

A Mesoscale Landscape Model to Predict Biological Hotspots in the US Caribbean: Towards Identifying Marine Protected Areas

Presented By:

John D. Christensen

Chris Caldow

Wendy Morrison

Chris Jeffrey

Matt Kendall

Mark Monaco

Michael Coyne

Jenny Waddell

Steve Plater

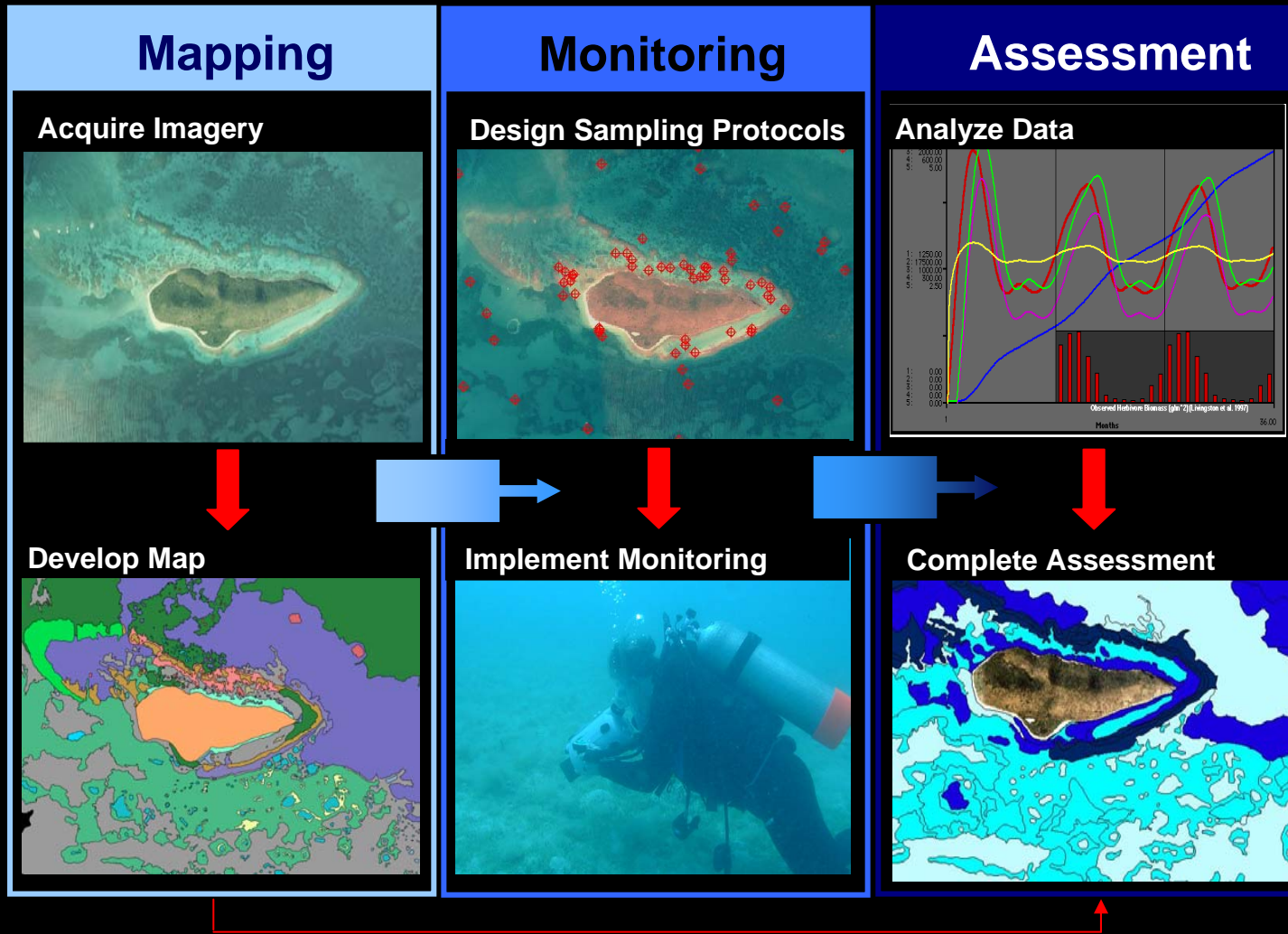


**NOAA National Ocean Service
Biogeography Program**



INTRODUCTION

Biogeography Program Reef Fish Monitoring & Assessment





INTRODUCTION

Biogeography Program Reef Fish Monitoring & Assessment

• 170 Dives

Objective - Quantify Effects of
MPA Boundary Closure

St. John



SW Puerto Rico

Objective - Ecologically-relevant
Marine Protected Areas

• 250 Dives



Buck Island, St. Croix

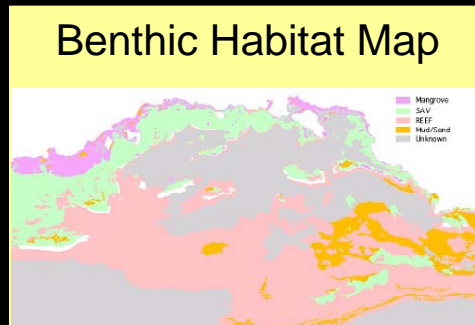
Objective - Monitor Fish
Abundance & Distribution in Monument

• 270 Dives



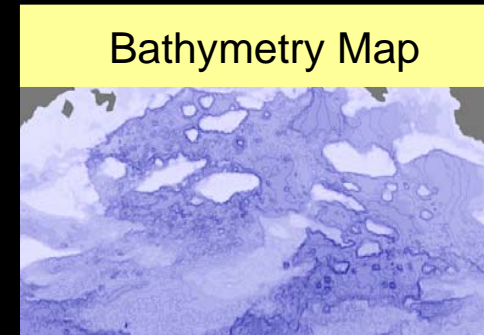
OBJECTIVES

ANALYTICAL APPROACH



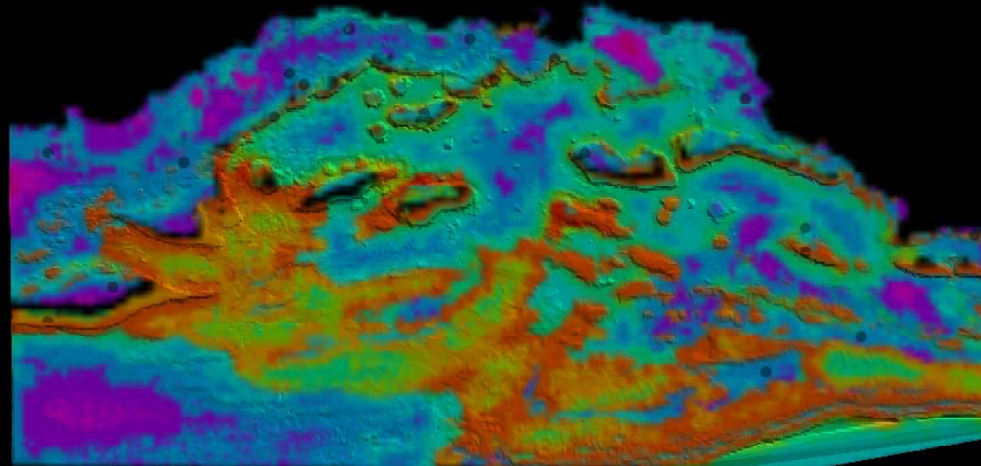
And Derivatives

**Canonical
Correlation**



And Derivatives

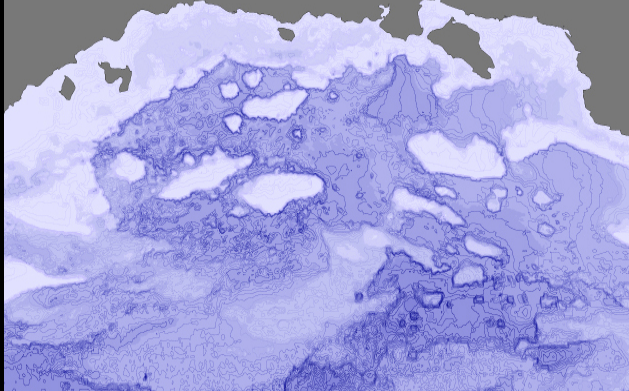
Biological Relevant Boundaries of MPA's and EFH





METHODS: Spatial Data Development

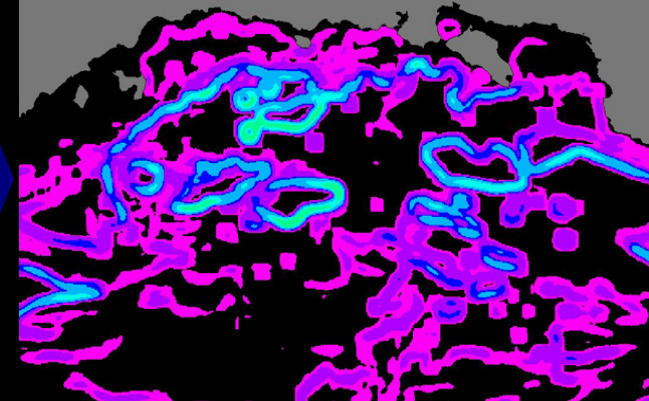
Raster Bathymetric Surface



Interpolate Bathymetric Surface
IDW, Kriging, Spline, etc.

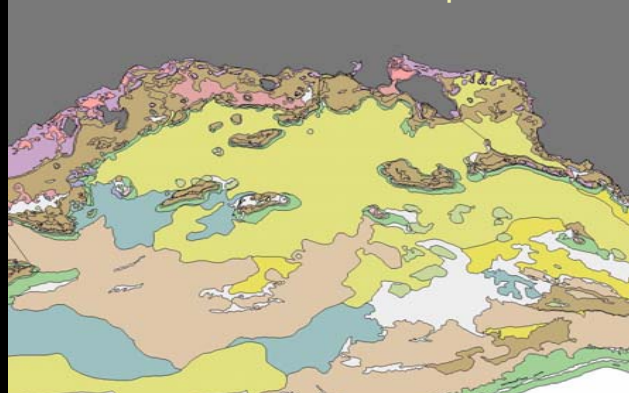
Arc View
Neighborhood Statistics

Raster Variance Map



Calculate Spatial Variance
60, 100, 200, 300, 500, 1000 m

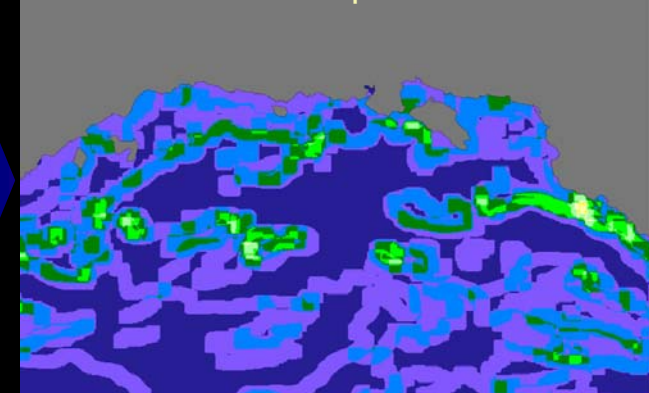
Raster Benthic Habitat Map



Develop Benthic Habitat Maps
Photo-interpretation, Auto recognition, etc.

Arc View
Neighborhood Statistics

Raster Variance Map

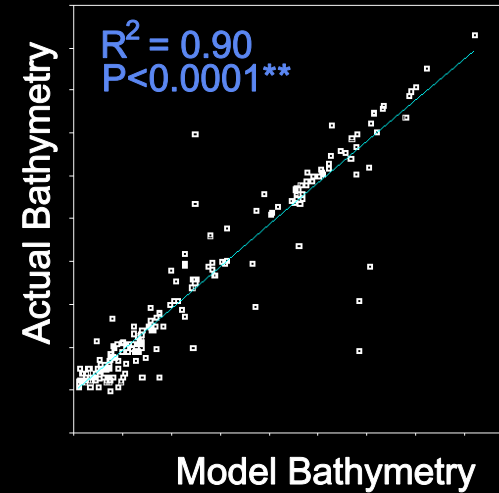
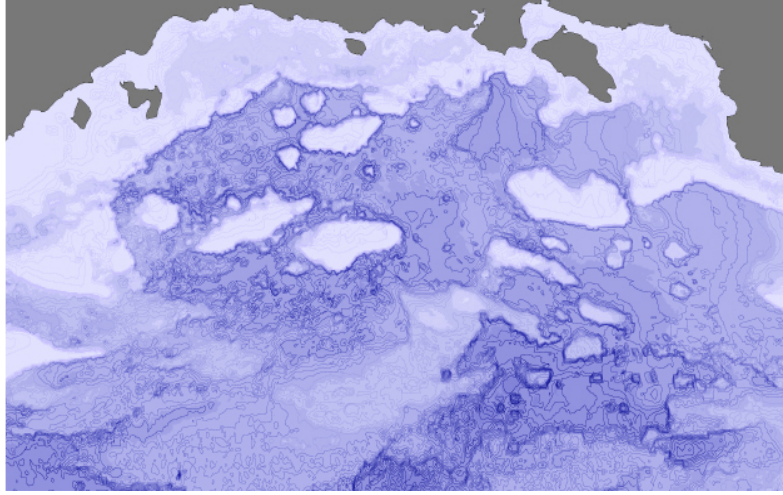


Calculate Spatial Variance
60, 100, 200, 300, 500, 1000 m

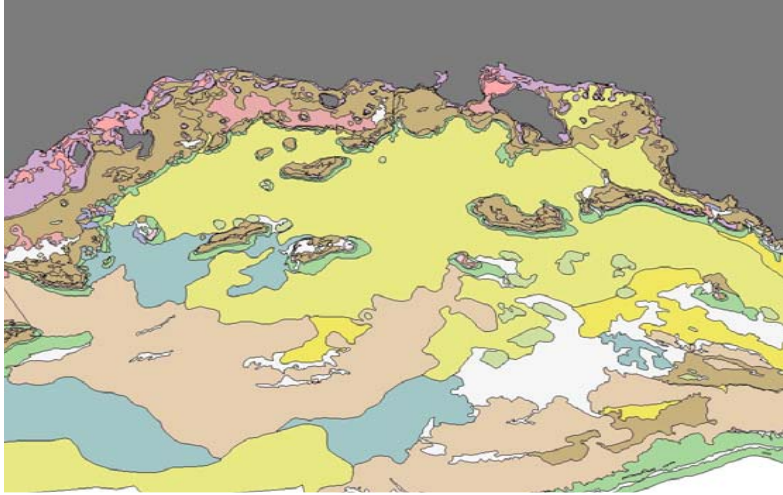


METHODS: Spatial Data Validation

Bathymetry



Benthic Habitat

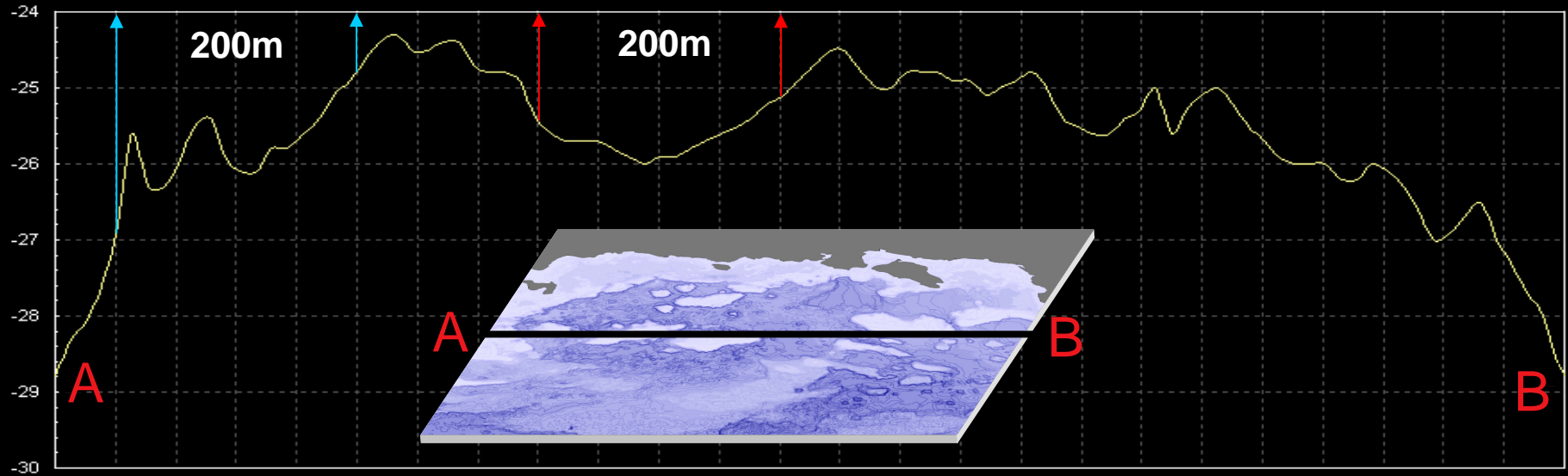


OVERALL MAP ACURACY = 94%

Reef	Seagrass	Sand/Mud
92%	99%	100%



METHODS: Calculating Spatial Variance



m1n1	m1n2	m1n3
m2n1	s^2	m2n3
m3n1	m3n2	m3n3

2	3	4
2	2	3
2	3	3

Example: BATHYMETRIC VARIANCE

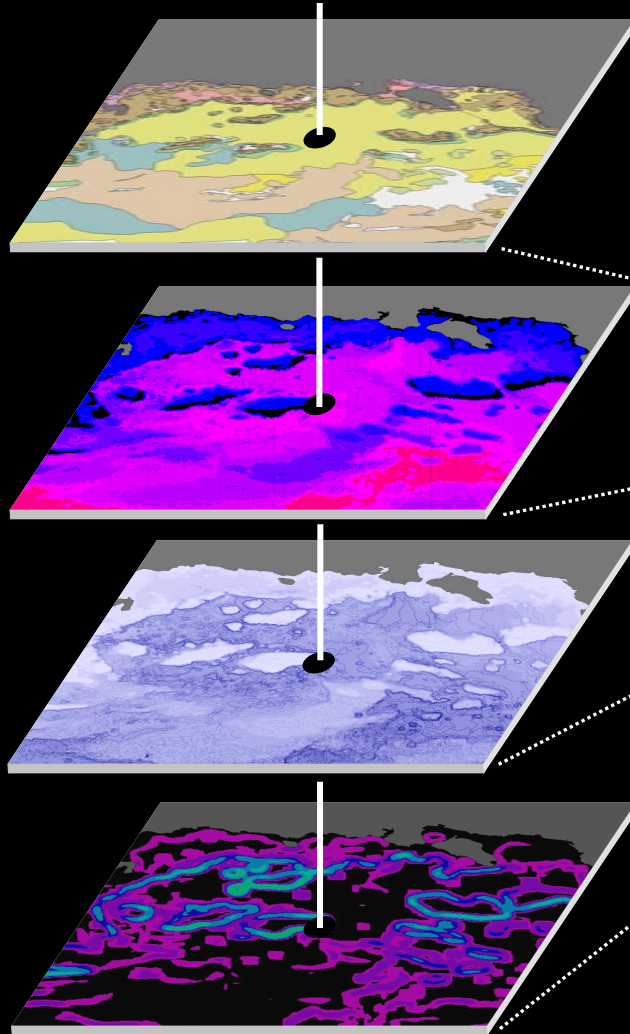
2	3	4
2	0.707	3
2	3	3

Spatial Variance Calculated at:
60, 100, 200, 300, 500, 1000 m
For both Habitat & Bathymetry



METHODS: Creating the Matrix

Drill Through Spatial Layers
Example: STATION X



CREATING THE ANALYSIS MATRIX

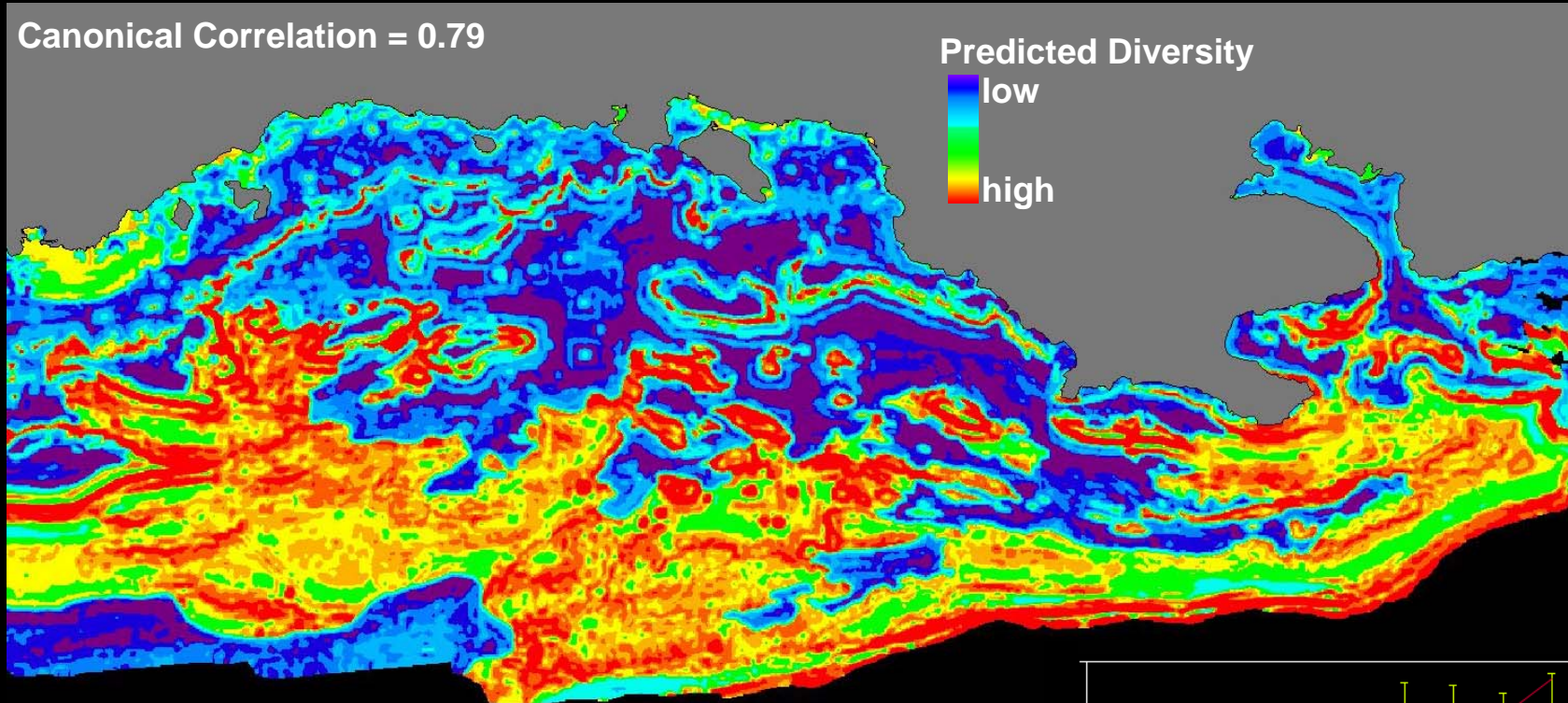


This is Done for the Following Variance Resolutions:
60,100, 200, 300, 500, 1000 m
Base Resolution for all Grids is 20 meters



RESULTS: Southwestern Puerto Rico

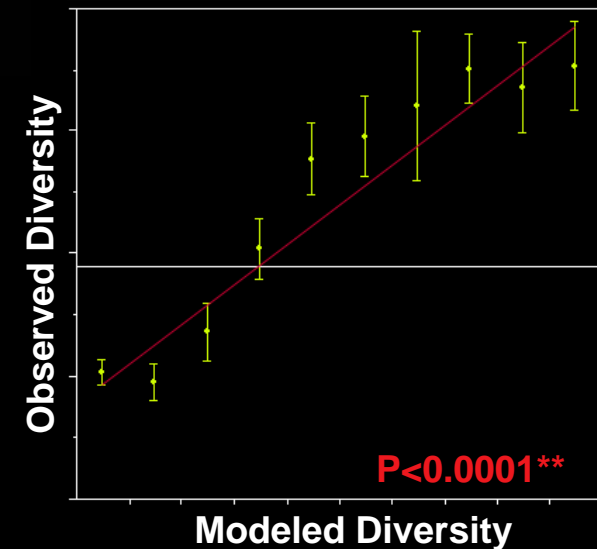
Canonical Correlation = 0.79



This map represents the canonical solution between landscape-level physiographic and fish community structure data.

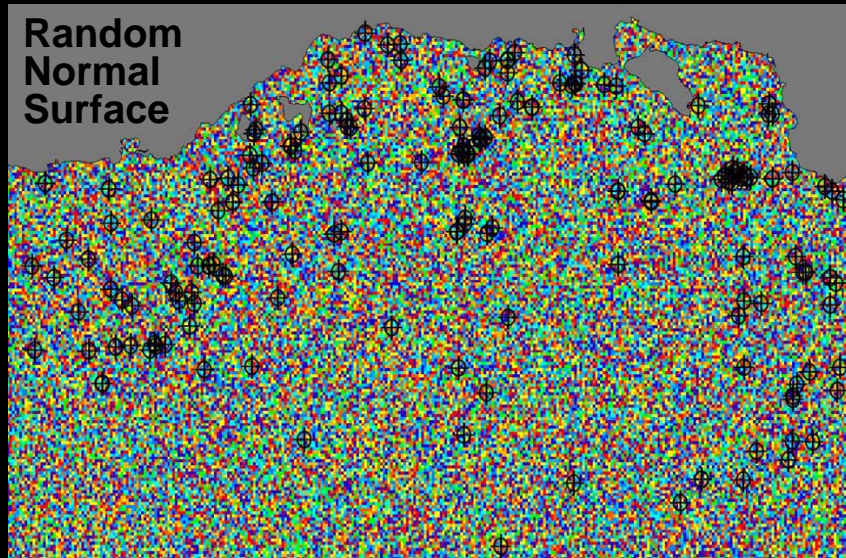
MAP ACCURACY

OVERALL
0.77

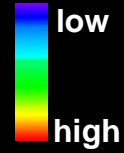




RESULTS: The Null Model

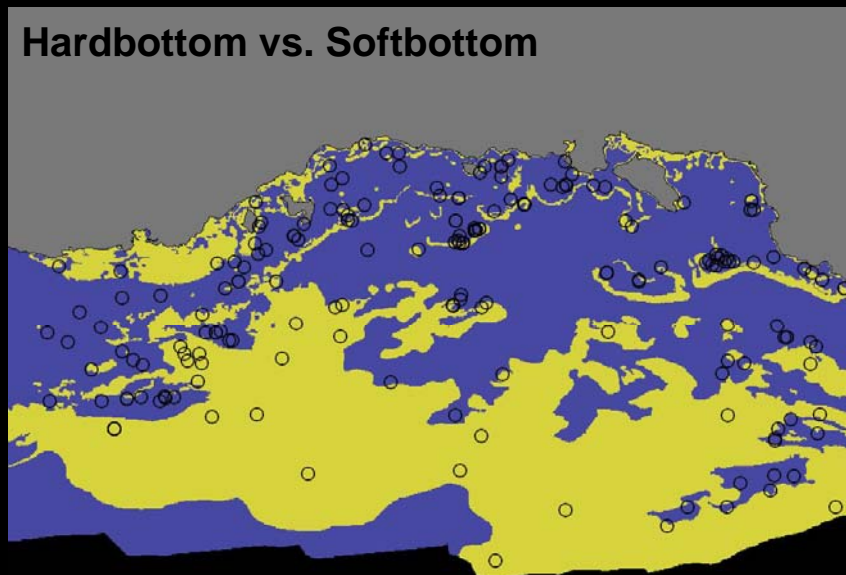
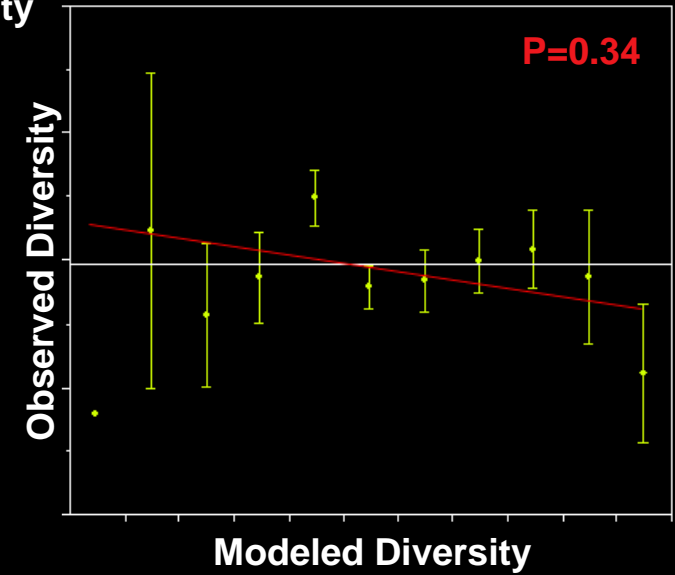


Predicted Diversity



MAP ACCURACY

OVERALL
0.46

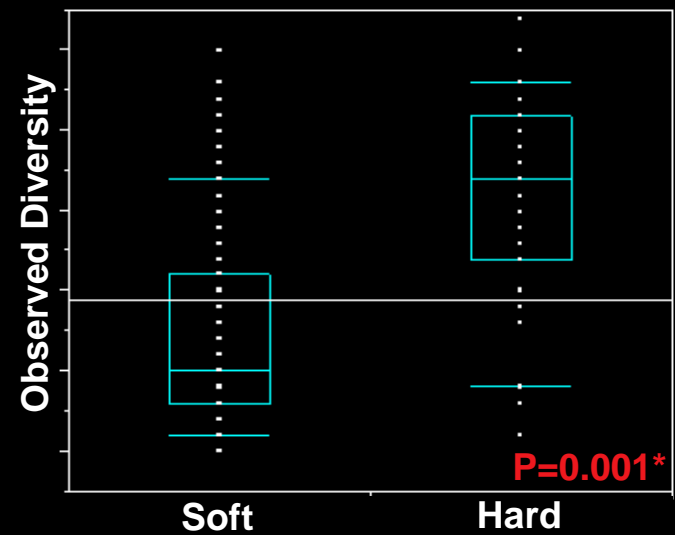


Habitat

- Hardbottom
- Softbottom

MAP ACCURACY

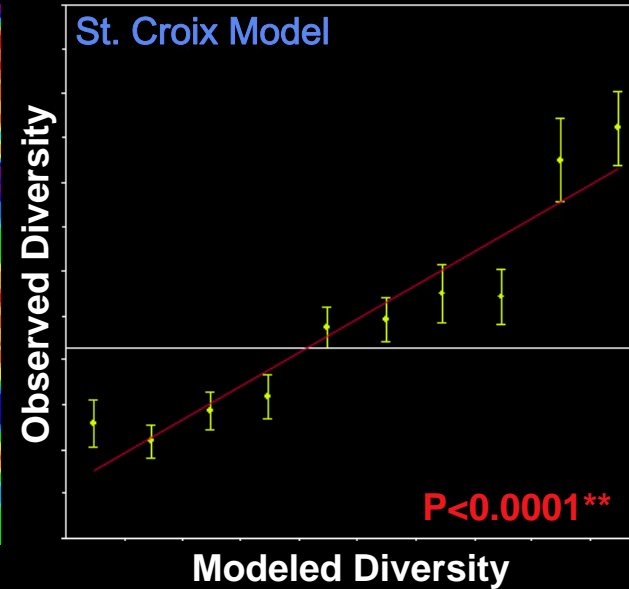
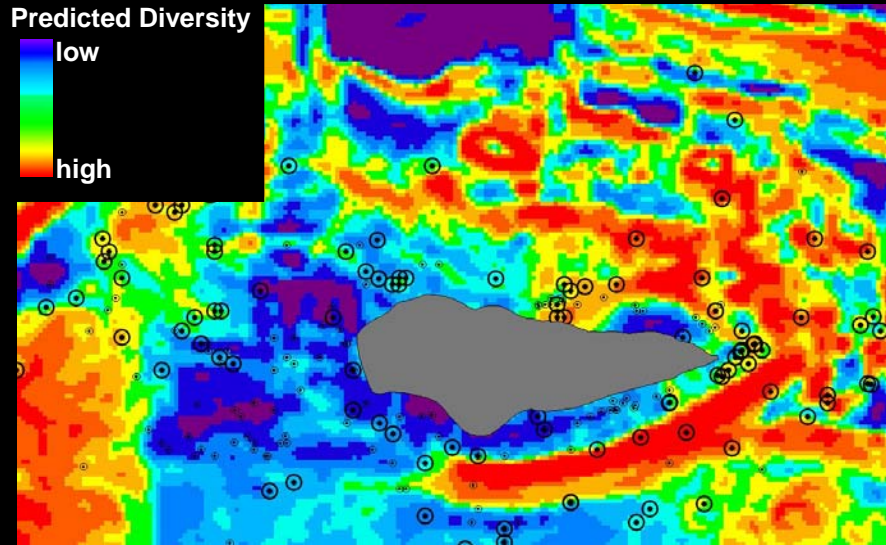
OVERALL
0.68





RESULTS: Buck Island - St. Croix, USVI

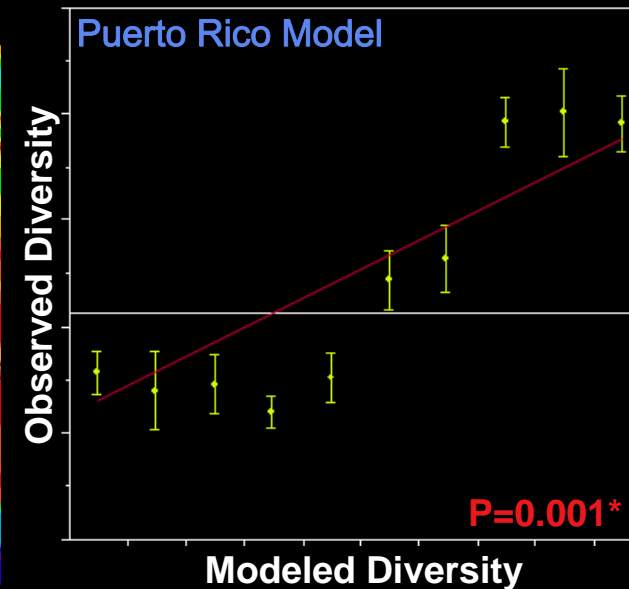
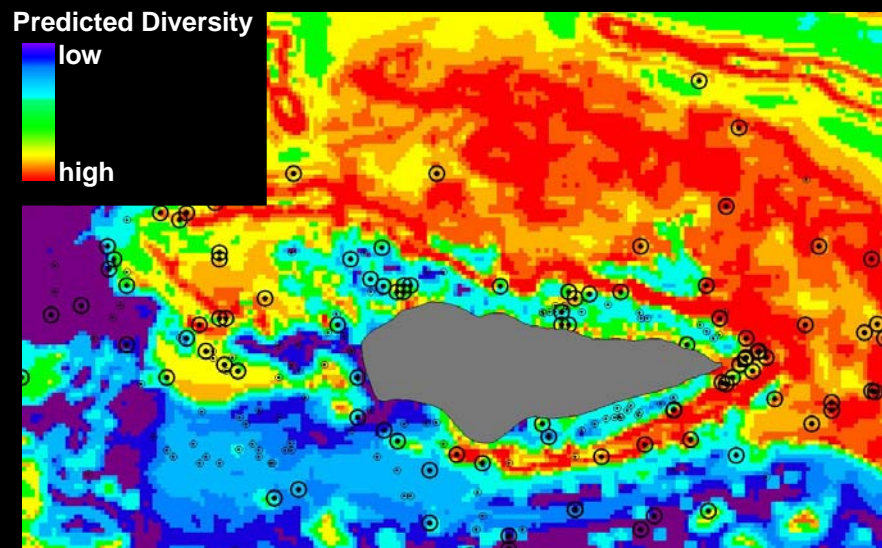
Canonical Correlation = 0.56



MAP ACCURACY

OVERALL
0.67

Spatial Correlation Between Model Results = 0.21



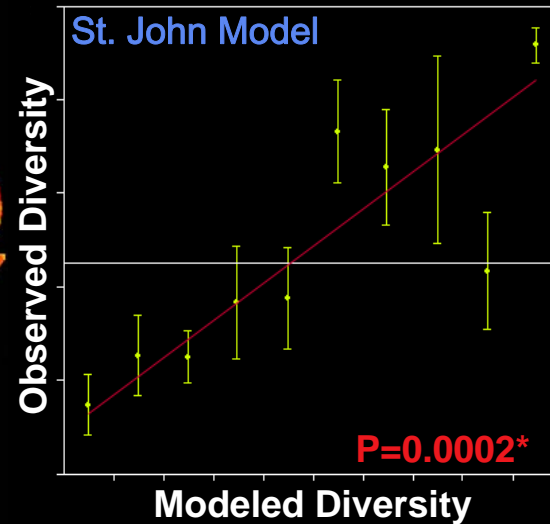
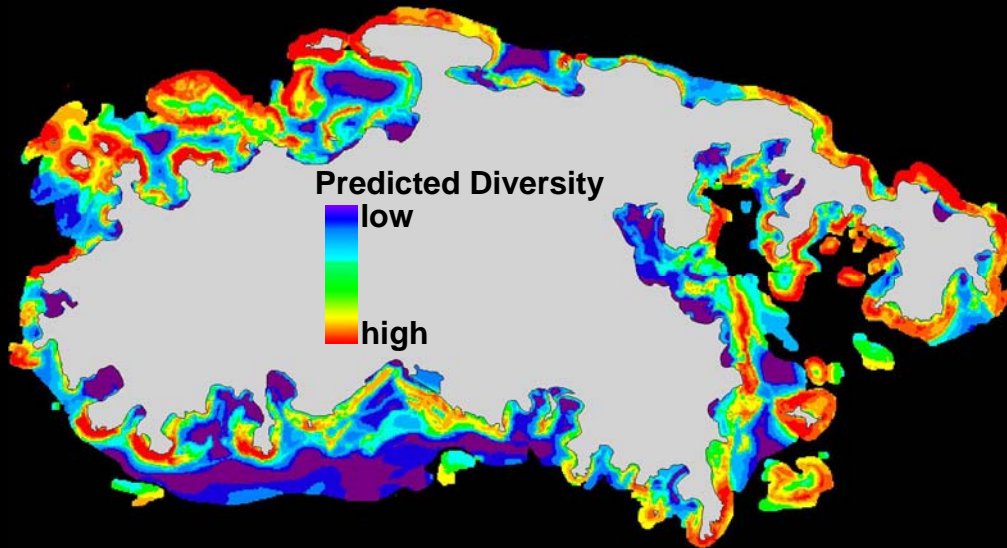
MAP ACCURACY

OVERALL
0.74



RESULTS: St. John, USVI

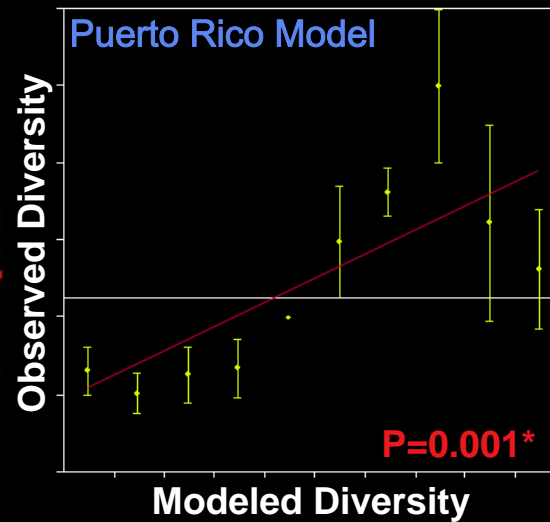
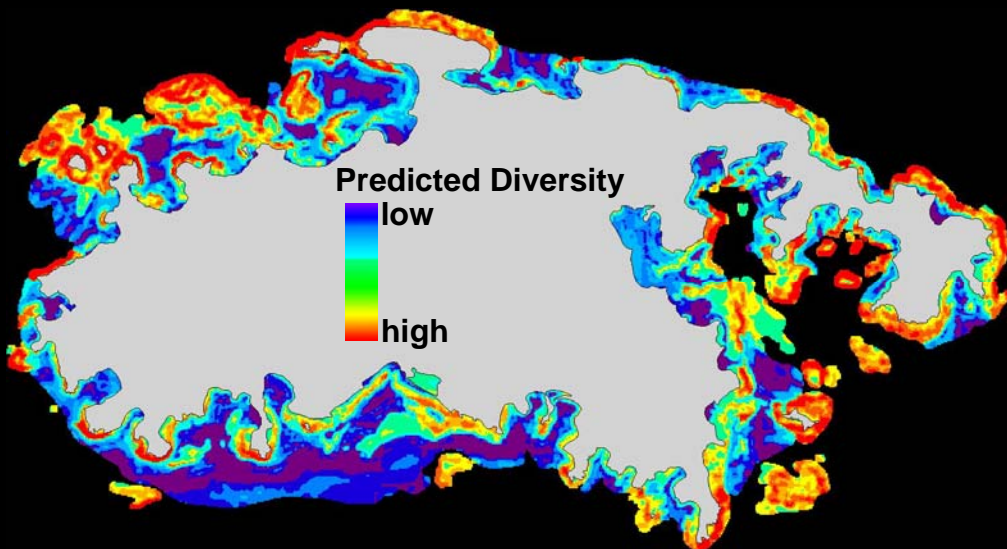
Canonical Correlation = 0.65



MAP ACCURACY

OVERALL
0.71

Spatial Correlation Between Model Results = 0.88



MAP ACCURACY

OVERALL
0.77



CONCLUSIONS

- ❖ Model surfaces of predicted fish diversity are positively, and significantly, correlated to observed diversity
- ❖ Models are different from random, and “perform” better than habitat alone
- ❖ Results suggest that models may be transferable (HANDLE WITH CARE!)
- ❖ Models may prove to be a useful tool for managers to identify locations/patterns in the landscape that have potential to “guide” MPA boundary delineation

With that said...

- ❖ More work is needed to test alternate model configurations
- ❖ A more robust set of Null models also must be tested
- ❖ A *posteriori* sampling needs to be conducted for further validation