Patch Metrics: A cost effective method for short and long term monitoring of Chesapeake Bay wild brook trout populations?

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Eastern Brook Trout JOINT VENTURE

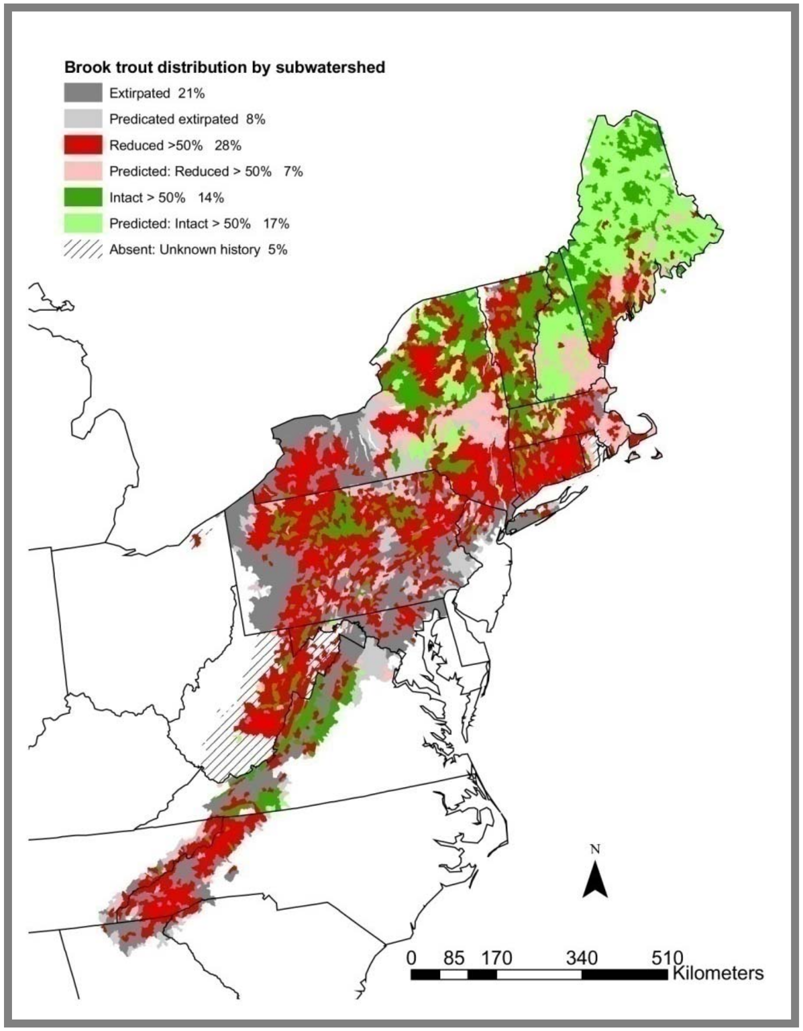
Introduction

Case History: Eastern Brook Trout Joint Venture

1. Evaluate the distribution of brook trout for the 2005 EBTJV assessment.

2. Context:
   -lots of states
   -inconsistent fine scale data

3. Hudy et al. 2008 NAJFM 28:1069-1085



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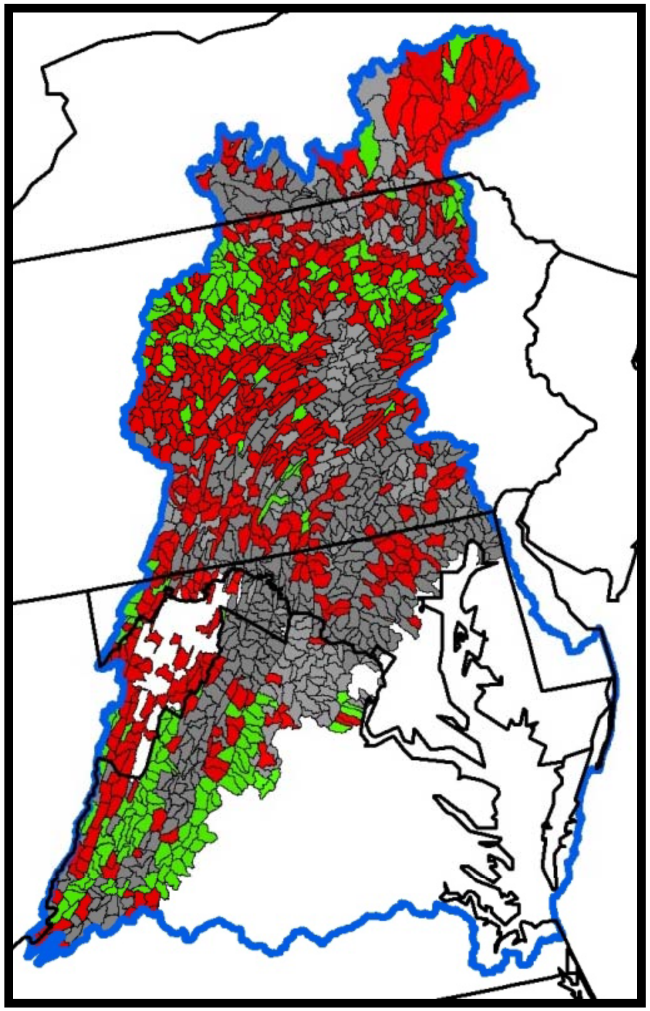
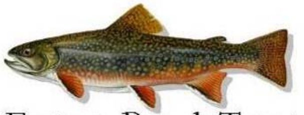
Brook Trout Range

- 1,433 subwatersheds
  - 226 intact (green)
  - 542 reduced (red)
  - 595 extirpated (gray)





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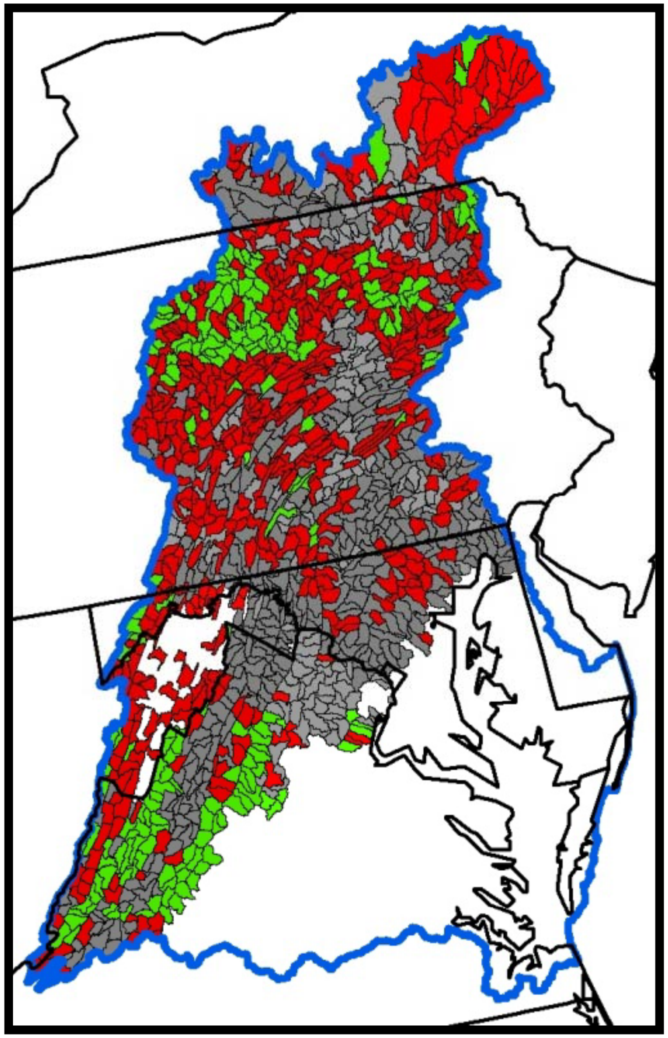
CART Model : Extirpated (76%); Reduced (64%); Intact (79%)

1. % Forest
2. Deposition kg/ha
3. % Agriculture
4. Road Density km/km^2
5. % Forest Riparian



While many extirpations and losses occurred at the turn of the century, many documented losses have occurred in the last ten years.

Threats:

- Dams
- Roads
- People
- Exotics
- Land use
- Genetic integrity
- Climate Change

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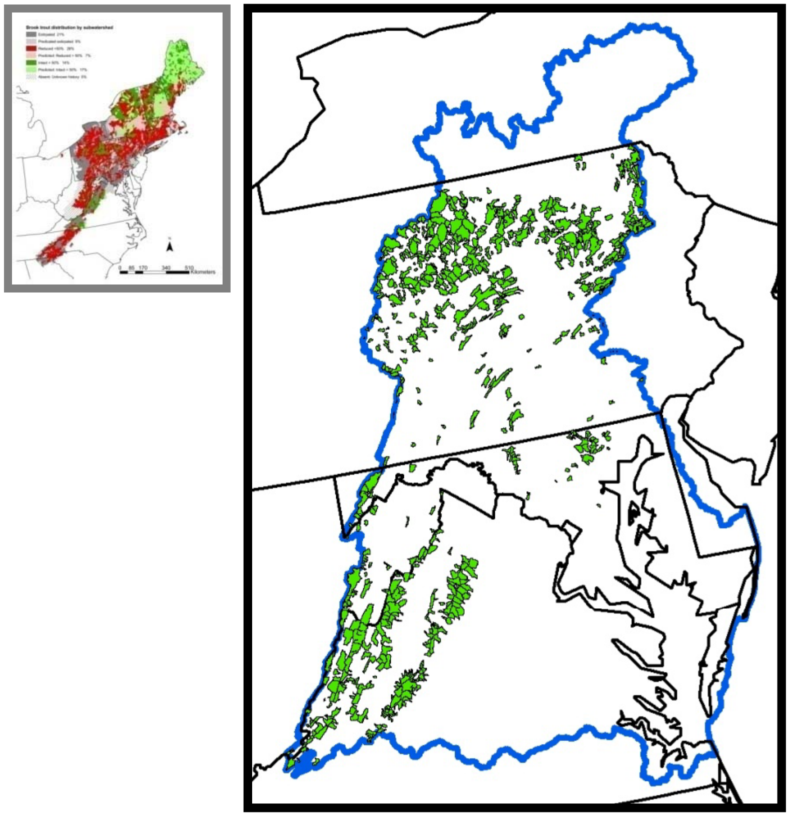
Objectives

Today's Objectives

1. Develop Metrics:
   - a) correct scale
   - b) cost effective
   - c) detect meaningful change
2. Develop monitoring protocol for brook trout populations in the Chesapeake Bay watershed.



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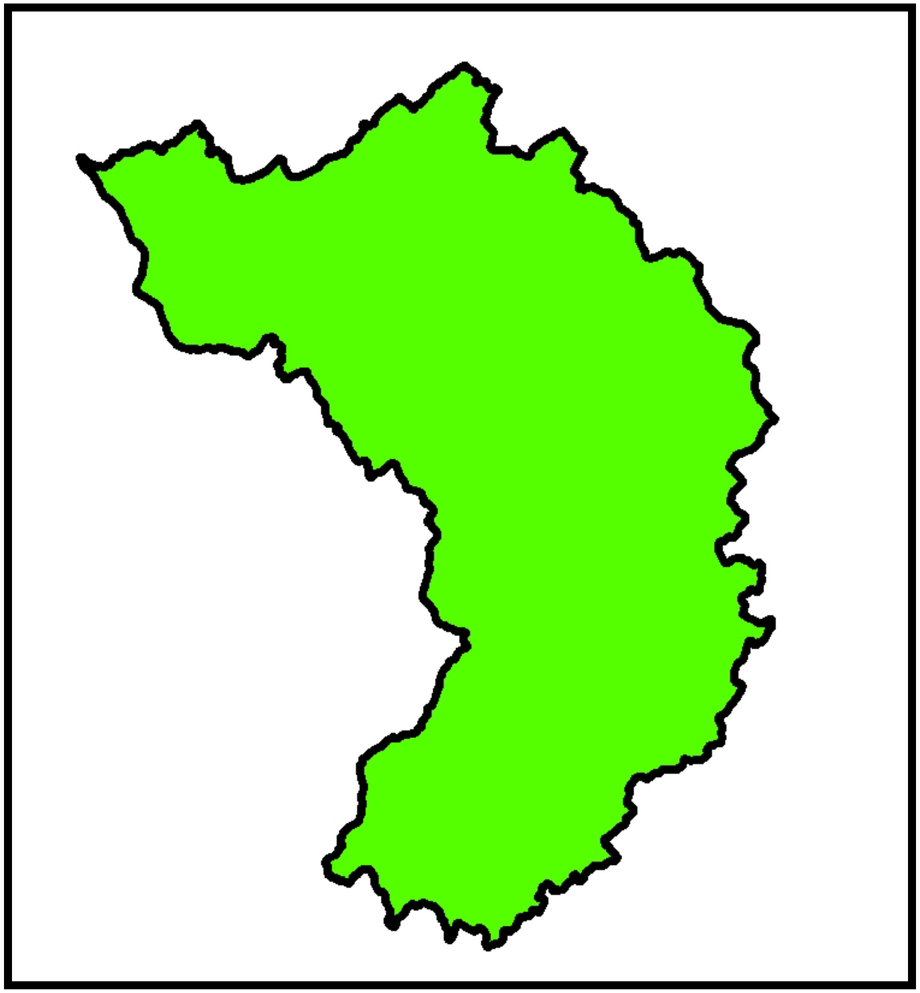
Scale

Sub-basins (4th HUC)
100%



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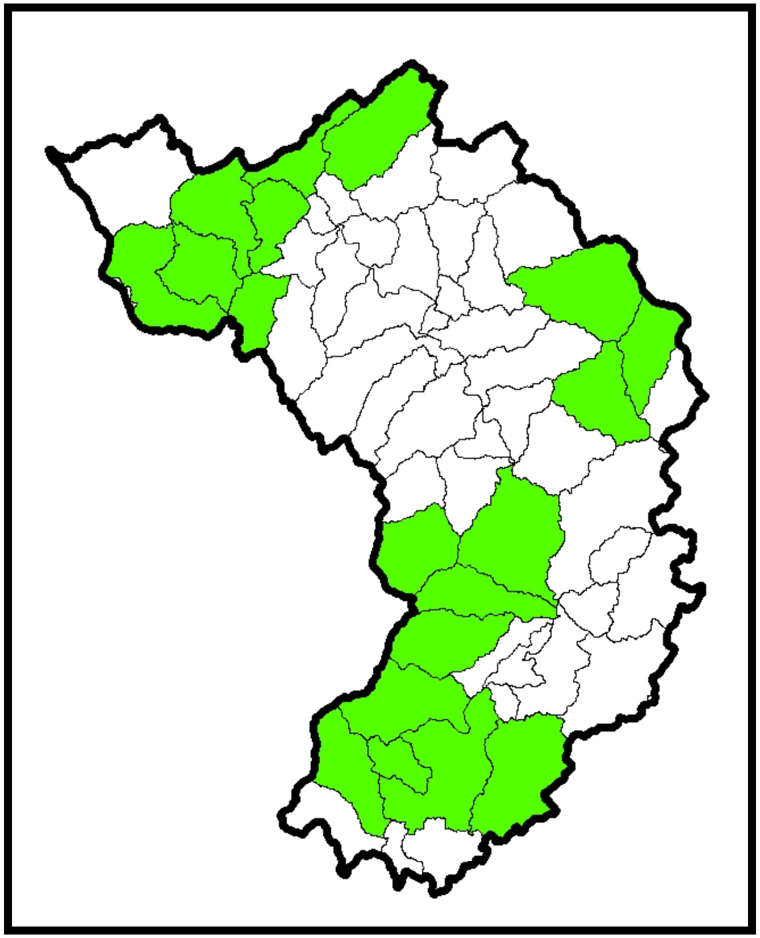
Subwatersheds (6th HUC) 33%



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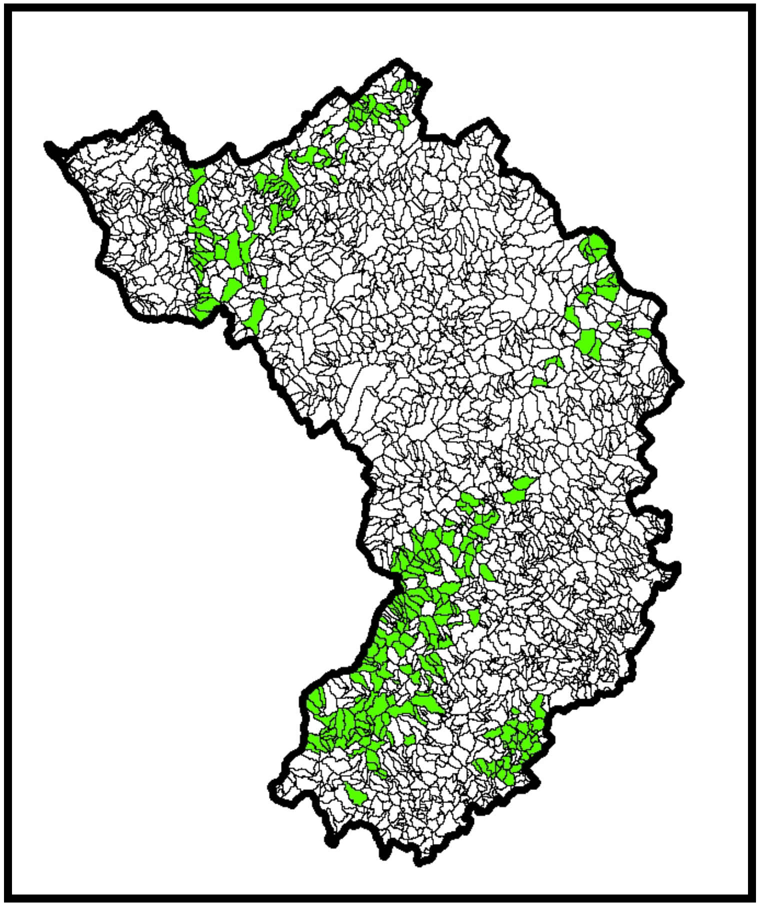
Catchments
11%



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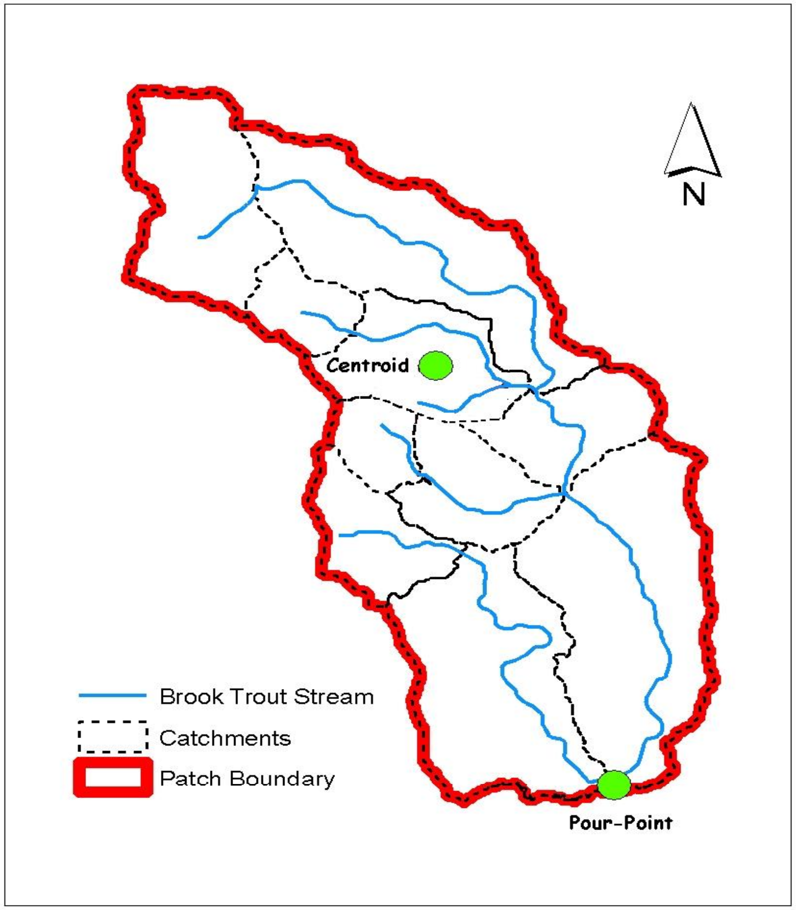
Fine Scale Occupancy Assessment

- In Chesapeake Bay Watershed*:
  - 3,003 catchments: Allopatric Brook Trout Populations
  - 1,716 catchments: Sympatric Populations (with Brown or Rainbow Trout)
  - 1,966 catchments: Only Exotic Trout Species

* excluding NY

Identification of Brook Trout “Patches”

- “Patch”= a group of contiguous catchments occupied by wild brook trout.
- Patches not connected physically
  - Dams, warm water habitat, downstream invasive species
- Assumed to be genetically isolated populations



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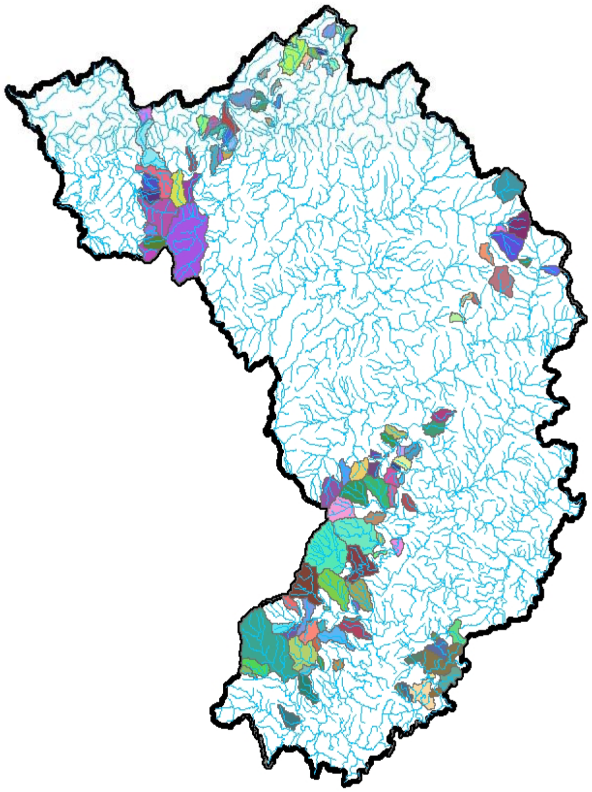
Patches



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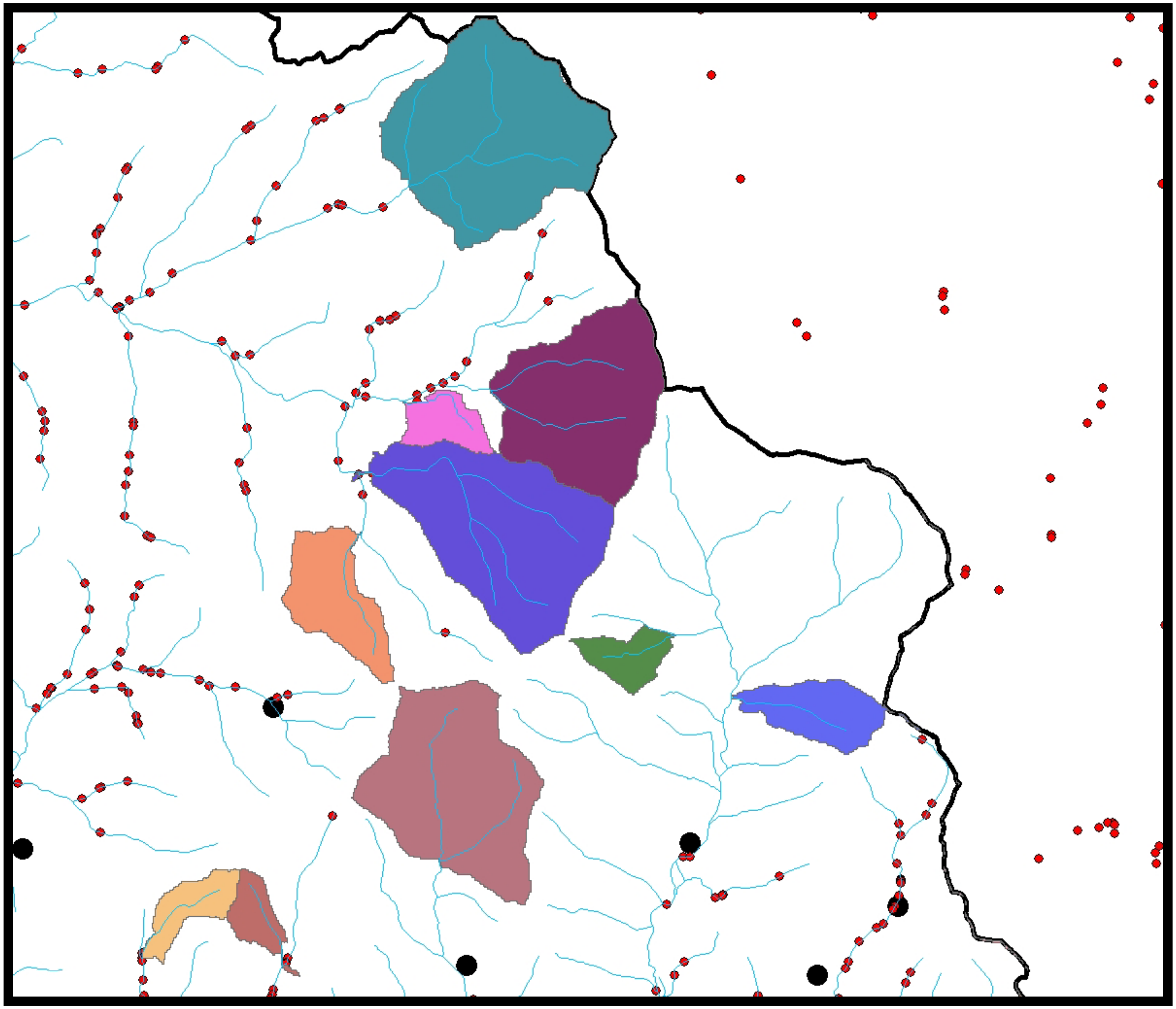

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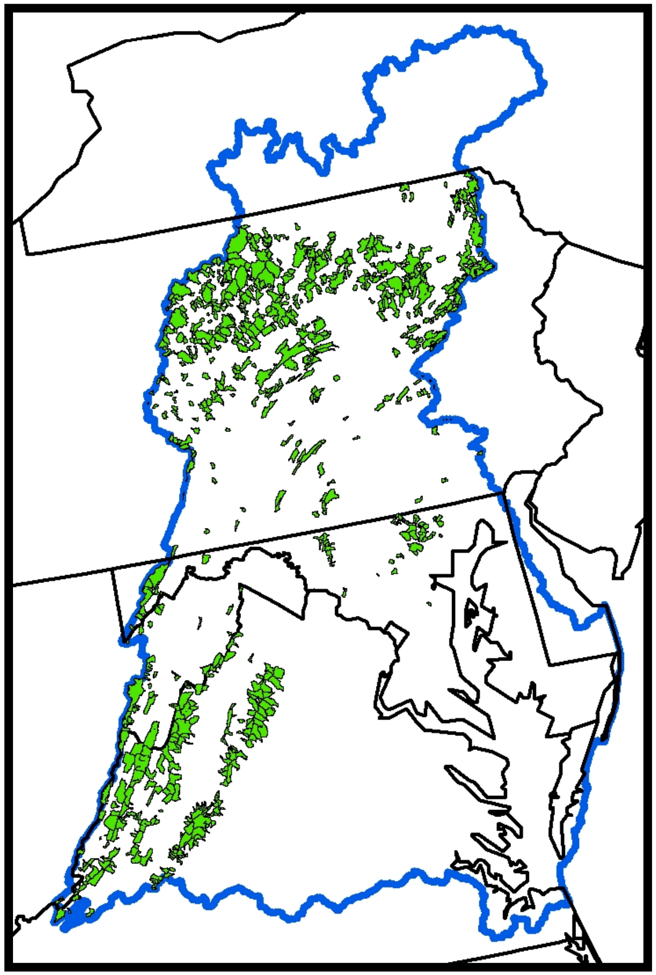
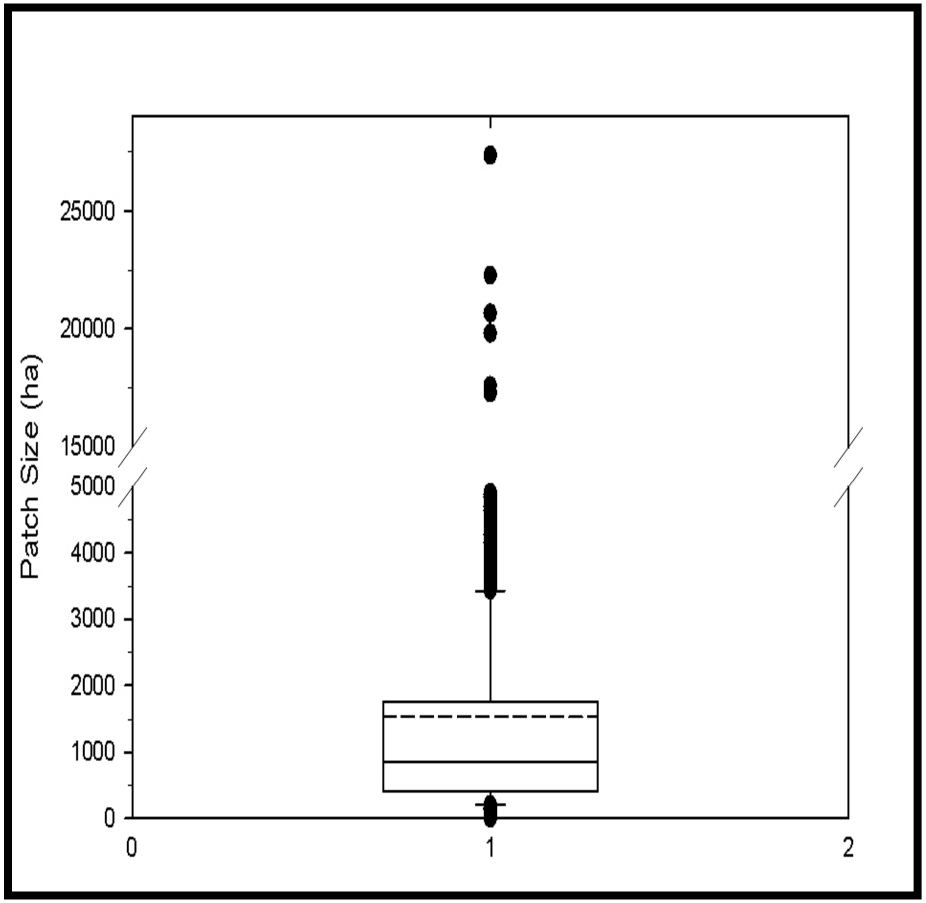
Chesapeake Bay Brook trout Patches
(n=868)



Patch - "Populations"

- Number of patches
  868
- Average size
  1,541 ha
- Median size
  855 ha



Lessons Learned

Current Population Estimates

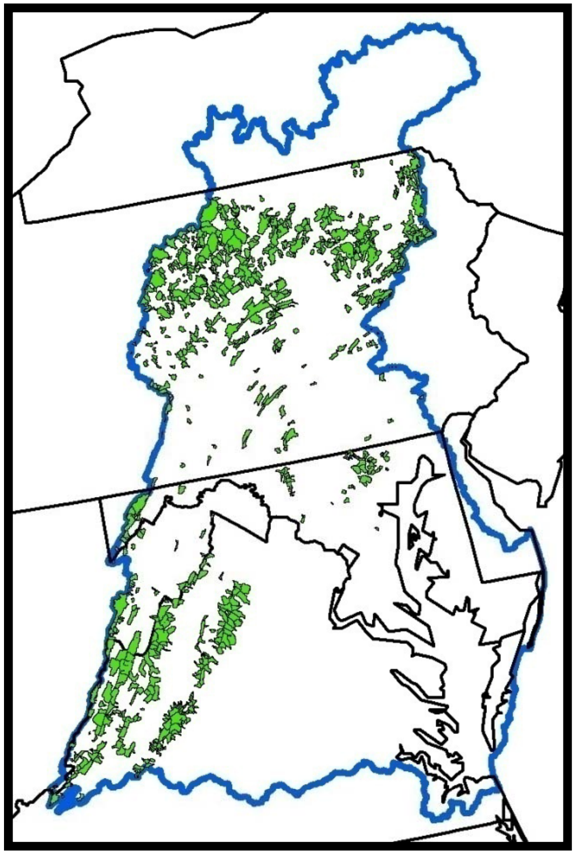
- Mark-Recapture
- Depletion Removal
- Problems:
  - Not viable for large scale monitoring
  - Expense
  - Inability to detect trend (i.e. large coefficient of variation % 50 adults; % 121 YOY)
  - Expansion to entire stream

Patch Metrics

Patch Metrics

Spatial Metrics

A. # of patches
B. # of patches with increasing size/connectivity(additional upstream and downstream catchments with brook trout)
C. # of patches decreasing in size/connectivity(loss of catchments)
D. Average patch size of the entire resource
E. # of patches with allopatric or sympatric(with brown or rainbow) populations



Genetic Patch Metrics

Two Genetic Monitoring Metrics

1. Estimates of the amount of genetic diversity within a patch can evaluate changes in relative abundance
2. Estimates of N_b (# of individual brook trout(regardless of age) contributing to year class; Whiteley et al. 2012)

Can serve as surrogate for estimates of census population size (N)

Can be used to directly test changes in population size (Tallmon et al. 2010)

Interpreting the N_b Metric

- Increasing N_b trends: positive response from improved habitat or increasing population.
- Decreasing N_b trends: suggest habitat loss and decreasing populations.

Benefits of N_b as a Sampling Protocol

- N_b directly relates to annual recruitment.
- Easy to obtain reliable estimates
- Cost-benefit suggests N_b alone can be a valuable surrogate for risk.
  - VA pilot study
    - Found number of breeders(N_b) often very low (<100 individuals)
- Monitoring patch metric changes(N, size, genetic diversity, and N_b) potentially a very cost-effective tool for monitoring wild populations of brook trout.

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Genetic Sampling vs. Genetic Monitoring

Sampling:

- Cost effective surrogate for population estimates (Tallmon et al. 2010).
- Taken at single point in time.
- Provides information on past population size (large populations retain more genetic diversity).
- Also provides insight into future resiliency to environmental changes.

Monitoring:

- Sampling the same population at multiple points in time.
- Genetic monitoring can quantify temporal changes in population genetic metrics, as opposed to a snapshot population genetics assessment taken at a single point in time (Schwartz et al. 2007).

Results

Virginia Pilot Study

Stream Name	Patch Size (Ha)	Adult N (95% CL)	YOY N (95% CL)	N_b (95%CL)	N_b/N
Fridley's Gap* (above Karl's dam)	590	822(740-915)	460(358-587)	131 (95-192)	0.16
Skidmore Fork (above Todd Lake)	993	90(73-130)	70(50-117)	28 (14-93)	0.31
Dry Run (above Dry Run Dam)	1217	46(42-44)	23(22-24)	5 (3-9)	0.10
Briery Branch (above Briery Branch Lake)	2438	129(104-175)	139(91-215)	26 (21-33)	0.20
Dry River (above Switzer lake)	3807	616(529-719)	1009(795-1275)	67 (58-77)	0.10
Little River (above Hearthstone Lake)	4121	323(236-438)	677(519-882)	46 (40-53)	0.14

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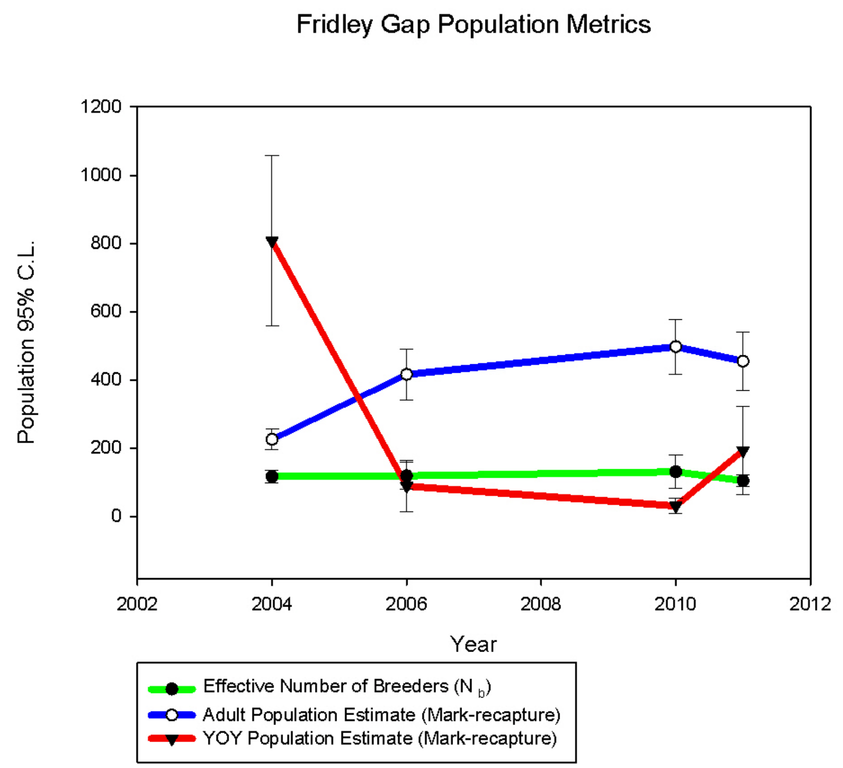
Virginia Pilot Study



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Monitoring Design

Proposed Monitoring Design and Methods

Cluster analysis to subsample existing 886 patches:

- Sentinel samples- (yearly trends)
- Panel samples every 5 years (long-term trends)

Example:

- 250 sites from cluster analysis-
  - 25 are designated "sentinel" to be sampled yearly.
  - Additional 45 sites sampled yearly on a rotating panel (each site visited every 5 years)
  - Equals 75 sites monitored per year.

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Advantages of N_b for Large Scale Monitoring

1. Estimate represents entire “patch” or population, not just the representative reach.

2. N_b values are less than N(10-50%), and require fewer samples for accurate estimation making them better suited for determining trends at numerous sites.

3. N_b provides reliable “at risk” evaluation that integrates yearly variation of N.

4. Bonus information: genetic diversity within a patch indicates past population size and resilience for future.

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Thanks to the Partners!

Virginia Tech

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