Patch-Scale Brook Trout Monitoring in Chesapeake Bay Headwaters

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Goals of project

Our Contribution:

Robust monitoring platform across a large basin that tracks occupancy and status at appropriate scale to document management **success** and prioritize **action**

Near term:

1. Update patch layer and occupancy as new data arrive
2. Use genetic metrics that will assess resilience and habitat quality

    - » Help prioritize management dollars
    - » Keep what we have by identifying vulnerability

Ultimate goal: Document an 8 % increase in occupied brook trout habitat

Brook trout (*Salvelinus fontinalis*)

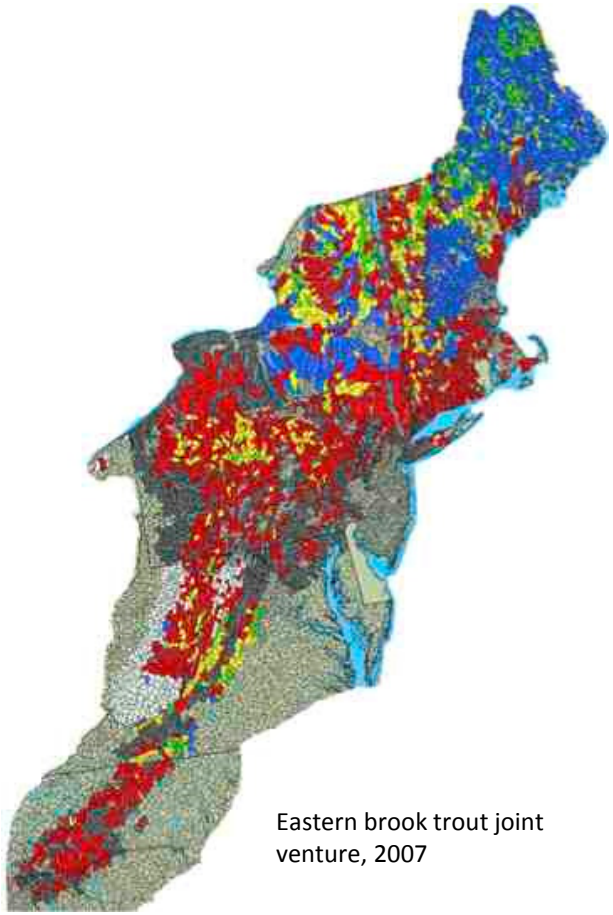
- U.S. native range Maine – Georgia
- Strong invader outside of native range
- Primarily occupy low-order streams in Cheasapeake headwaters

Brook trout life history

- Spawn in fall
- Embryos overwinter in stream gravel
- Fry emerge in spring

Brook trout ecology

- Require clean cold water
- Sentinal species for headwater habitat

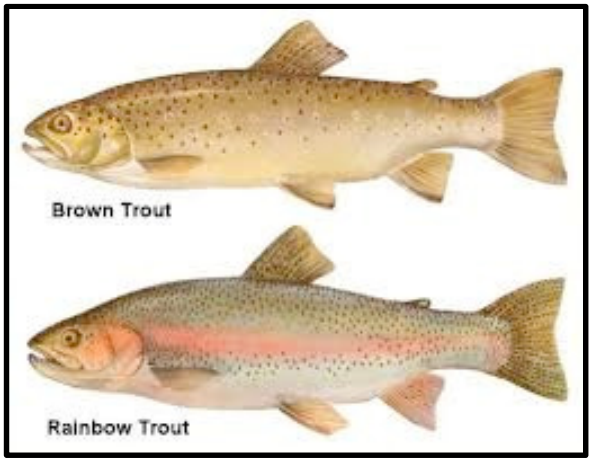


Eastern brook trout joint venture, 2007

Threats to brook trout and the bay

Threats to Population Persistence

- Barriers (dams, culverts, etc.)
- Exotic species
- Anthropogenic land use
- Climate change



Project History – Appropriate Landscape Scale

- Mark Hudy began a range-wide subwatershed assessment in mid-2000's. (Hudy *et al.* 2008)
  - This clarified the need for a better management scale
- Jason Coombs began working with EBTJV to delineate habitat "patches"
- Ben Letcher (USGS) and Jason Coombs (USFS) implemented rapidly updated web-based tool for EBTJV patches, occupancy, and stream temperature modeling.

http://www.ecosheds.org

Project History – Genetic Monitoring

- The sampling difficulty and limited power for trend detection of population estimates
- Patch-level genetic metrics a better solution for status and vulnerability?
- Andrew Whiteley and Jason Coombs developed a sampling protocol for N_b. (Whiteley *et al.* 2012)
- Recent work substantiates link between N_b, habitat quality, and cohort-specific reproductive success *(*Whiteley *et al. 2016)*.

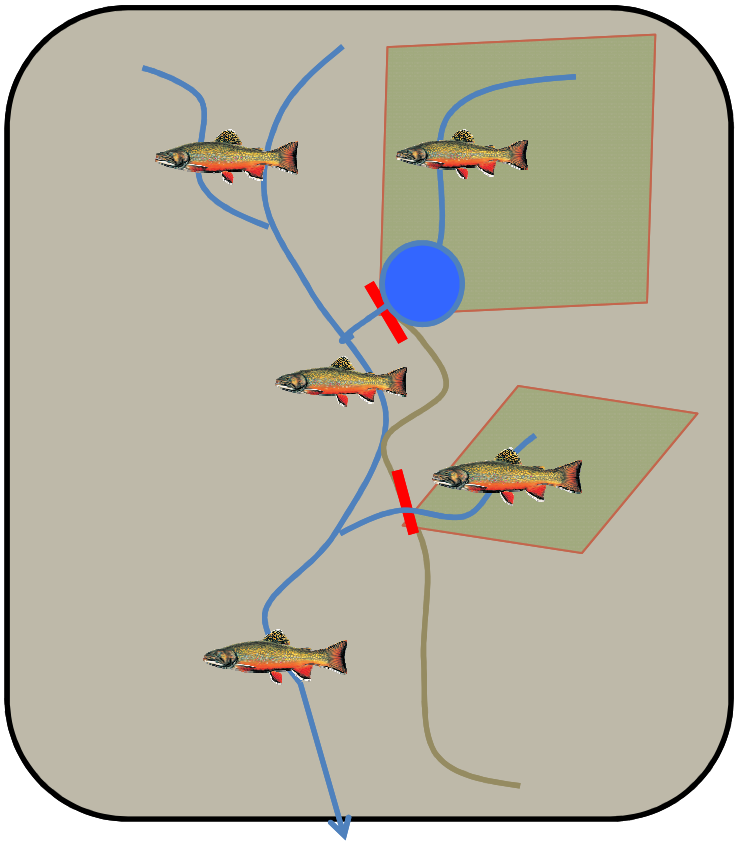
Project History – Collaboration

- States throughout the native range engaged in patch layer development
- Began genetic monitoring with VDGIF support in Virginia, 2013
- Engaged VA, PA, NY, MD, and WV state agencies for patch sampling in 2015
- Currently have 2 year state commitments to continue sampling in Chesapeake states
- Leveraged additional dollars (NFWF) ($130k)

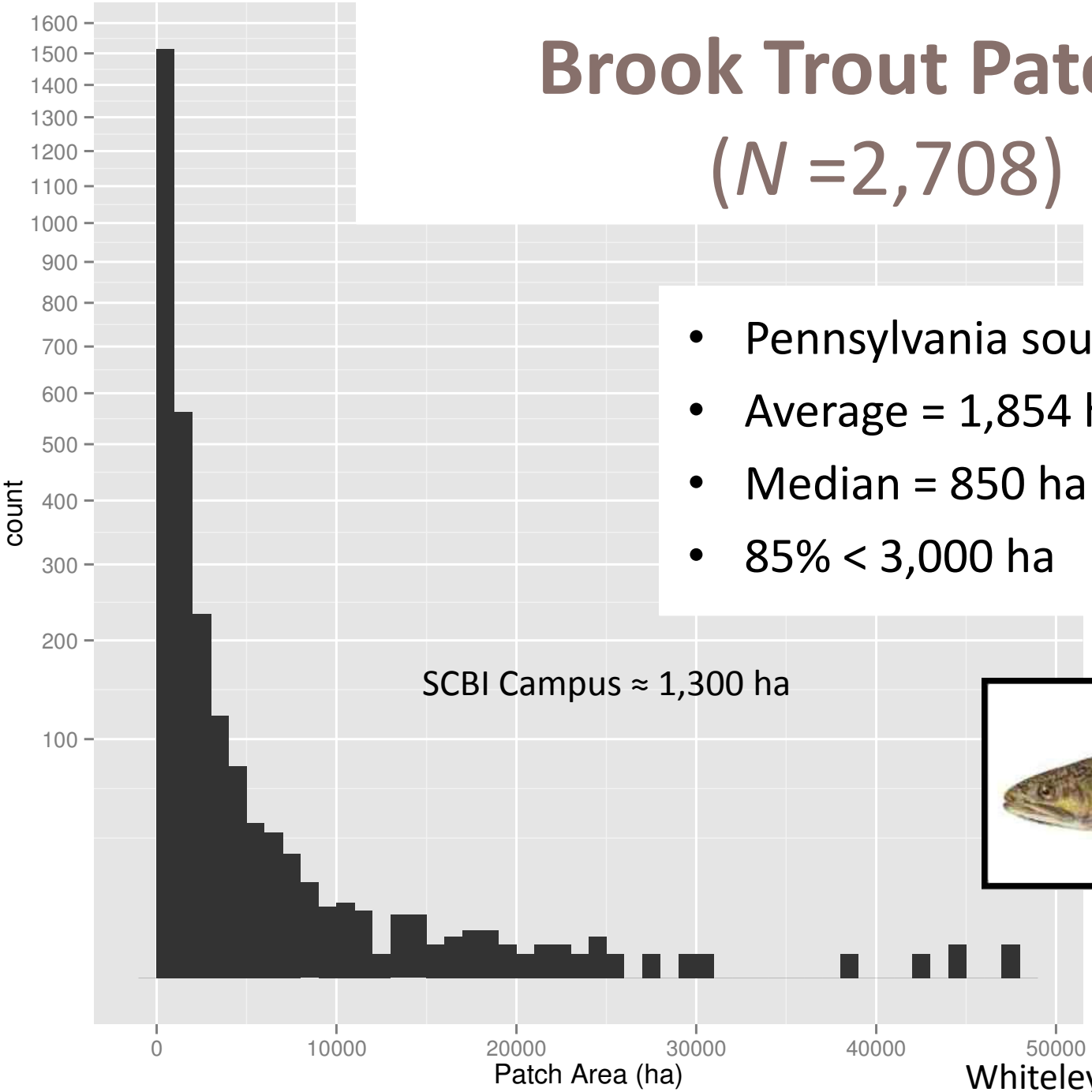
Patch layer construction

- We defined a patch for brook trout as a group of occupied contiguous hydrologic catchments

Three patches are not necessarily better than one

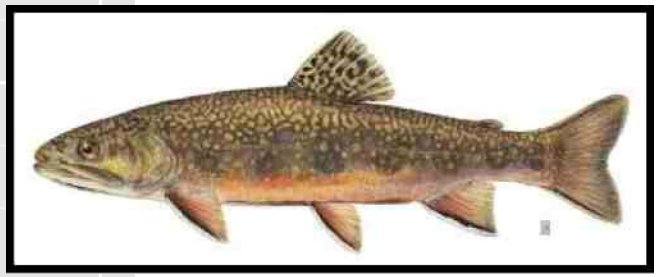


Brook Trout Patches
(*N* =2,708)



- Pennsylvania south
- Average = 1,854 ha
- Median = 850 ha
- 85% < 3,000 ha

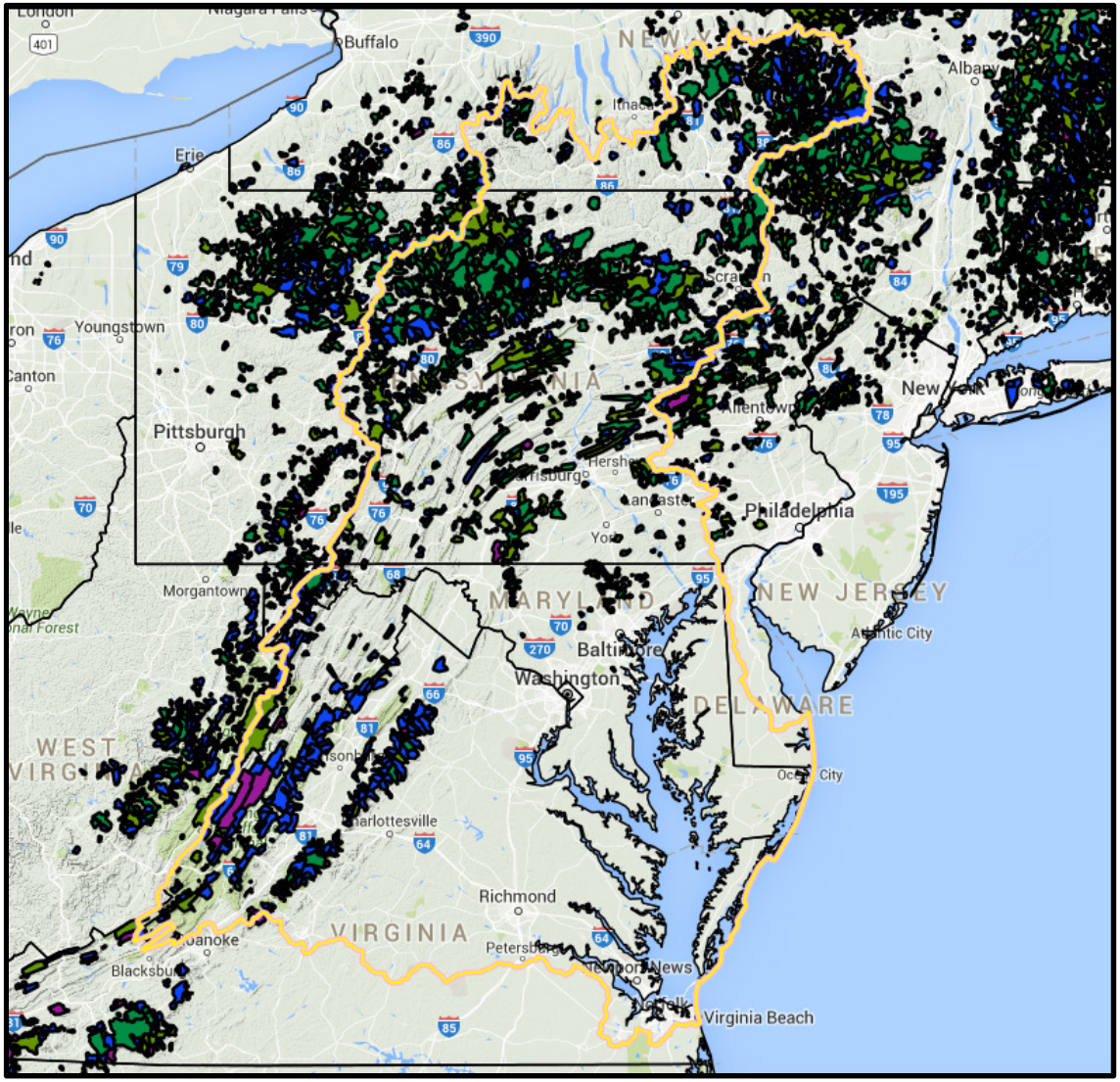
SCBI Campus ≈ 1,300 ha



Whiteley et al. 2014, *Wild Trout XI*

Brook Trout Patches in the Chesapeake Watershed

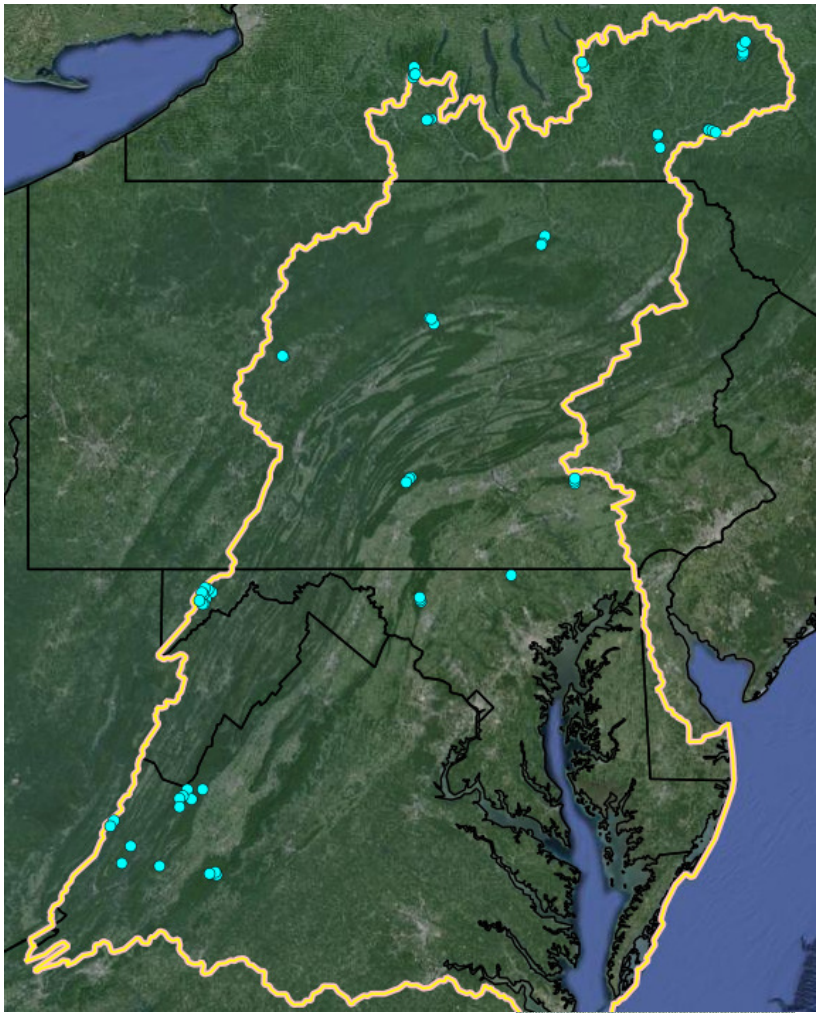
- 4,719 occupied catchments
- 868 occupied patches
- 2.69 million acres



Brook Trout Patches in the Chesapeake Watershed

- Sampling with strategy from Whiteley *et al*. 2012
- Working with states to collect two more years
- Will add WV for the next two years

State	Patches sampled 2015
MD	5
NY	6
PA	5
VA	8



8 % increase in occupied area

- Baseline established with our patch layer
- 2.9 million acres of Brook trout habitat
- 215,200 acres of habitat to be occupied by brook trout by 2025
- Strategies to meet this goal
  - Must monitor occupancy
  - Balance gains and losses
    - Resilience/Vulnerability
  - Add to size of existing patches or add new patches?
  - Patch quality and prioritization

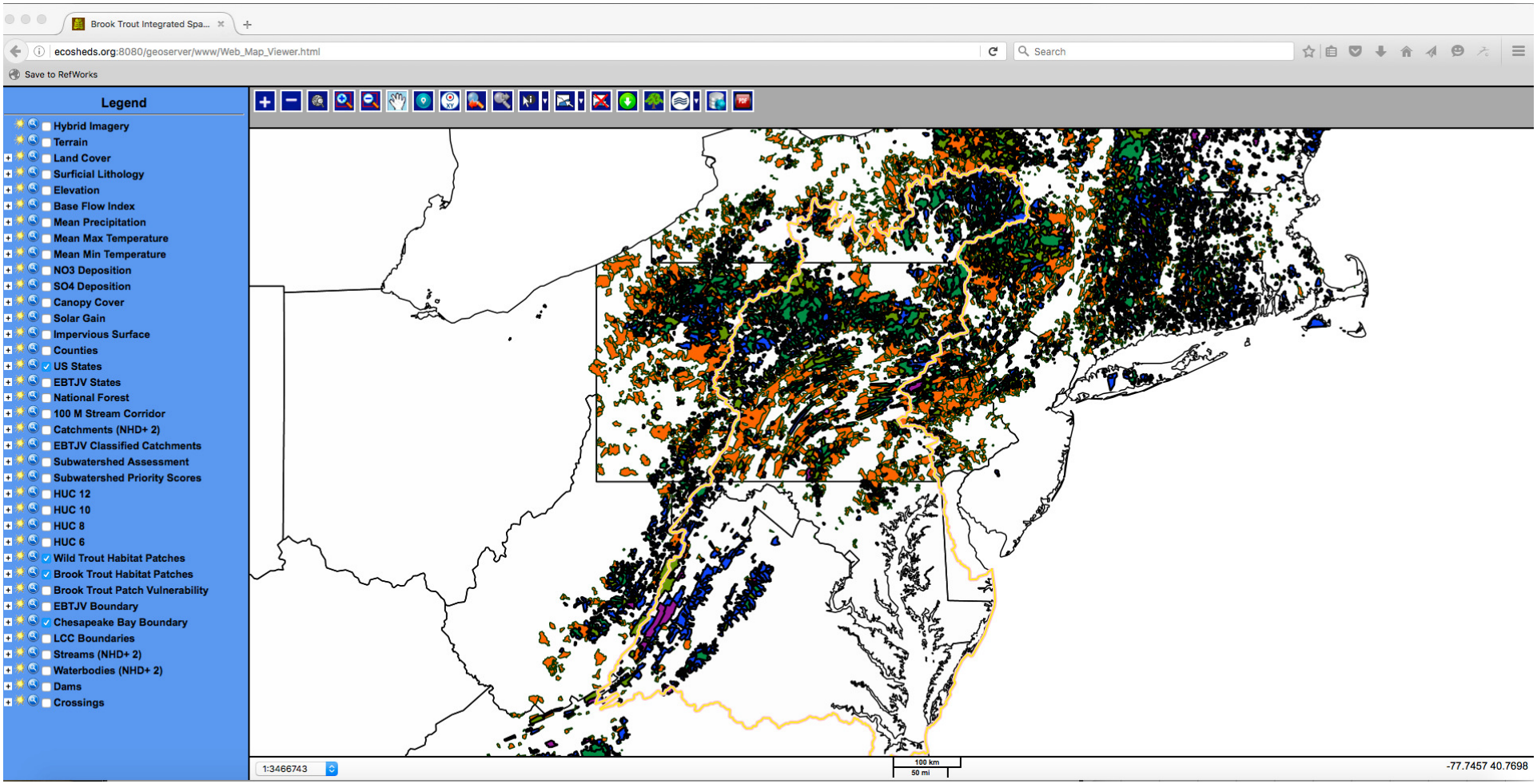
8 % increase in occupied area

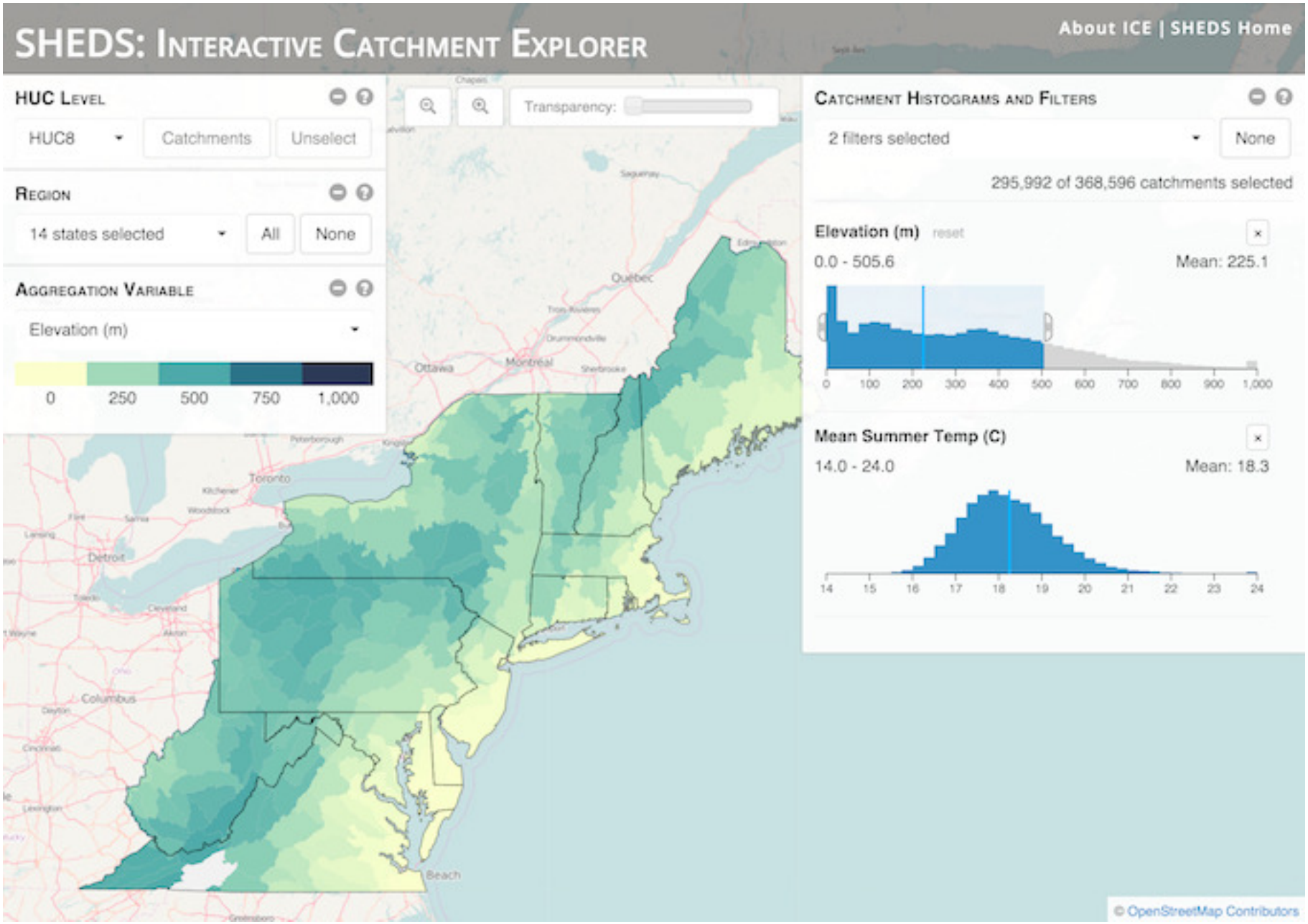
- Increased monitoring may reveal losses from baseline
  - Must balance gains and losses
- Our genetic monitoring will flag populations at risk and help prioritize resources

8 % increase in occupied area

- Existing patches may be expanded by habitat improvement and barrier removal
  - Our genetic monitoring can document success
- Adding new patches
  - Locate areas likely to be successful
  - Locate appropriate source population
  - Replace invasive trout with brook trout
  - ≈ 47 average patches meets 8% goal
- Prioritize expanding largest patches ?
  - Large metapopulations are resilent to extripation
- Our patch layer can be readily updated and is publically viewable through user-friendly web-based platform

Ecosheds.org




SHEDS: Interactive Catchment Explorer
About ICE | SHEDS Home
HUC Level
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Catchments
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Aggregation Variable
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Genetic tools

Can establish:

- Which patches are most vulnerable
- What are the effects of habitat improvement, and what strategies are most effective
- Is it better to add to existing vs. add new patches?

Current metrics of interest

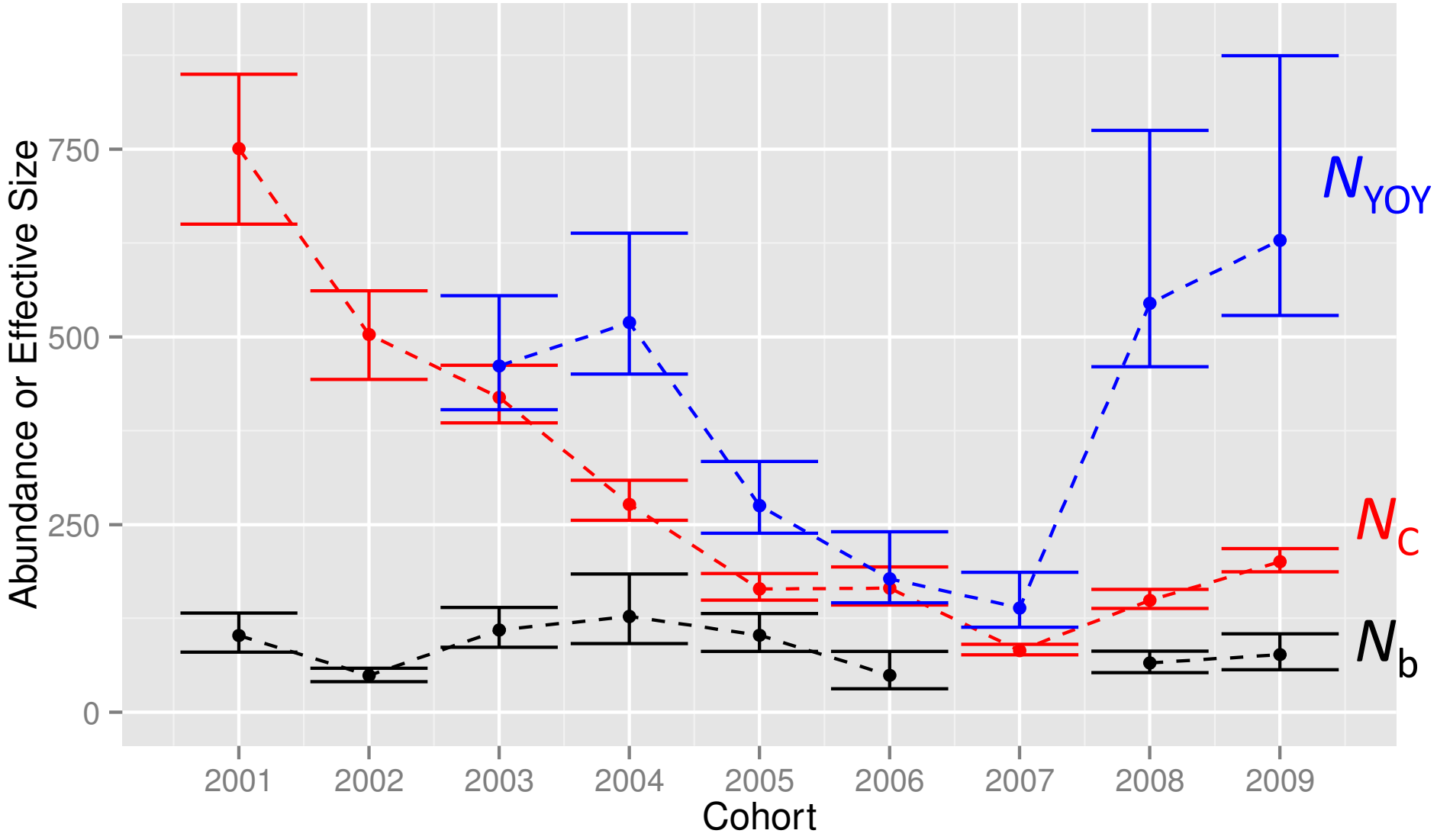
- Genetic diversity
  - Heterozygosity and allelic richness
- Effective number of breeders

Effective number of breeders N_b

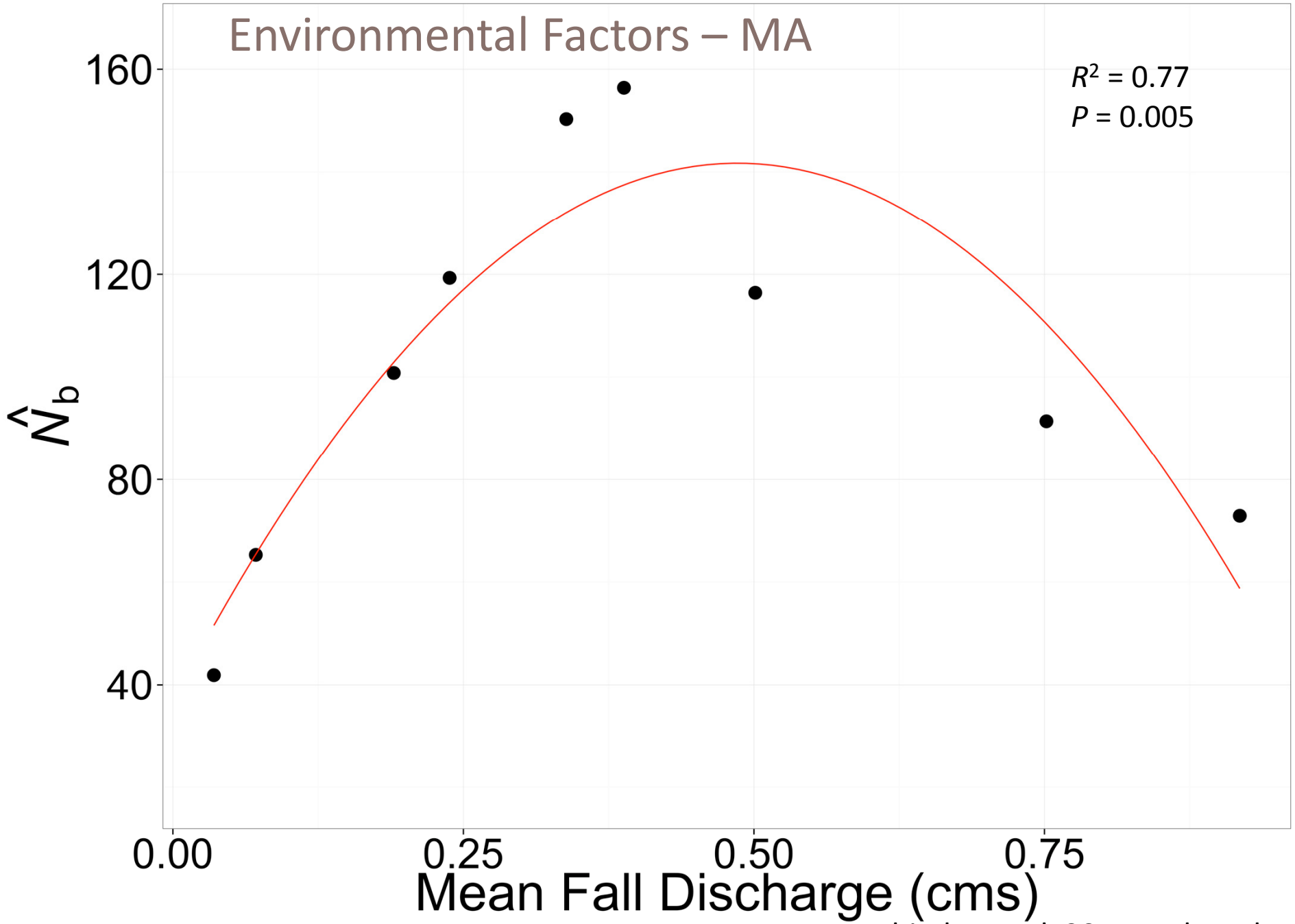
Genetic estimate of habitat patch quality

- Cohort-specific reproductive success
- Number of families
- Variance in family size
- Brook trout N_b appears to be limited by reproductive habitat
- More reproductive habitat coincides with higher N_b
- Linked to potential for population growth and thus resilience

Massachusetts – Value of N_b

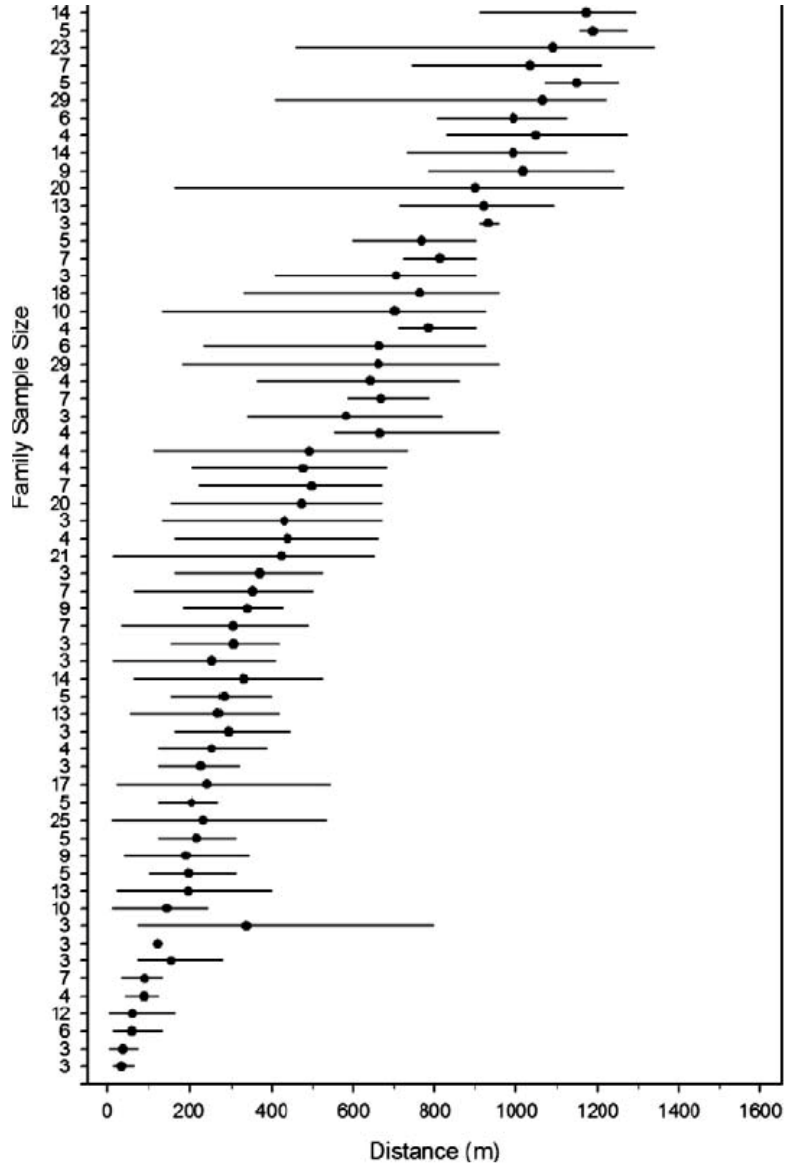


Environmental Factors – MA



Whiteley et al. 2015 Mol. Ecol.

Sampling for N_b?



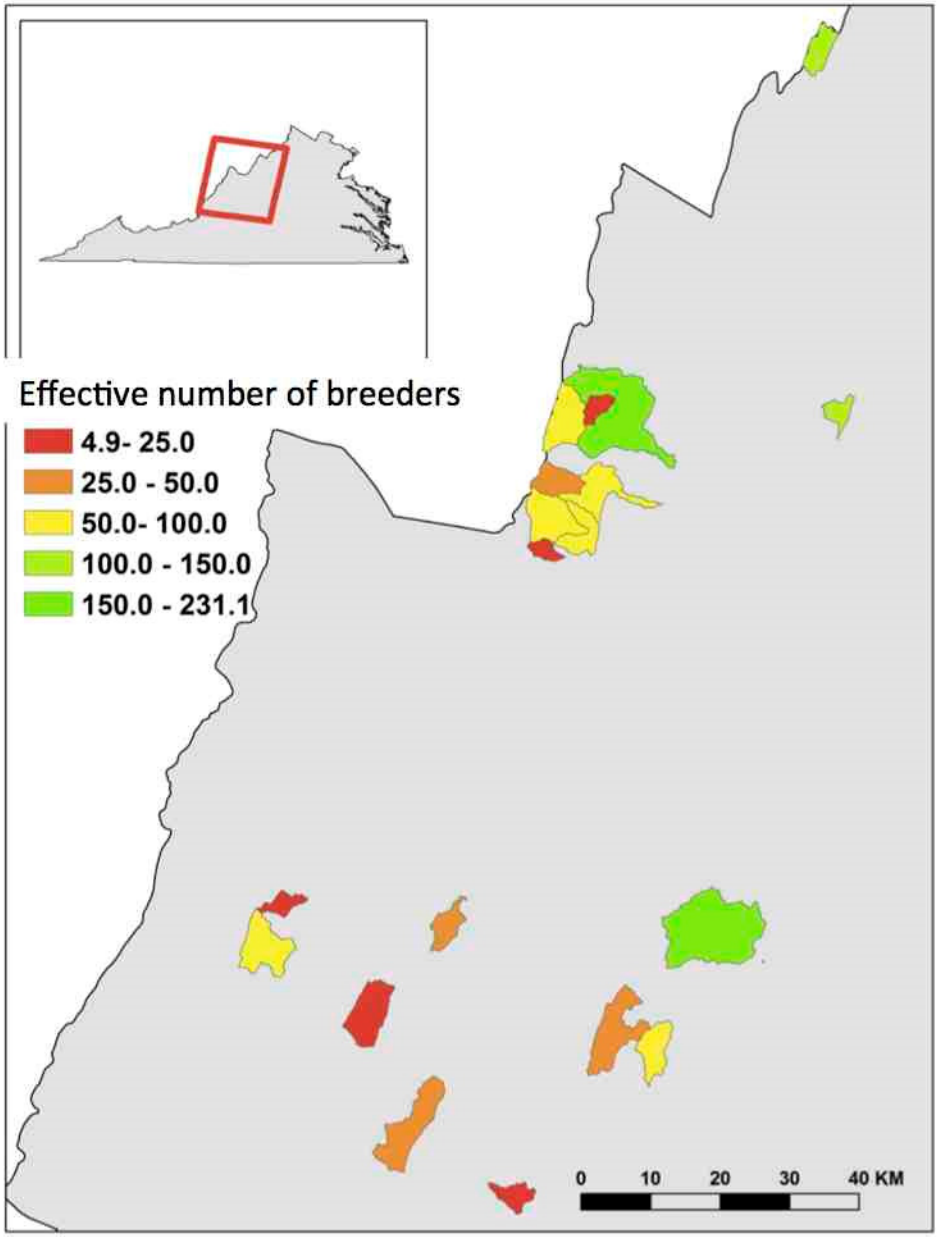
- Brook trout: target age 0 (YOY)
  - Field identifiable
  - Single cohort aids interpretation of N_b

Hudy et al. 2010, Transactions AFS
Whiteley et al. 2012 Cons. Genetics

N_b variation across populations

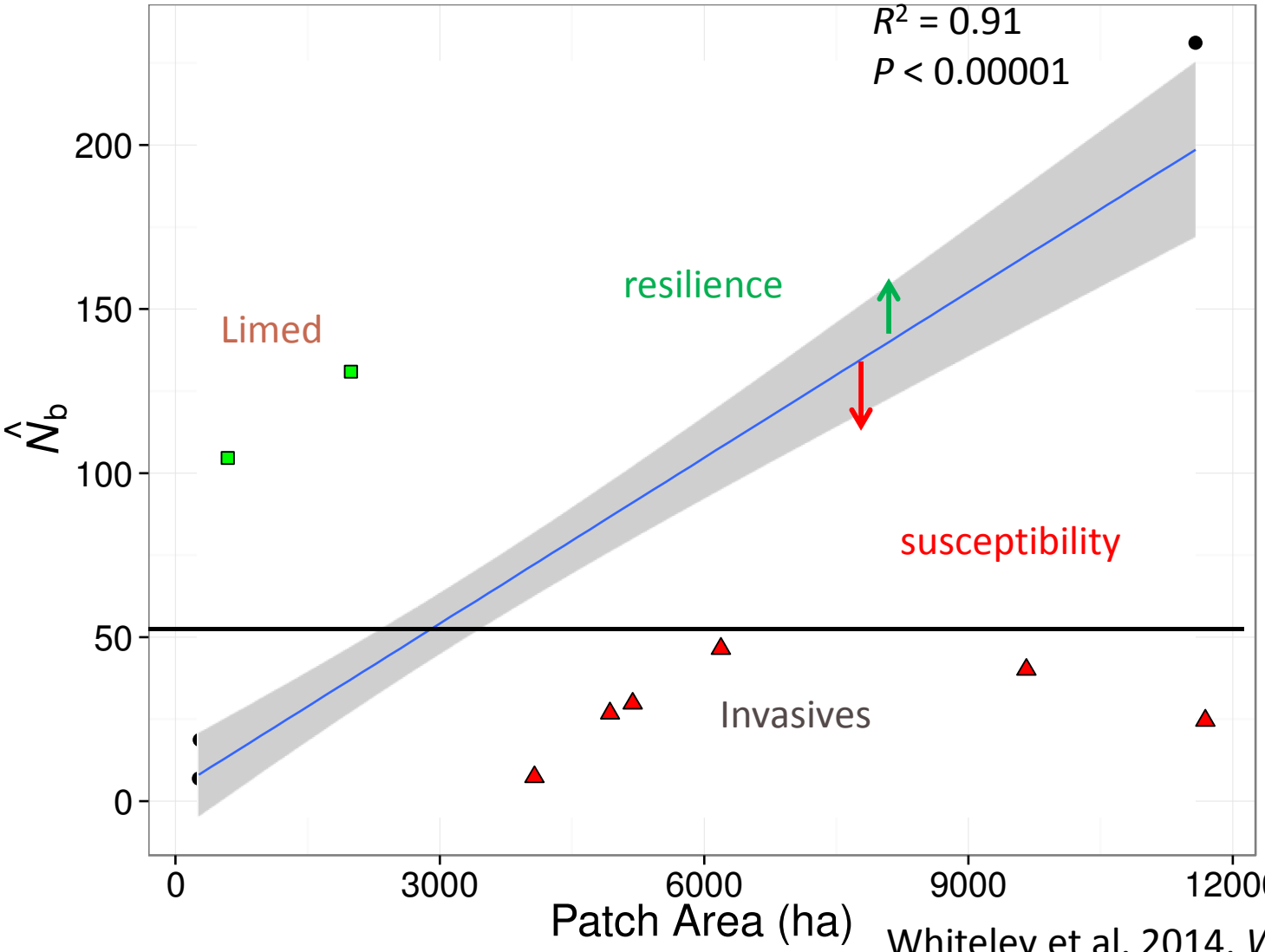
Genetic analysis of Virginia patches

Many patches
$N_b < 50$



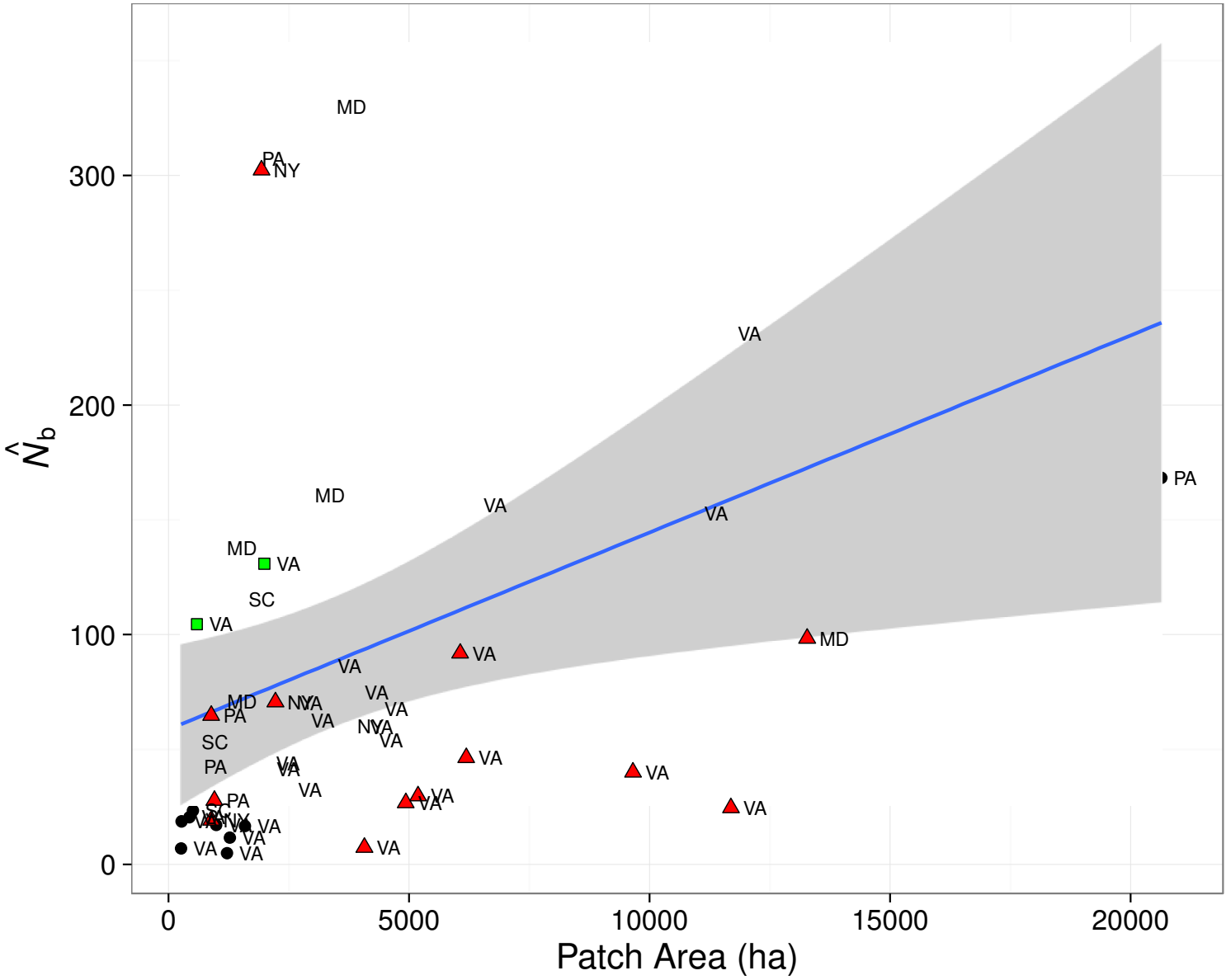
Whiteley et al. 2014, *Wild Trout XI*

N_b and Patch Size



Whiteley et al. 2014, *Wild Trout XI*

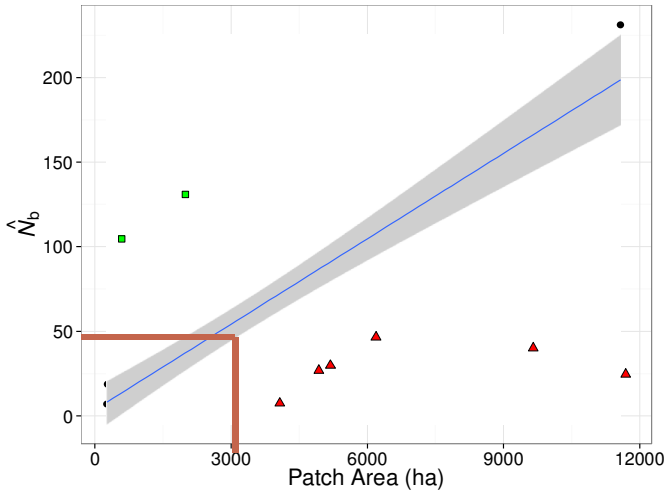
Chesapeake Sites

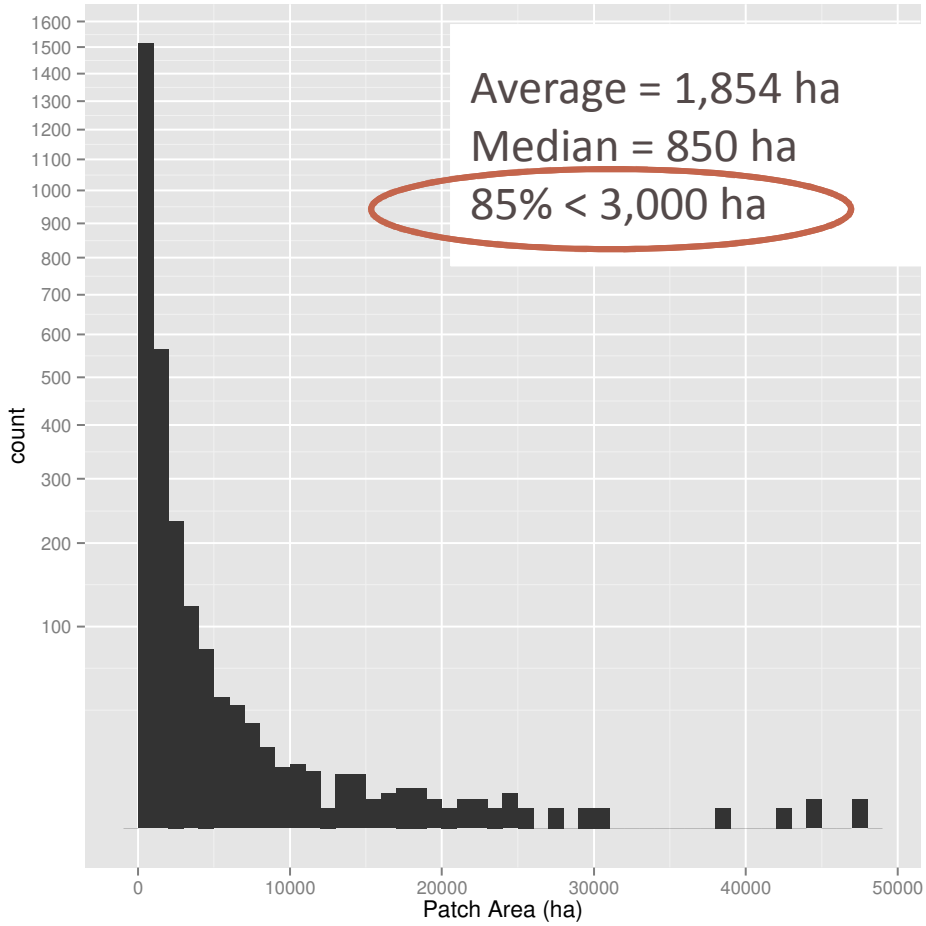


Vulnerable populations

Brook Trout Patches (*N* =2,708)

Many small patches on the landscape





Whiteley et al. 2014, *Wild Trout XI*

Predicting N_b at patch scale

Habitat quality

- Forest
- Solar gain/aspect
- Invasives
- Slope
- Catchment morphology
- Acid rain
- Road density

Use in conjunction with occupancy model

Prioritize currently unoccupied but potentially suitable habitats

Success of management measures

- We would like to team up with partners engaged in restoration.
- Increasing reproductive habitat quantity or quality increases N_b
- Single sample estimates of passage

Implementation and reaching goals

- Rotating panel design
  - Identify target patches return on five year cycle
  - Opportunistically sample other patches
- Include genetic metrics as habitat/status proxy
  - Allelic richness , heterozygosity, N_b
- Add genetic layer to web-based tool
- Future directions
  - eDNA can quickly and efficiently establish occupancy allowing better allocation of state and federal efforts
  - Link N_b to climate stress

Summary – Reaching the goal

- Habitat improvements
  - Increase habitat through patch expansion
    - Barrier removal
    - Reforestation/Riparian buffer
  - Genetic metrics can efficiently document success
- New Habitats
  - Using genetic metrics and occupancy predict suitable, but currently unoccupied habitat
  - Replace allopatric invasive populations populations
- Web-based tools makes successes readily available to public and managers

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