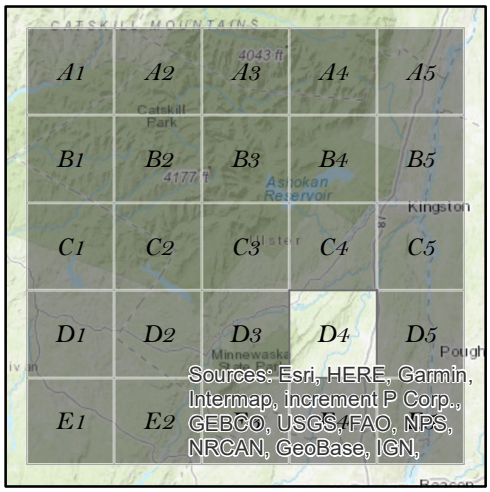
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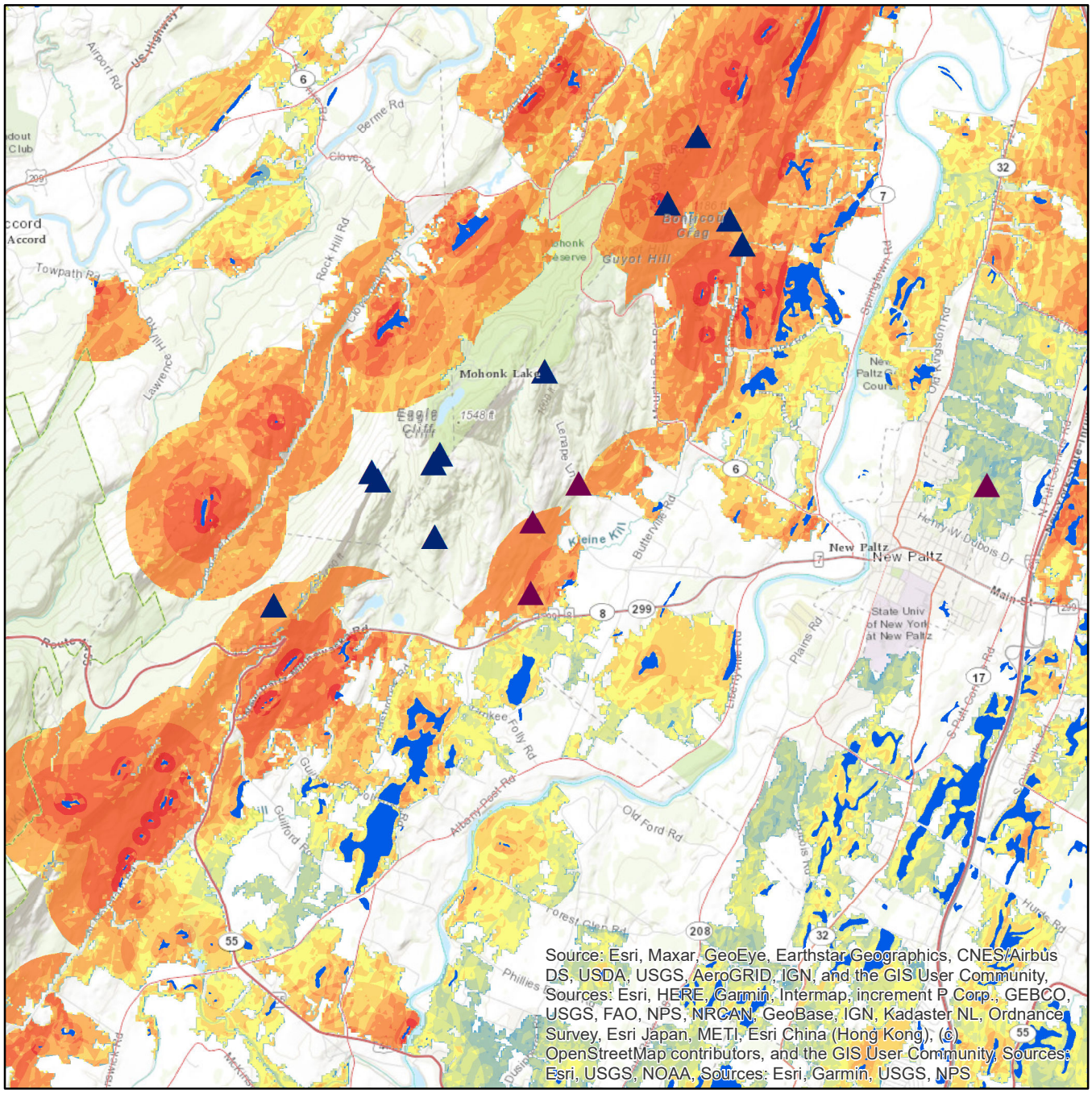
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Projection: Transverse Mercator

D4

0 10 20 40 60 80 Kilometers

N





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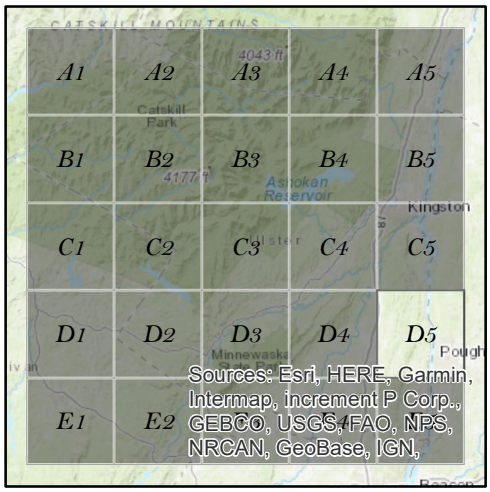
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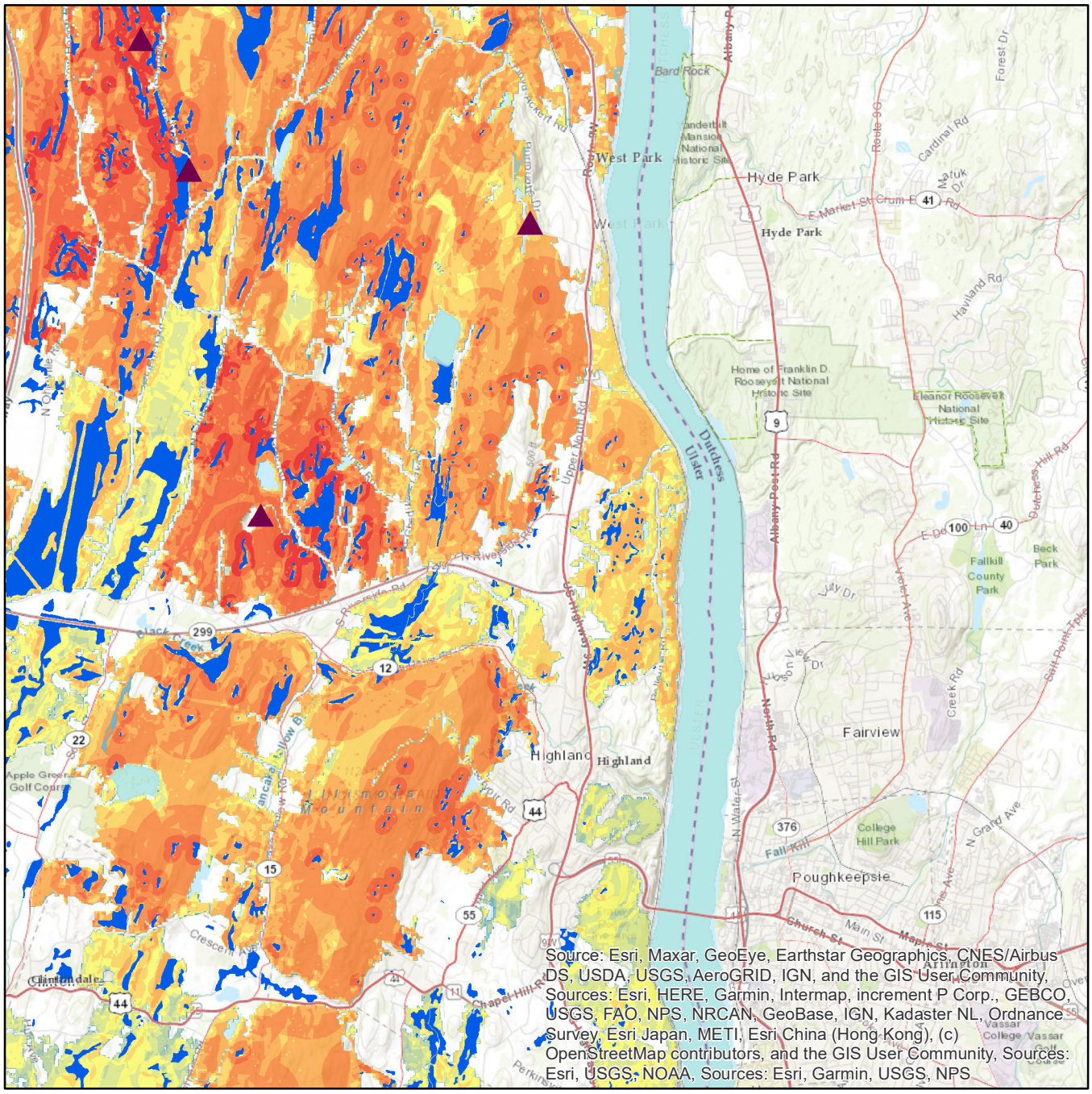
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Projection: Transverse Mercator

D5

0 10 20 40 60 80 Kilometers

N





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Mohonk Preserve Observations

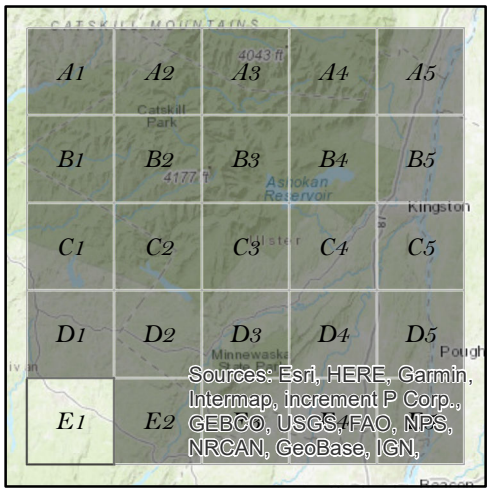
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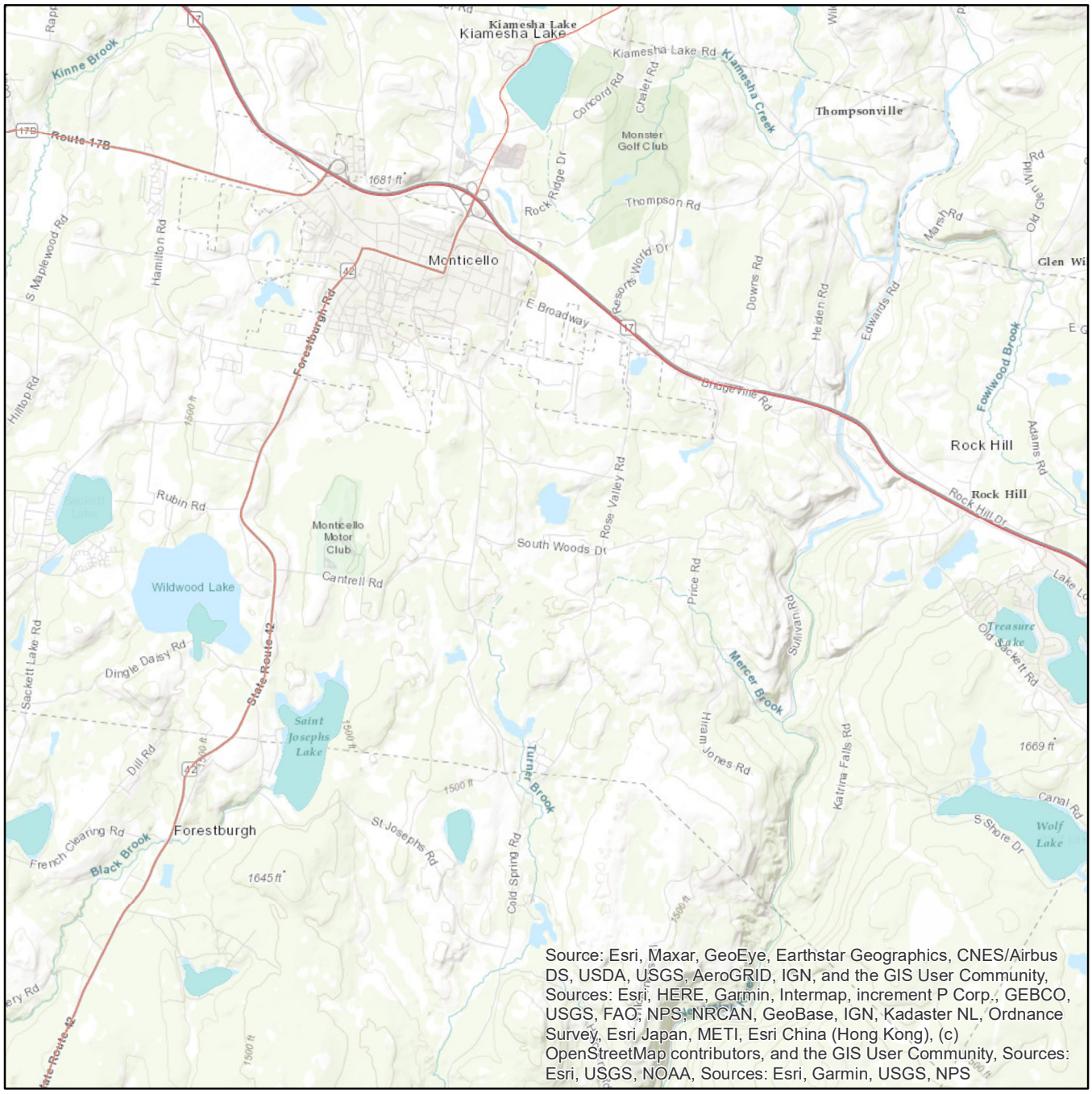
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Projection: Transverse Mercator

E1

0 10 20 40 60 80 Kilometers

N





Source: Esri, Maxar, GeoEye, Earthstar Geographics, CNES/Airbus DS, USDA, USGS, AeroGRID, IGN, and the GIS User Community, Sources: Esri, HERE, Garmin, Intermap, increment P Corp., GEBCO, USGS, FAO, NPS, NRCAN, GeoBase, IGN, Kadaster NL, Ordnance Survey, Esri Japan, METI, Esri China (Hong Kong), (c) OpenStreetMap contributors, and the GIS User Community, Sources: Esri, USGS, NOAA, Sources: Esri, Garmin, USGS, NPS

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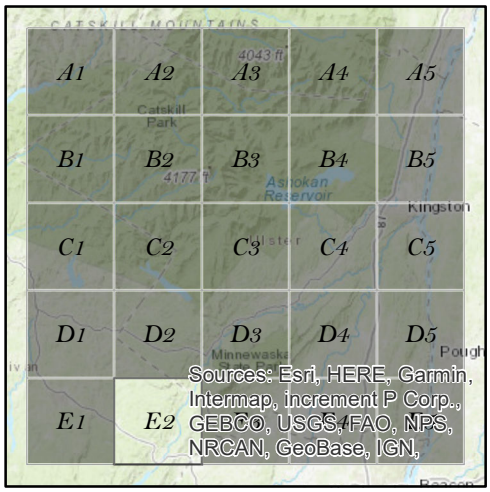
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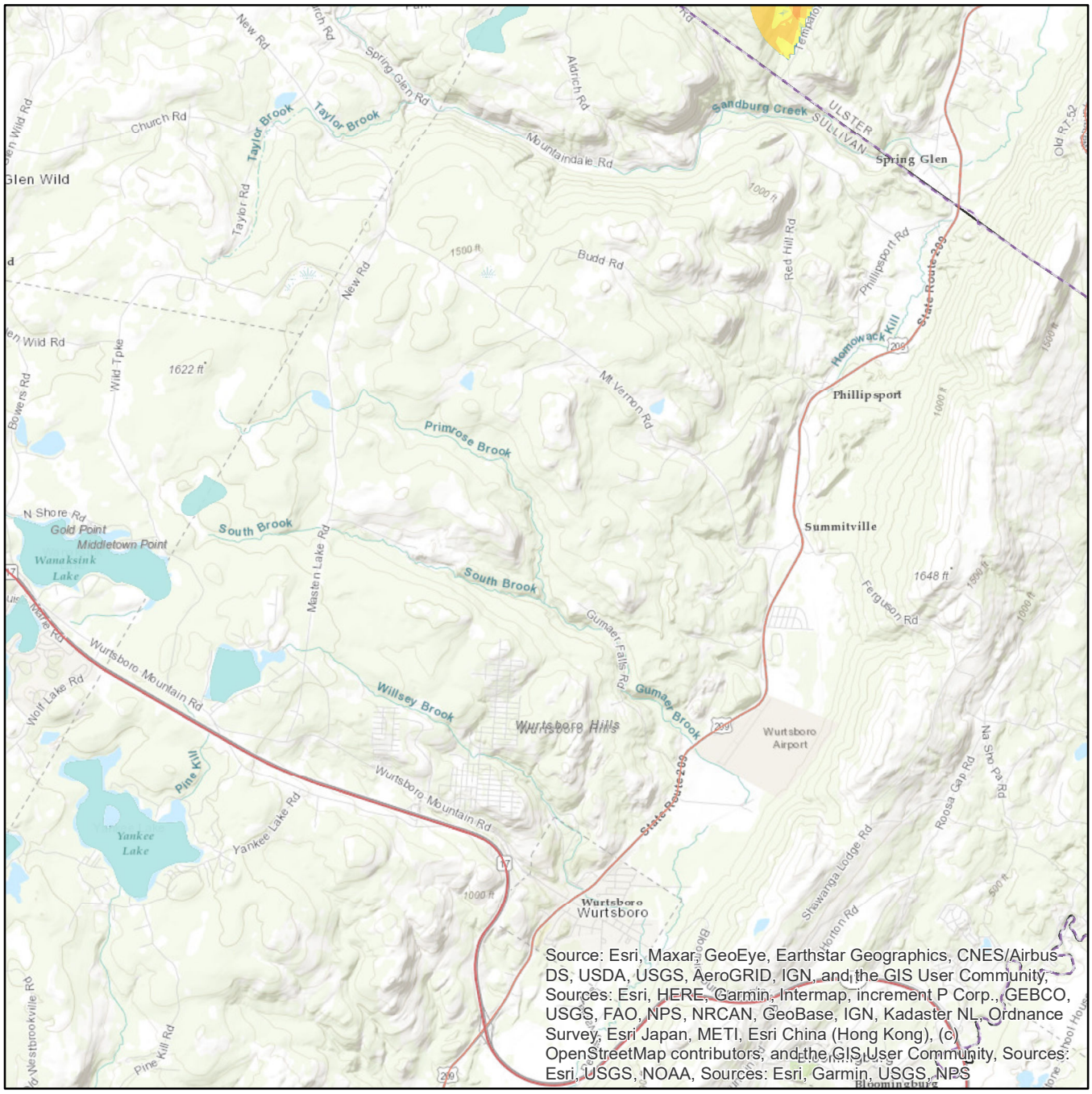
Coordinate System: GCS North American 1983 UTM Zone 18T (Calculated)
Projection: Transverse Mercator

E2

0 10 20 40 60 80 Kilometers

N





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iNaturalist Observations

Mohonk Preserve Observations

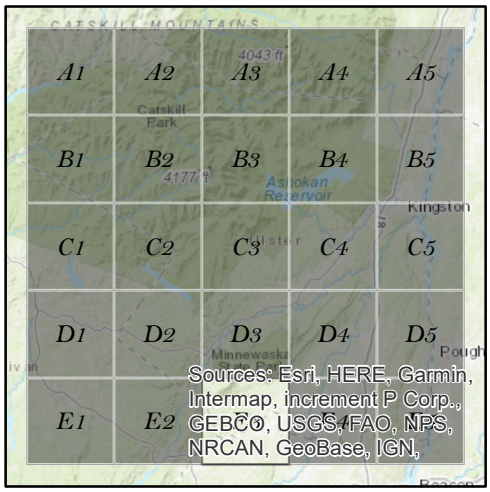
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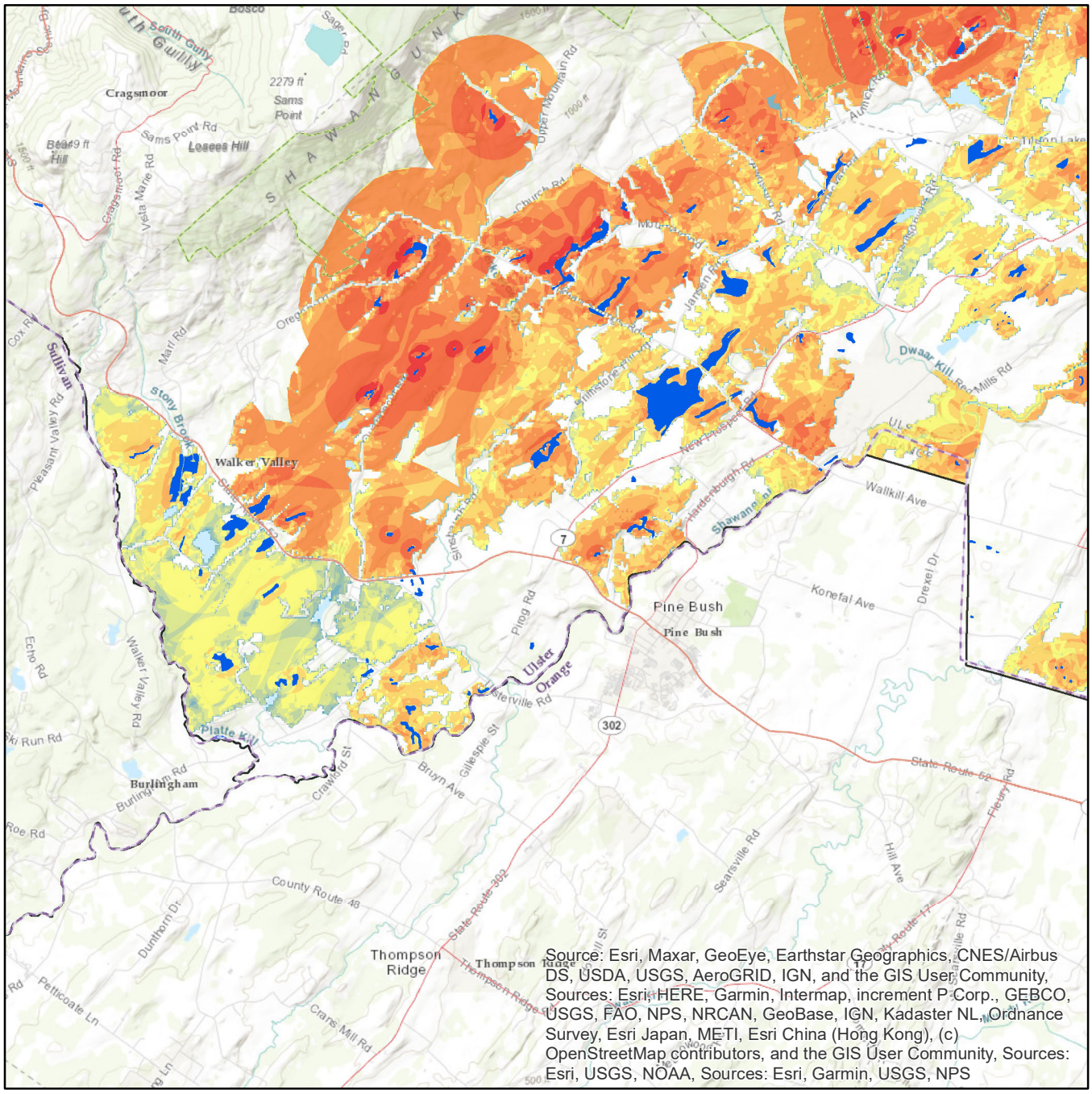
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Projection: Transverse Mercator

E3

0 10 20 40 60 80 Kilometers

N





Identifying Suitable Mole Salamander Migration Paths in Ulster County, NY

Author: Jay Locke *Date Saved: 7/22/2022*

iNaturalist Observations

Mohonk Preserve Observations

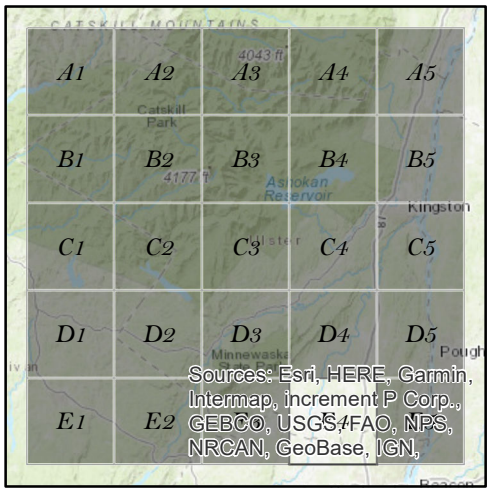
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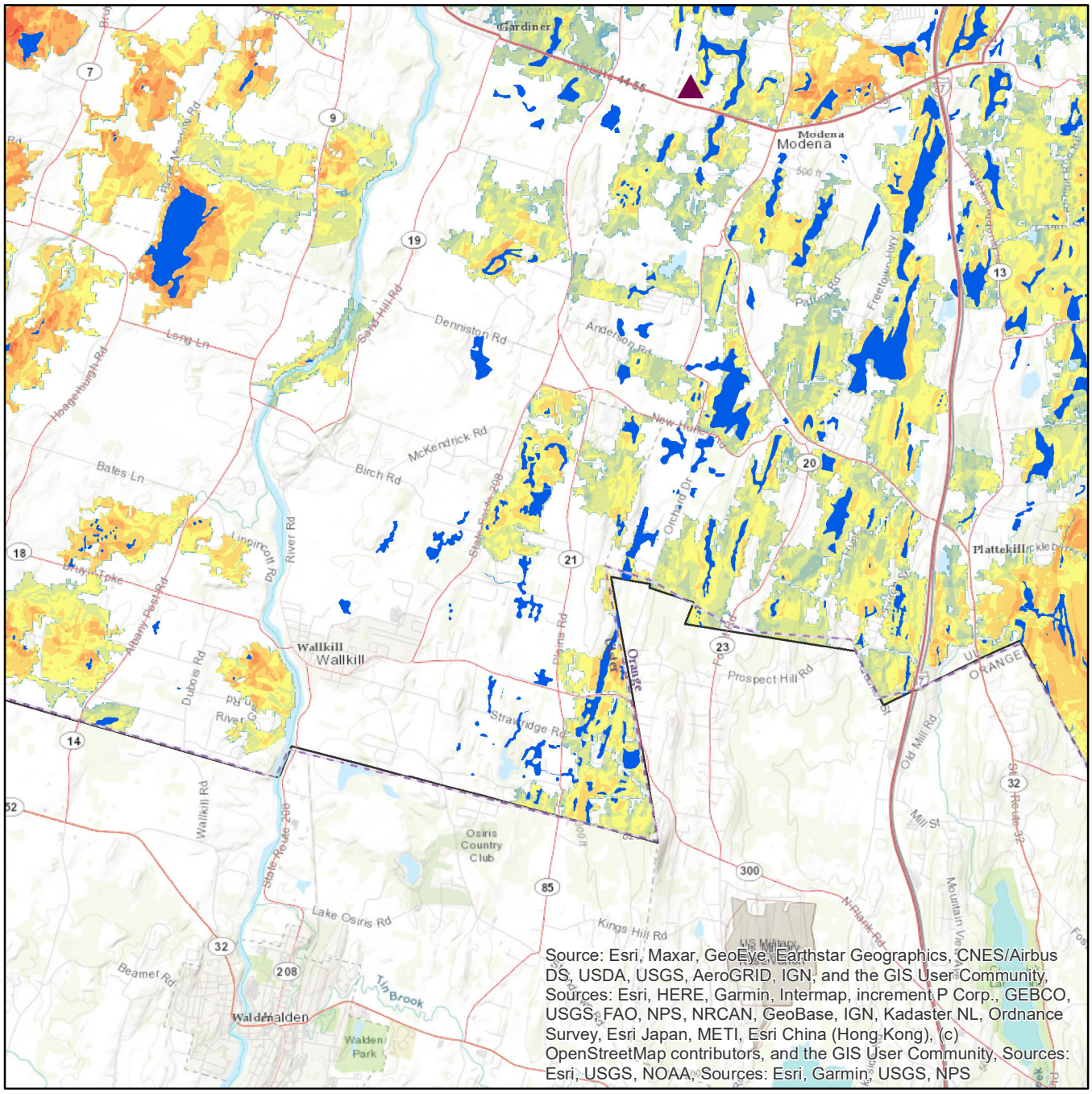
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Projection: Transverse Mercator

E4

0 10 20 40 60 80 Kilometers

N





Identifying Suitable Mole Salamander Migration Paths in Ulster County, NY

Author: Jay Locke *Date Saved: 7/22/2022*

iNaturalist Observations

Mohonk Preserve Observations

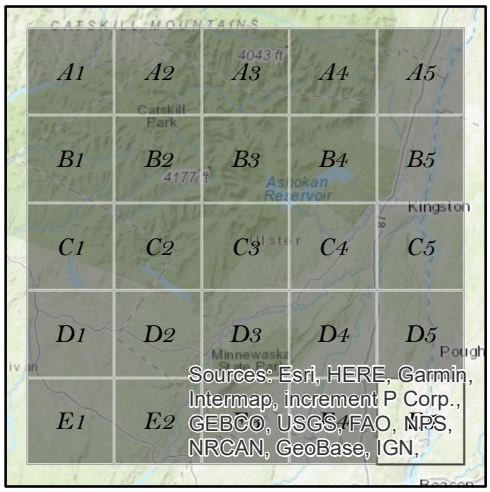
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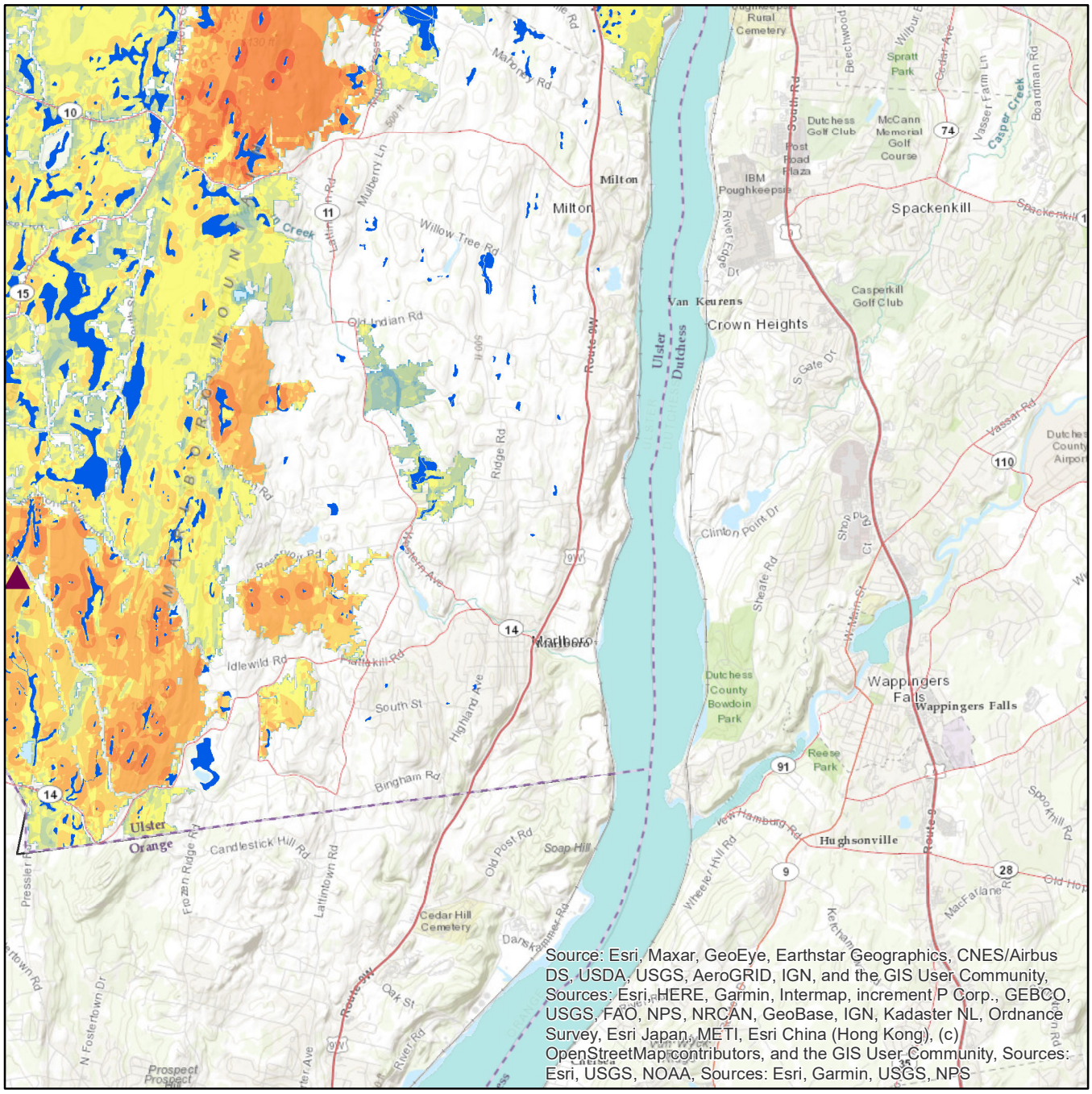
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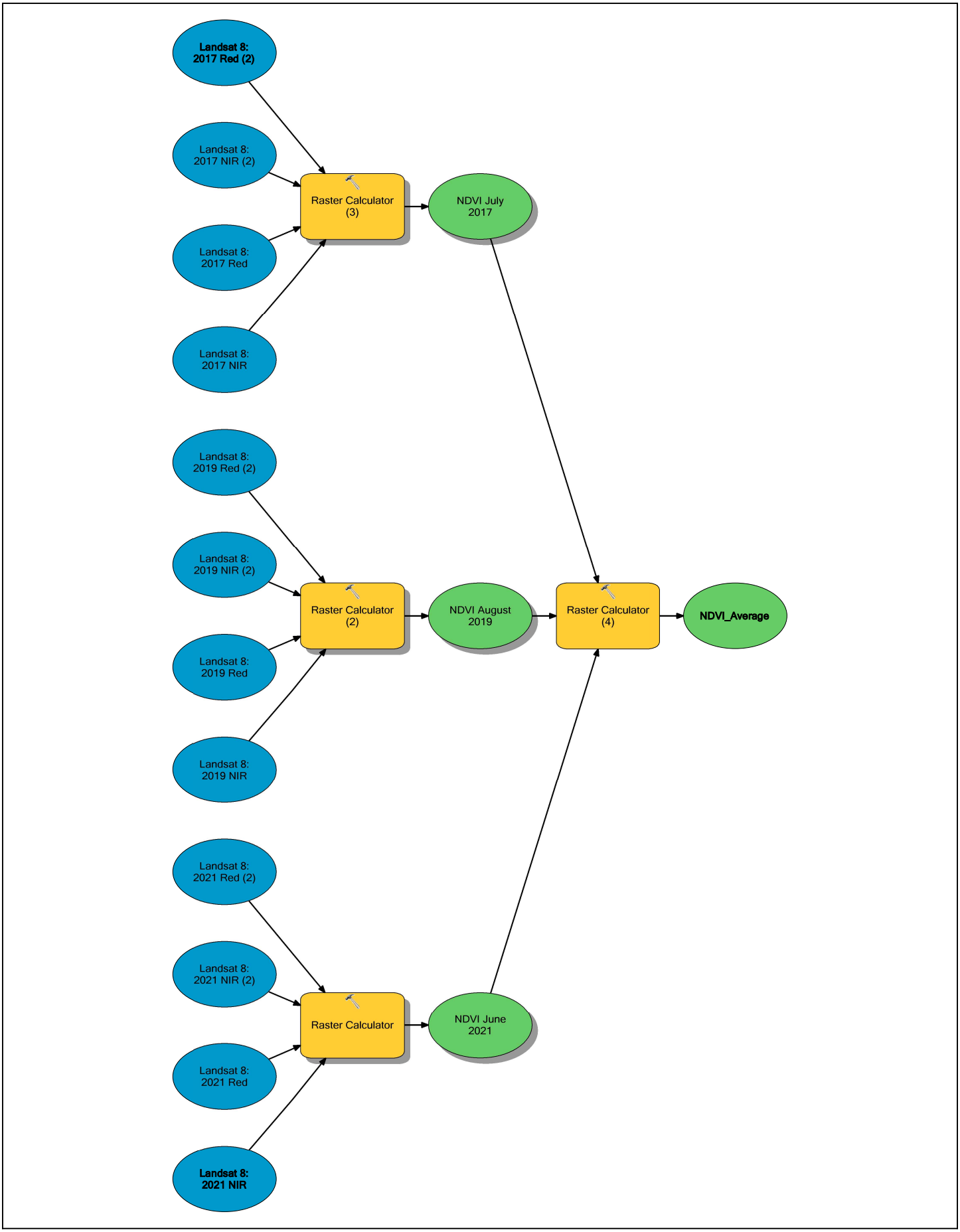
E5

0 10 20 40 60 80 Kilometers

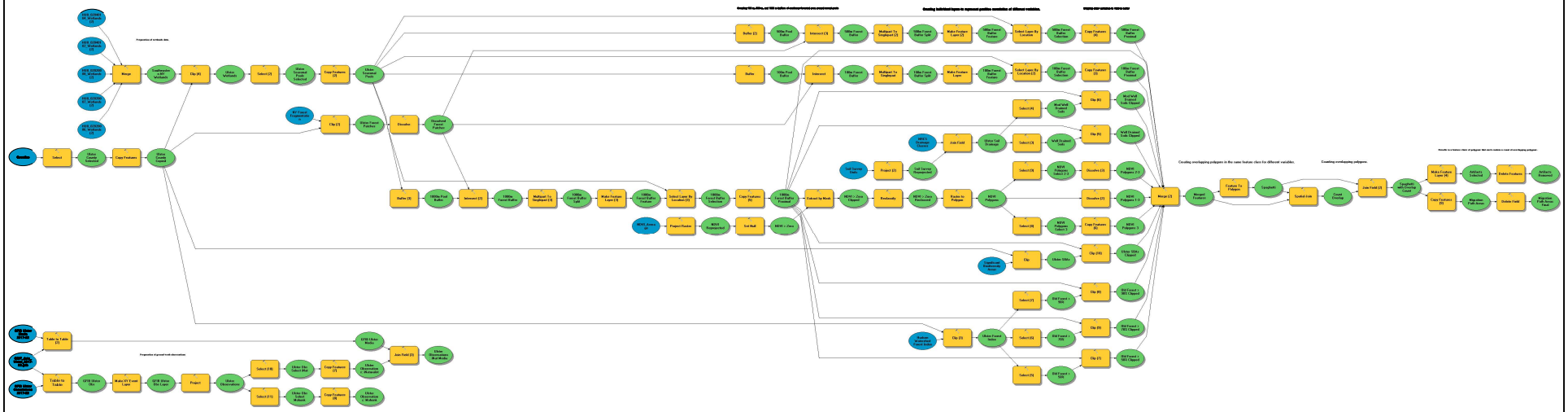
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Average NDVI Model



Migration Paths Model