

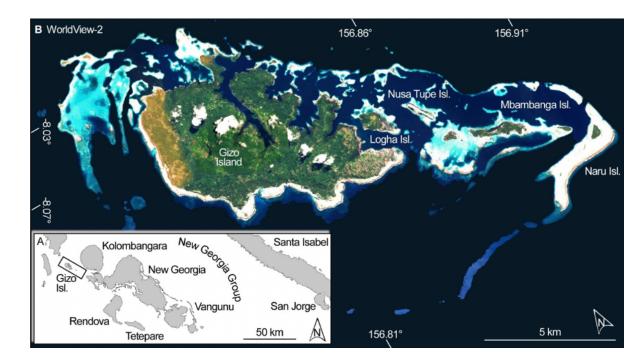
High-Performance Programming and Execution of a Coral Biodiversity Mapping Algorithm Using Chapel

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- 2. The Coral Reef Alliance San Francisco, California, USA
- 3. University of Miami Coral Gables, Florida, USA
- 4. Hewlett Packard Enterprise Spring, Texas, USA 4. Hewlett Packard Enterprise Spring, Texas, USA

• **Problem:** Coral reefs are widespread, but small and hard to reach. Surveying and measuring is difficult, time-consuming, and expensive.

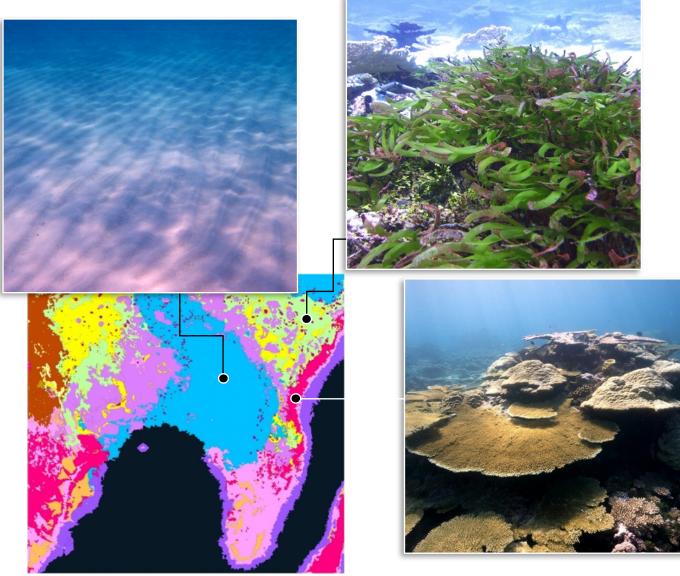
Do corals and fish correspond to seascape patterns in the reef as seen by satellite?



B WorldView-2 ۲ 156.91° D Habitat Map 156.86° 156.91° 156.86° lusa Tupe Abambanga -8.03 Naru Isl -8.07° New Georg Santa Isabel Kolombangara New Georgia Giz P Vangunu San Jorge [m] Rendova 5 km 50 km 156.81° 156.81° Tetepare

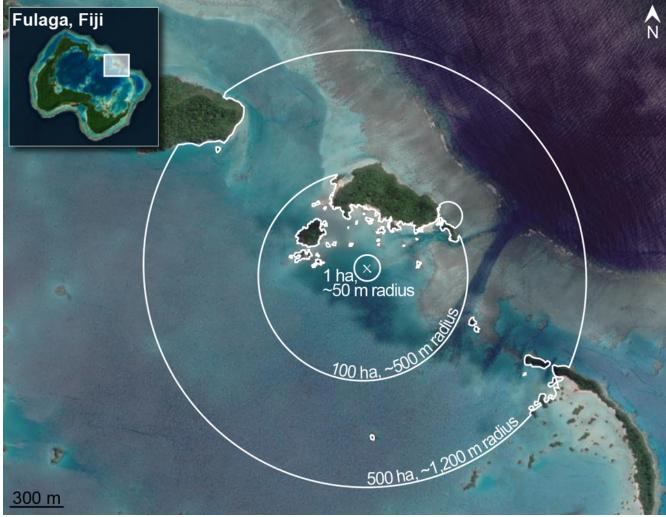
Satellite image

Rasterized habitat map



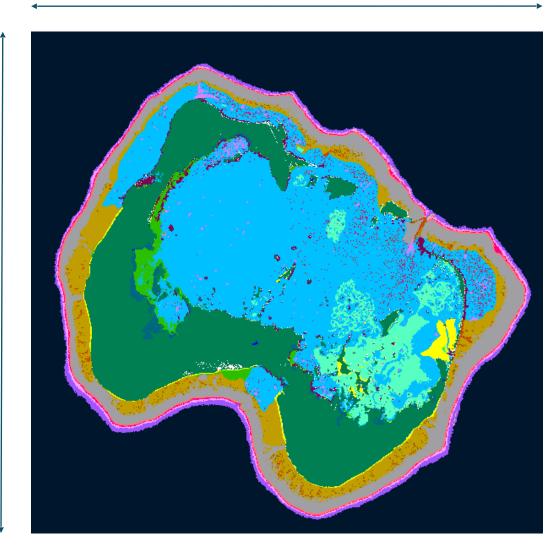
Challenge: How much habitat diversity occurs in a circle of size X?

Need to perform this calculation for each point in the image.



1. Read in a (M x N) raster image of habitat data

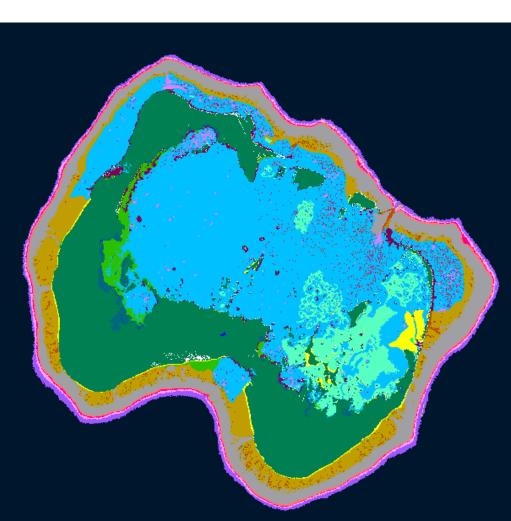
Μ



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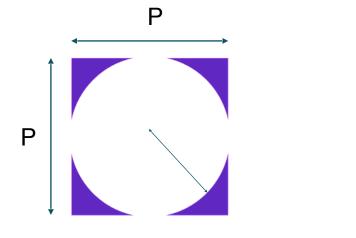
2. Create a (P x P) mask to find all points within a given radius.

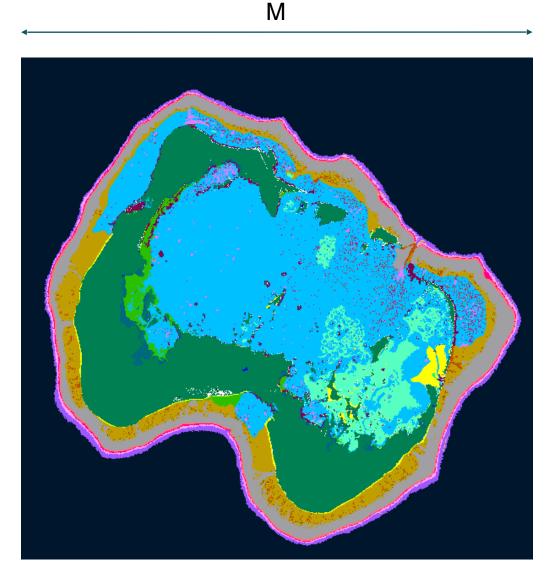
P P Ν



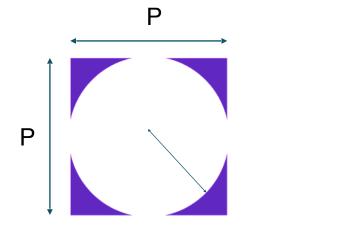
Μ

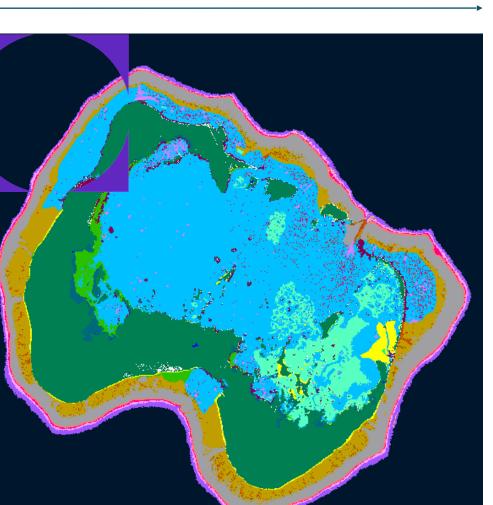
- 1. Read in a (M x N) raster image of habitat data
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- 3. Convolve this mask over the entire domain and perform a weighted reduce at each location.



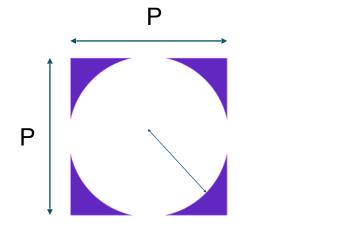


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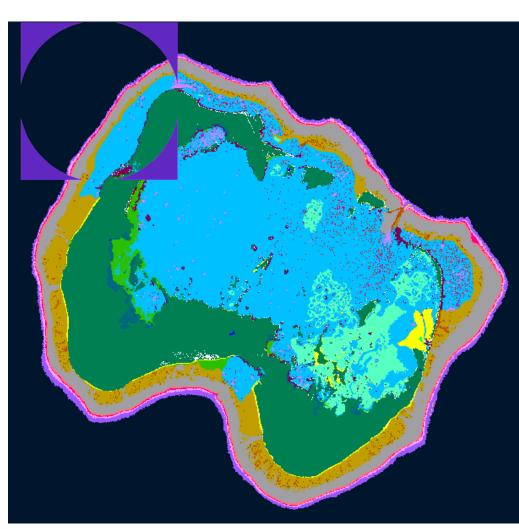




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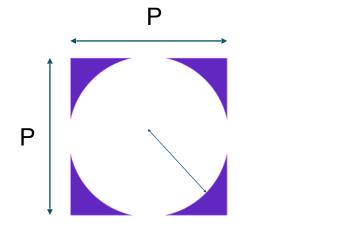


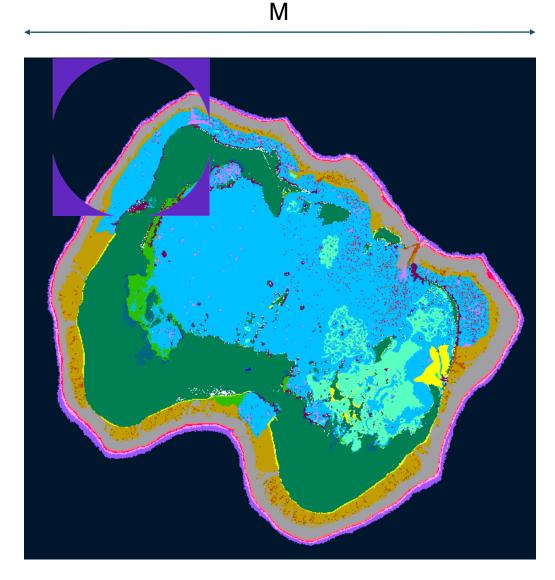
Ν



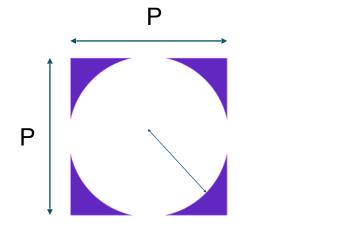
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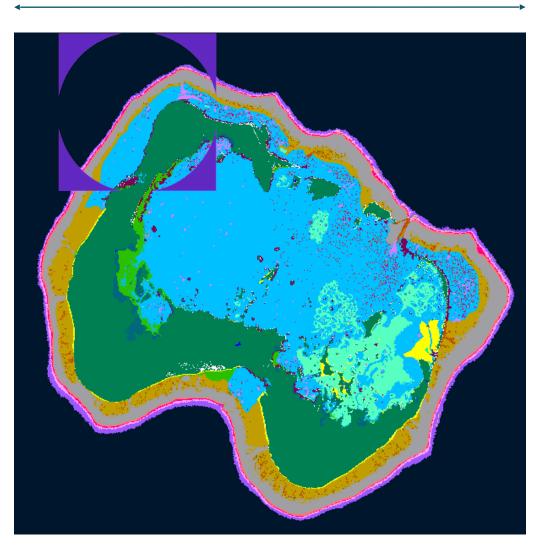
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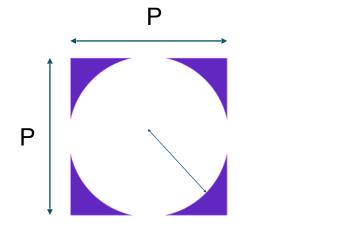


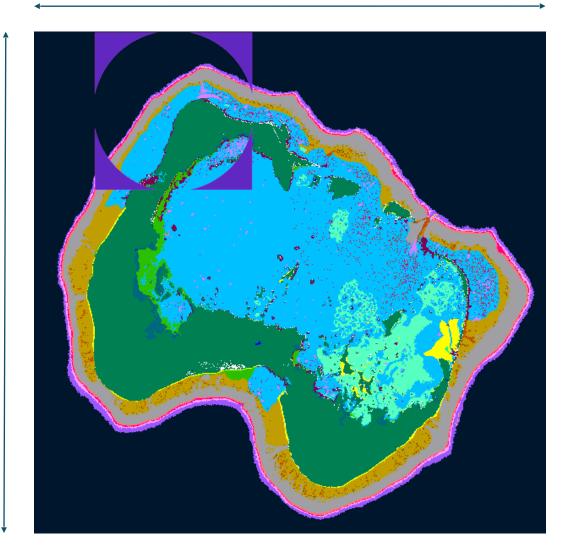
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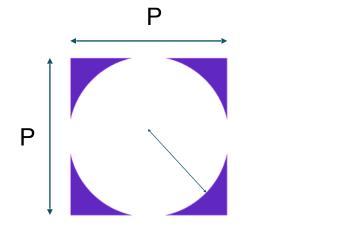


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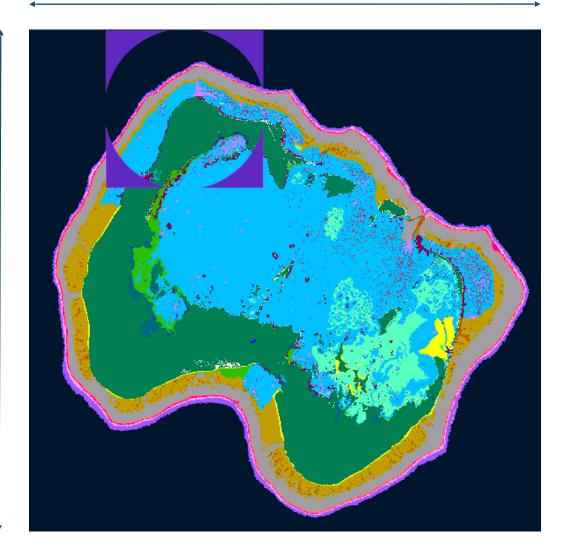




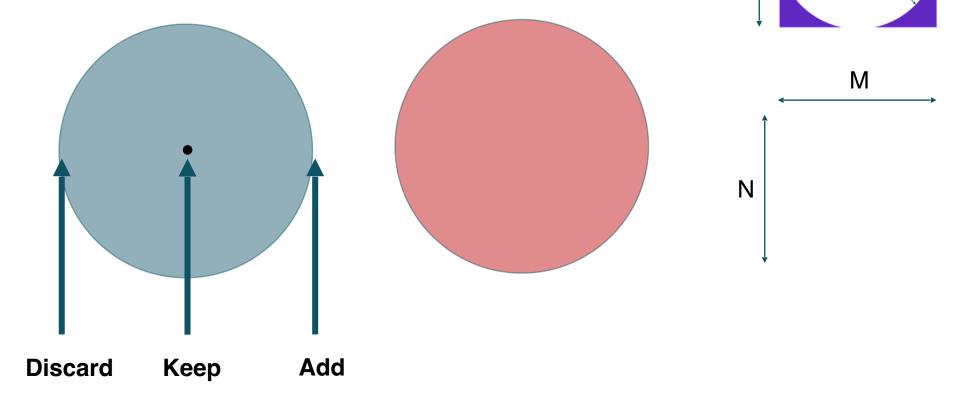
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The basic algorithm essentially involves calculating a histogram at each point. *"How many habitats of each type are in the neighborhood?"*



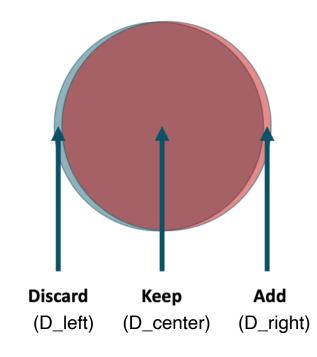
• Saves roughly a factor of *P* calculations.

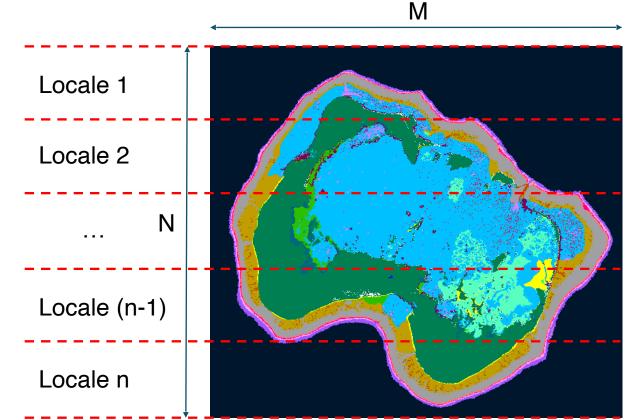
Overall algorithm is O(MNP) instead of $O(MNP^2)$

Ρ

Ρ

```
proc create_distance_mask(radius : real, dx : real, nx : int) {
 const D : domain(2, int) = \{-nx..nx, -nx..nx\};
 var D_center : sparse subdomain(D);
 var D_left : sparse subdomain(D);
 var D_right : sparse subdomain(D);
 var dist : [D] real;
 var center_mask : [D_center] bool;
 var left_mask : [D_left] bool;
 var right_mask : [D_right] bool;
                 . . .
 // Define center mask.
 for (i,j) in dist.domain do {
    dist[i,j] = dx * sqrt(i**2 + j**2);
   if (dist[i,j] < radius) {</pre>
      D_center += (i,j);
    }
 }
```





```
// Create Block distribution of interior of PNG
const offset = nx;
const Inner = ImageSpace.expand(-offset);
const myTargetLocales = reshape(Locales, {1..Locales.size, 1..1});
const D = Inner dmapped Block(Inner, targetLocales=myTargetLocales);
var OutputArray : [D] real;
```



coforall loc in Locales do on loc {

const locImageDomain = Image.domain; const locImage : [locImageDomain] Image.eltType = Image;

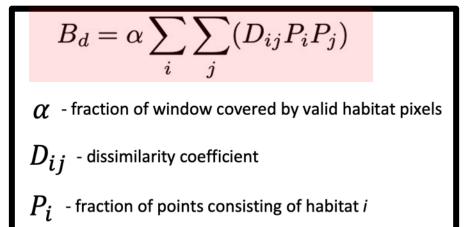
const locLeftMaskDomain = LeftMask.domain; const locCenterMaskDomain = CenterMask.domain; const locRightMaskDomain = RightMask.domain;

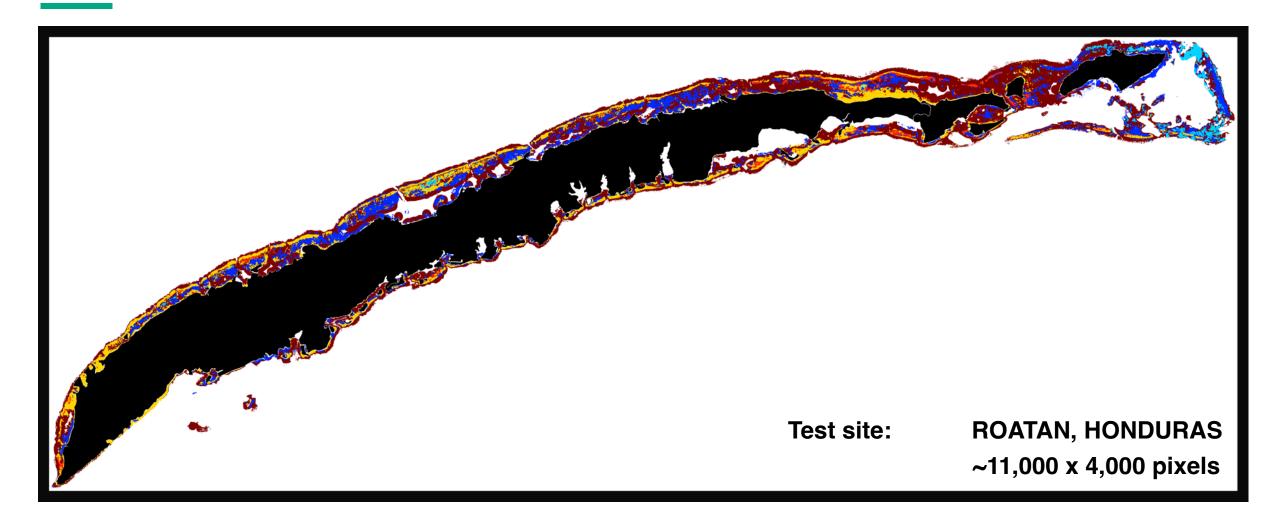
\bullet \bullet \bullet

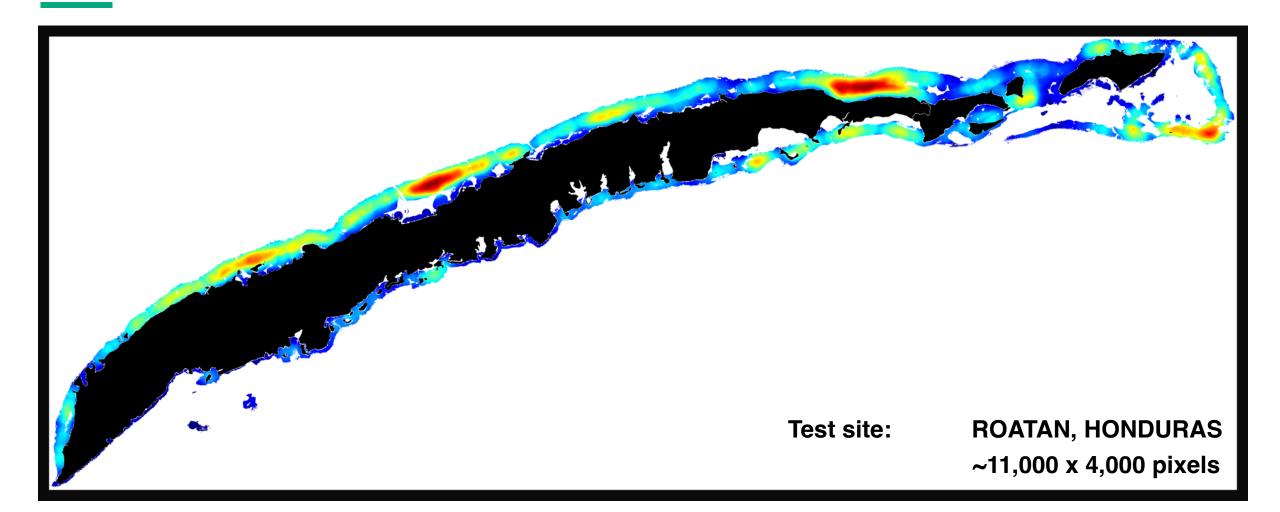
```
// If we are on a reef point, calculate beta diversity
var num_habitat_pixels = (+ reduce B[1..(d_size-2)]) : real;
var habitat_frac = num_habitat_pixels / Mask_Size;
```

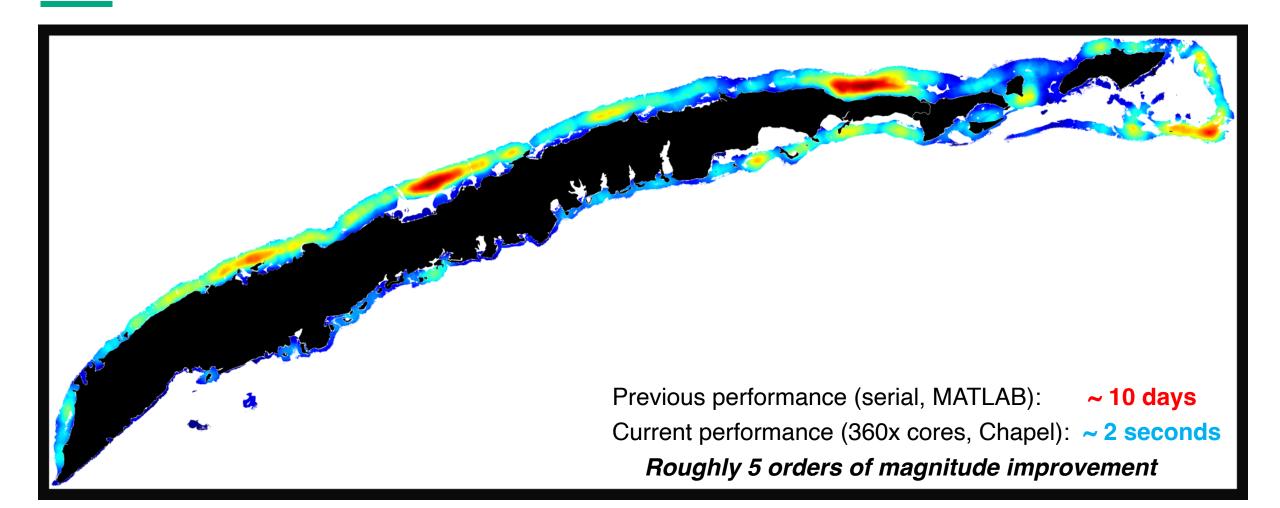
```
var P = B / num_habitat_pixels;
```

```
var beta = + reduce (dissimilarity * outer(P,P));
Output[center,point] = habitat_frac * beta + eps;
```

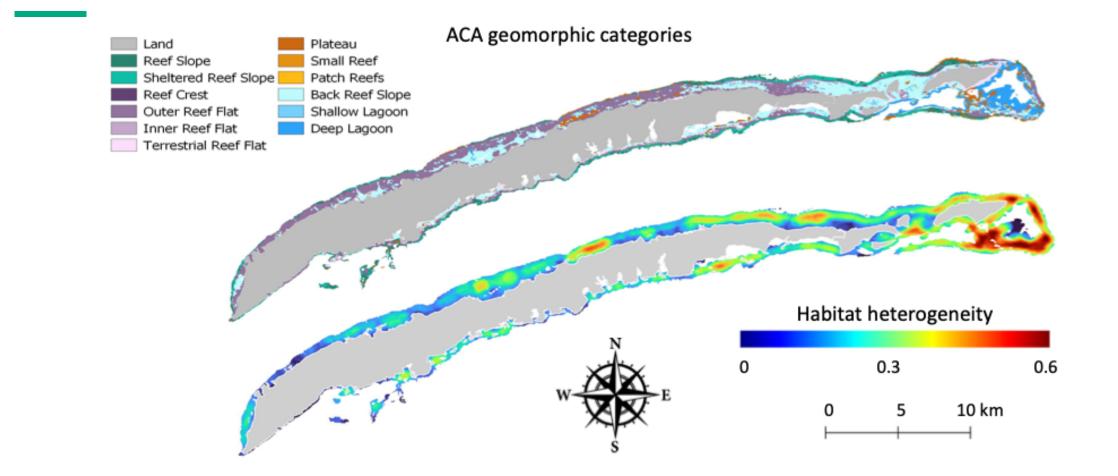




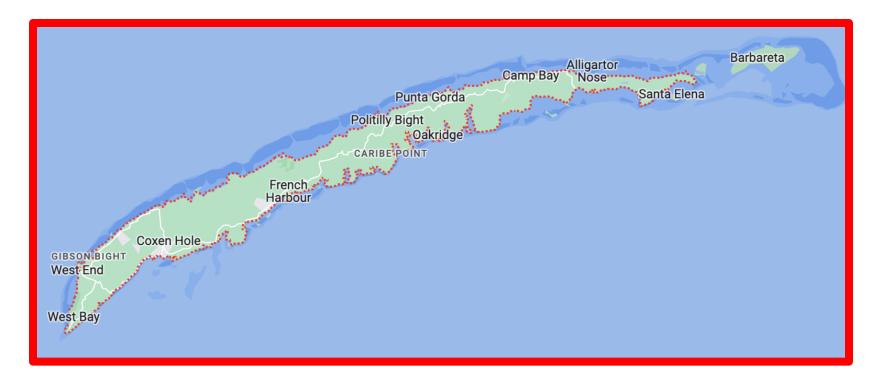




- Collaborations/discussions w/ U. Miami, Coral Reef Alliance, U. Leeds (UK), U. Hawaii
- Unexpected shoutout here(!): https://www.youtube.com/watch?v=tlp2_DI6Nal

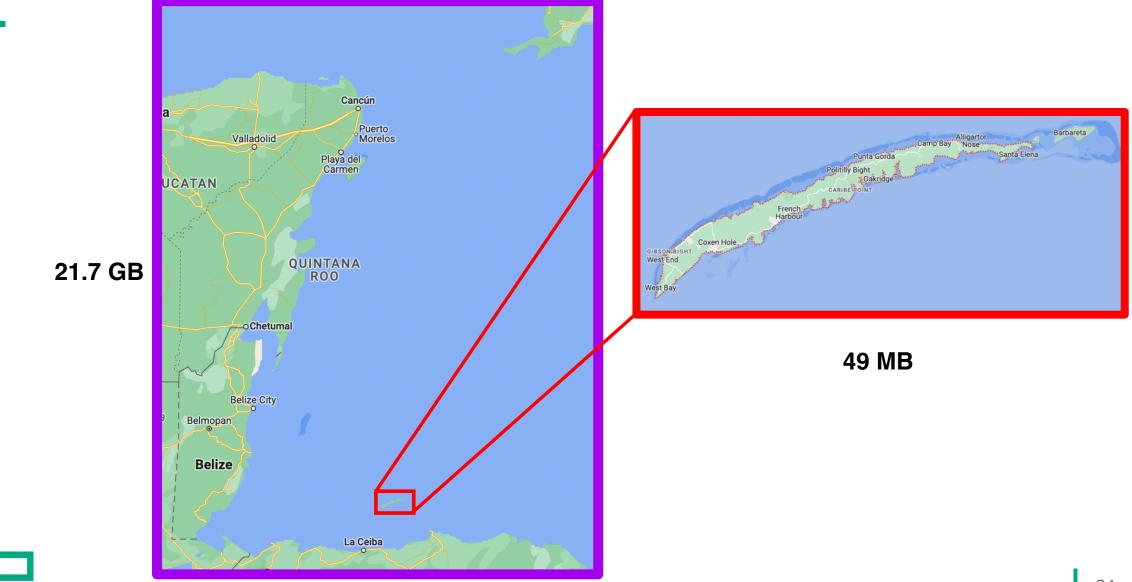


Previous performance (serial, MATLAB): ~ Multiple days Current performance (360x cores, Chapel): ~ 2 seconds *Roughly 5 orders of magnitude improvement*

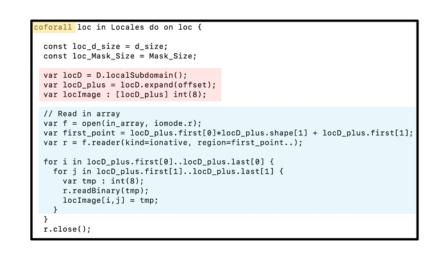


Can we try bigger regions?

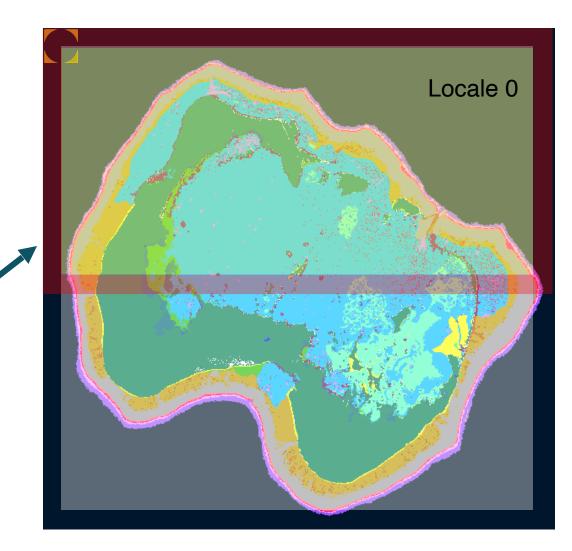




```
coforall loc in Locales do on loc {
                                                     Distributed read
 const loc_d_size = d_size;
                                                    of the input image
 const loc Mask Size = Mask Size;
 var locD = D.localSubdomain();
 var locD_plus = locD.expand(offset);
 var locImage : [locD_plus] int(8);
 // Read in array
 var f = open(in_array, iomode.r);
 var first_point = locD_plus.first[0]*locD_plus.shape[1] + locD_plus.first[1];
 var r = f.reader(kind=ionative, region=first point..);
 for i in locD_plus.first[0]..locD_plus.last[0] {
   for j in locD_plus.first[1]..locD_plus.last[1] {
     var tmp : int(8);
     r.readBinary(tmp);
     locImage[i,j] = tmp;
 r.close();
```



Passes the local Subdomain + a halo equal to half the mask width



Scaling Up

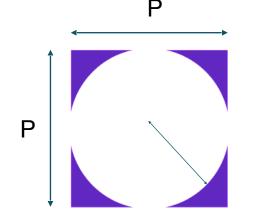
Distributed write of the output image (using Cinteroperability)

```
proc WriteOutput(filename : string, ref arr_out: [?D] real(32), ImageSpace : ?, varid
_in : int, offset : int) {
coforall loc in Locales do on loc {
 var ncid : c_int;
 var varid = varid_in : c_int;
 extern proc nc_open(path : c_string, mode : c_int, ncidp : c_ptr(c_int)) : c_int;
 nc_open( filename.c_str() , NC_WRITE, c_ptrTo(ncid));
 /* Determine where to start reading file, and how many elements to read */
 // Start specifies a hyperslab. It expects an array of dimension sizes
    var start = tuplify(D.localSubdomain().first);
 // Count specifies a hyperslab. It expects an array of dimension sizes
   var count = tuplify(D.localSubdomain().shape);
   var start_c : [0..#start.size] c_size_t;
    var count_c : [0..#count.size] c_size_t;
   for i in 0..<count.size {</pre>
     start_c[i] = start[i] : c_size_t;
     count_c[i] = count[i] : c_size_t;
    }
   extern proc nc_put_vara_float(ncid : c_int, varid : c_int, startp : c_ptr(c_size_
t), countp : c_ptr(c_size_t), op : c_ptr(c_float)) : c_int;
   nc_put_vara_float(ncid, varid, c_ptrTo(start_c), c_ptrTo(count_c), c_ptrTo(arr_ou
t[start]));
   nc_close(ncid);
```

Coral Reef Biodiversity (image analysis) Variant algorithms

Spectral diversity

"How much variation in the visible spectrum exists within a neighborhood?"

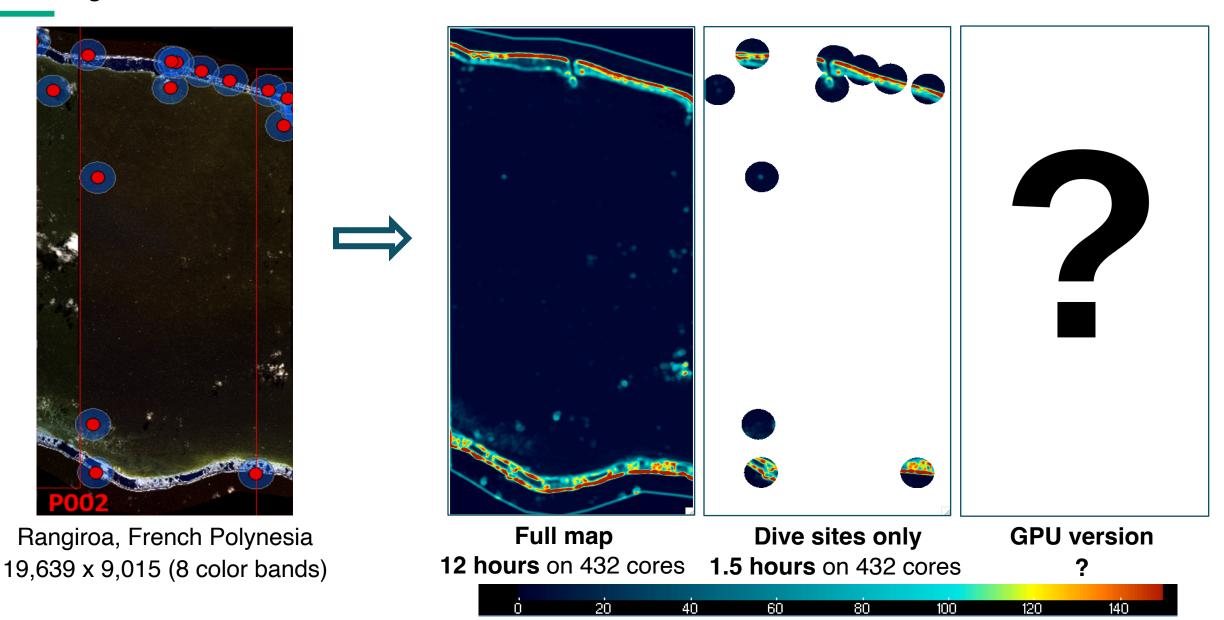


Habitat diversity: Count the number of points of each type Spectral diversity: For each point, compare spectrum against every other point

Habitat diversity:O(MNP)Spectral diversity: $O(MNP^3)$



Coral Reef Biodiversity (image analysis) Variant algorithms



Variant algorithms

Spectral diversity on GPU

foreach i in centerPoints.dim(0) {
//for i in centerPoints.dim(0) {
 assertOnGpu();

var tmpLL : real = 0; var tmpLC : real = 0; var tmpLR : real = 0; var tmpCC : real = 0; var tmpCR : real = 0; var tmpRR : real = 0;

calc_distance(Array, Masker.left(), Masker.left(), tmpLL, bs, be, i, first_point); calc_distance(Array, Masker.left(), Masker.center(), tmpLC, bs, be, i, first_point); calc_distance(Array, Masker.left(), Masker.right(), tmpLR, bs, be, i, first_point); calc_distance(Array, Masker.center(), Masker.center(), tmpCC, bs, be, i, first_point); calc_distance(Array, Masker.center(), Masker.right(), tmpCR, bs, be, i, first_point); calc_distance(Array, Masker.right(), Masker.right(), tmpRR, bs, be, i, first_point);

```
Distance circle has a radius of 5 points.

Elapsed time at start of coforall loop: 6e-05 seconds.

Starting coforall loop.

Distance circle has a radius of 5 points.

Made masker on 0

Starting convolution at 18.5078.

Before gpu 6..15236

6

10066

0 (gpu 0): main_GPU_iter2.chpl:38: kernel launch (block size: 512x1x1)

Took 0.005122 seconds to complete convolve.

Elapsed time to finish coforall loop: 18.6655 seconds.
```

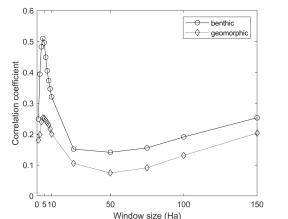
• Assessing whether habitat heterogeneity metrics may be linked to thermal variability and genetic diversity of reefs.

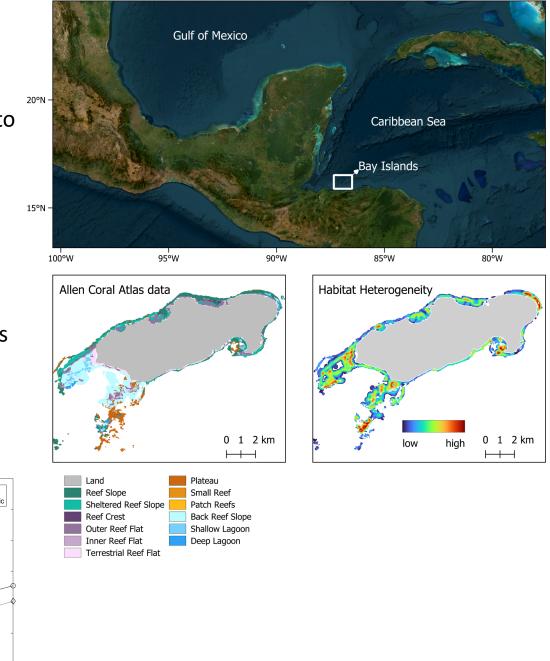
Methods:

- Publicly available maps of coral reef benthic and geomorphic zonation from Allen Coral Atlas used in RapidQ.
- 40 temperature loggers deployed for 24 months, genetic samples from coral species taken.

Initial Results:

- Daily temperature range at coral sampling sites correlated to habitat heterogeneity at window sizes of 4 and 5 Ha.
- Higher correlations in benthic habitat maps.





Applications and Projects

- Largest barrier reef system in the Western Hemisphere, stretching for >1000km along the coasts of Honduras, Guatemala, Belize and Mexico.
- Habitat heterogeneity layers created for entire reef system, currently evaluating against Marine Protected Area (MPA) status.
- End goal: deliver a product derived from satellite remote sending that can be used in effective global marine conservation planning.





Mesoamerican Reef Marine Protected Area boundaries

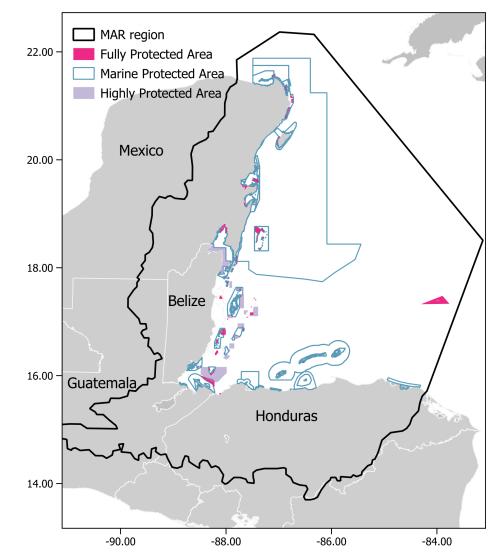
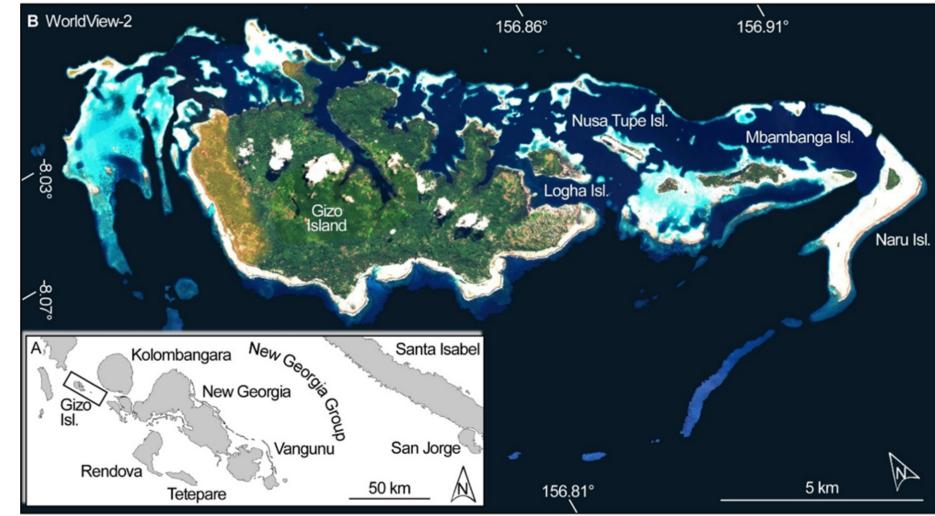


Photo credit Antonio Busiello

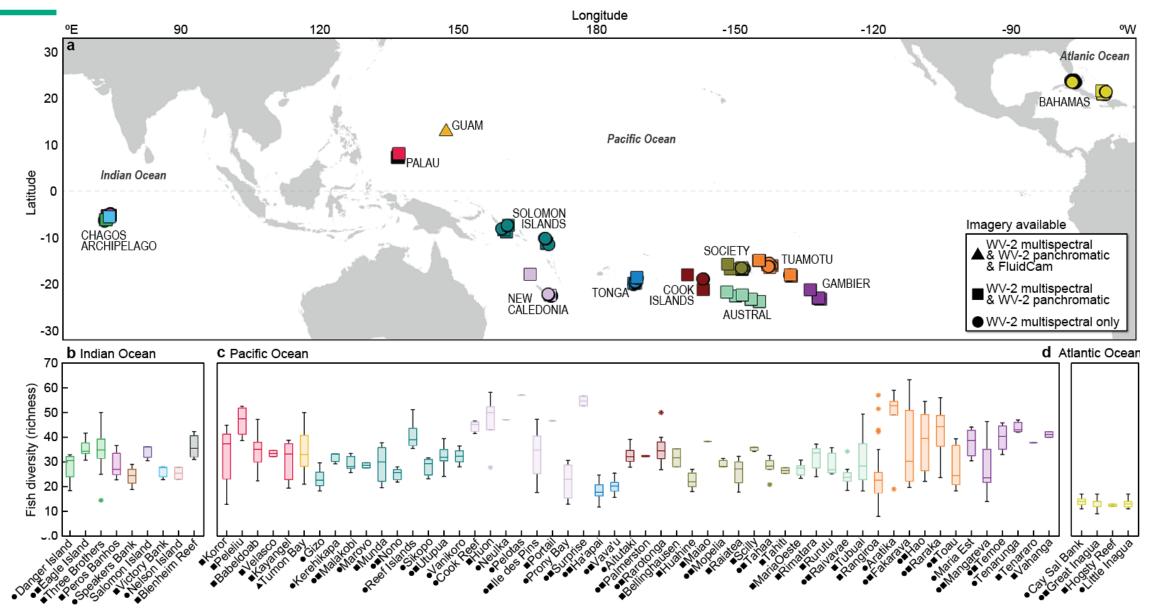
Coral Reef Biodiversity (image analysis) Measuring Diversity (in situ)

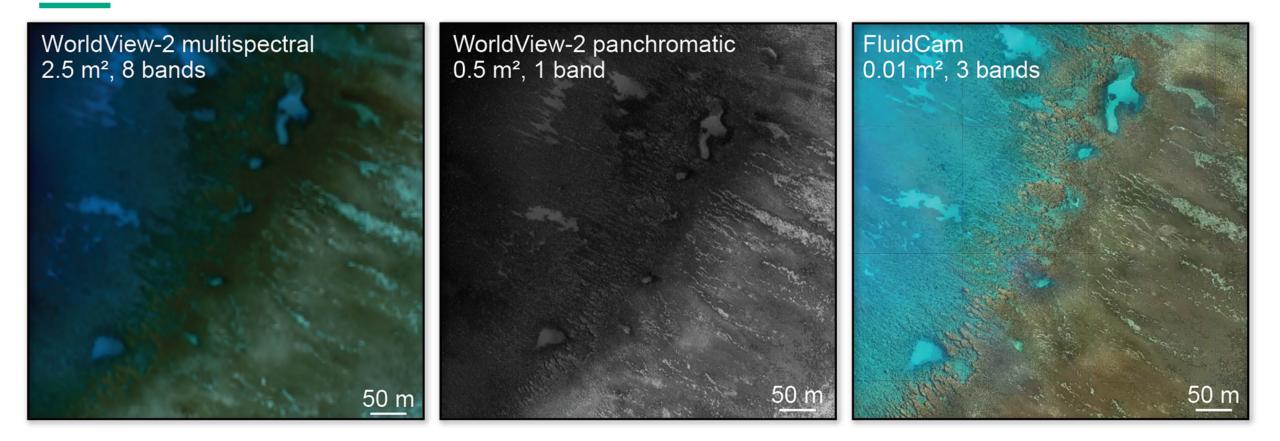
Coral Reef Biodiversity (image analysis) Measuring Diversity (remote)



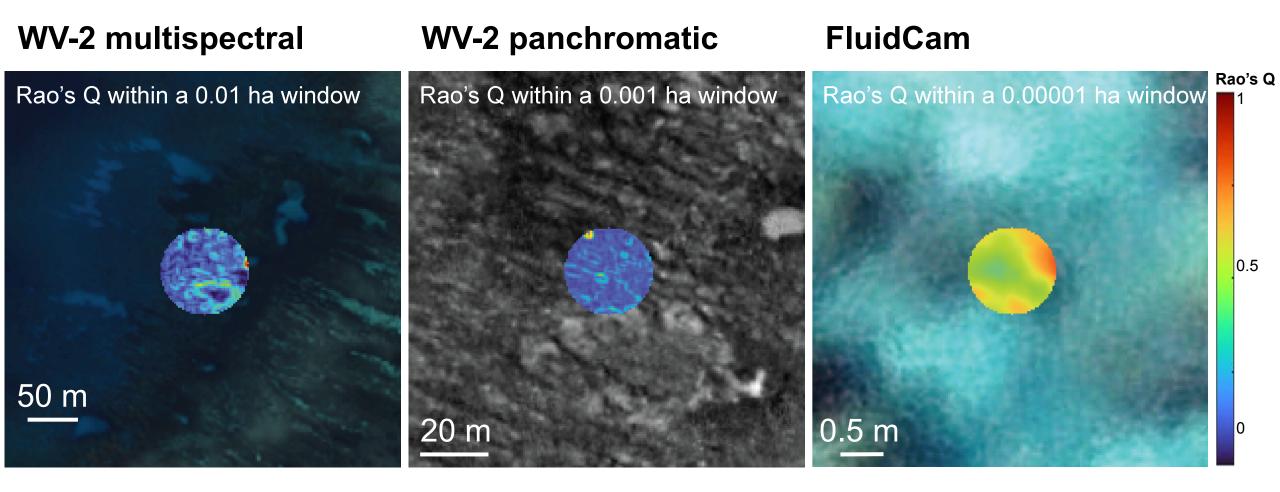


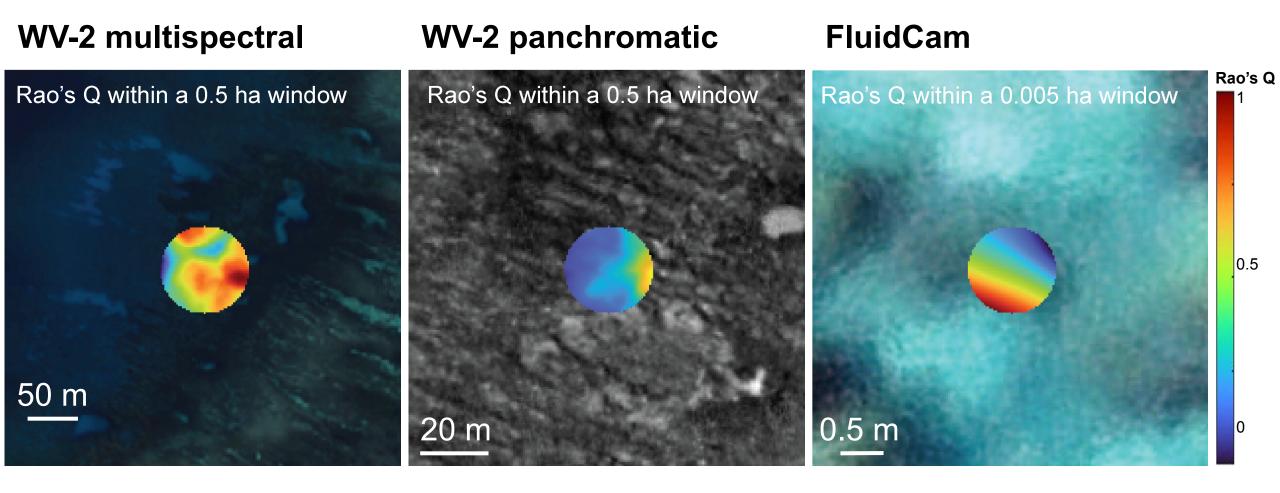
Applications and Projects



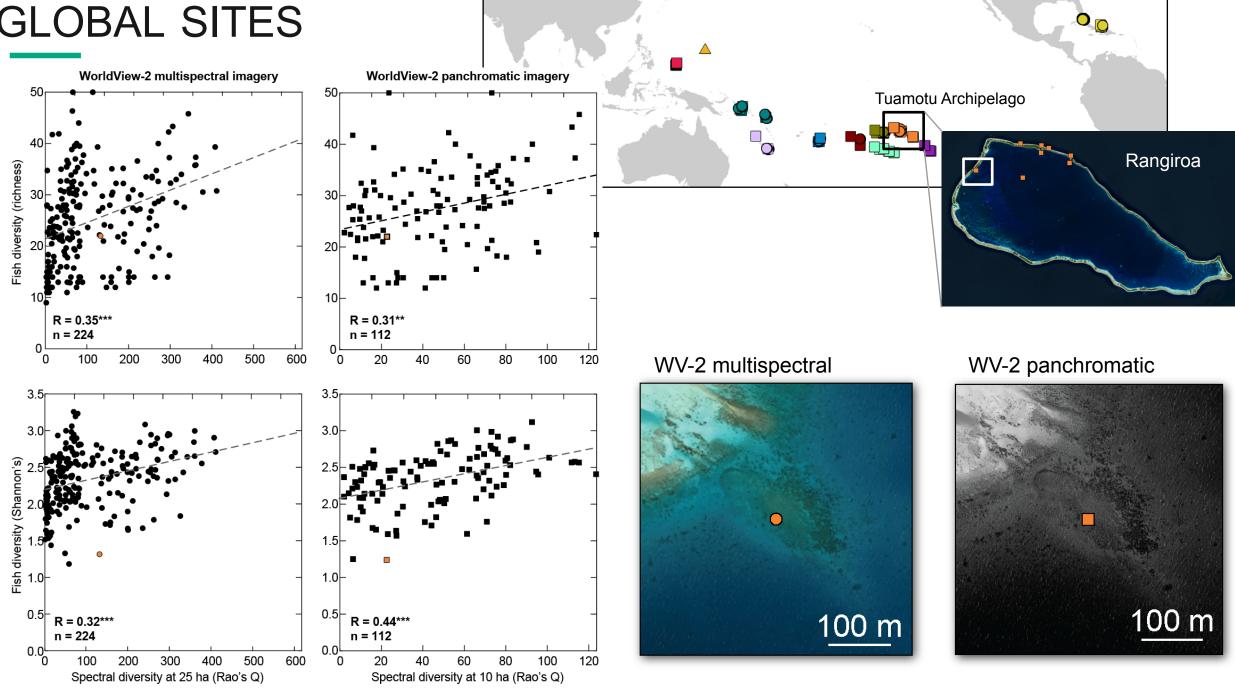


WorldView-2 multispectral 2.5 m², 8 bands WorldView-2 panchromatic FluidCam 0.01 m², 3 bands 0.5 m², 1 band <u>10 m</u> 10 m





GLOBAL SITES



Coral Reef Biodiversity (image analysis) Summary

- Chapel program to estimate reef biodiversity using satellite imagery
 - Embarrassingly parallel and scalable
 - Multiple orders faster than incumbent MATLAB program
 - <u>Very</u> exciting for my colleagues in the conservation world!
- Takeaway? Lots of applications out there (not necessarily complicated) that could benefit from what Chapel provides