

An aerial photograph of a body of water heavily infested with bright green algae. The water is dark blue, and the algae forms a dense, textured carpet. Several pieces of white plastic trash, including a bottle and a piece of paper, are scattered across the surface. The text 'DETECTION & MONITORING' is overlaid in the center in a white, sans-serif font.

DETECTION & MONITORING

SPECTRAL MIXTURE ANALYSIS FOR SURVEILLANCE OF HARMFUL ALGAL BLOOMS (SMASH): A NEW TOOL FOR INFERRING BLOOM TAXONOMY FROM REMOTELY SENSED DATA

Dr. Carl J. Legleiter – cjl@usgs.gov

Research Hydrologist

U.S. Geological Survey, Observing Systems Division



PROJECT SUMMARY

Spectral Mixture Analysis for Surveillance of Harmful Algal Blooms (SMASH): A framework for integrating hyperspectral images acquired in the lab and from space to not only detect the presence of an algal bloom but also identify which taxa are present and their fractional abundances

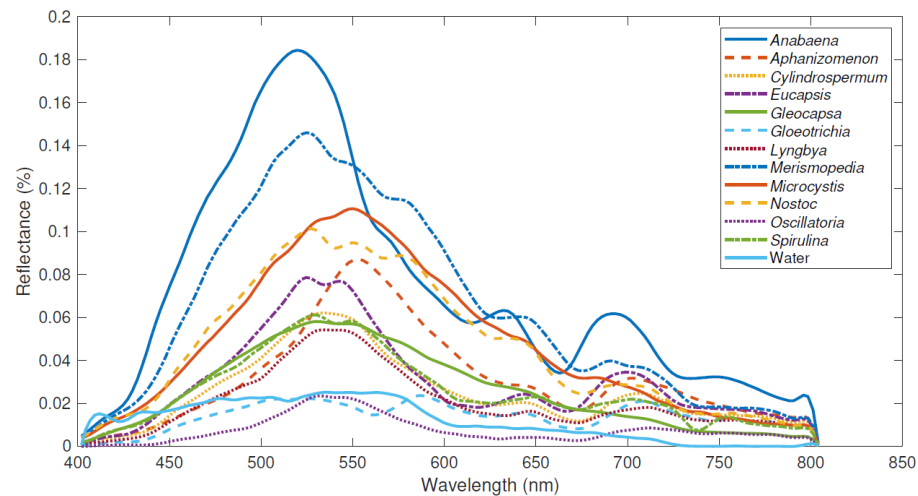
[Legleiter et al., 2022](#)



PROJECT SUMMARY

Spectral Mixture Analysis for Surveillance of Harmful Algal Blooms (SMASH): A framework for integrating hyperspectral images acquired in the lab and from space to not only detect the presence of an algal bloom but also identify which taxa are present and their fractional abundances

[Legleiter et al., 2022](#)



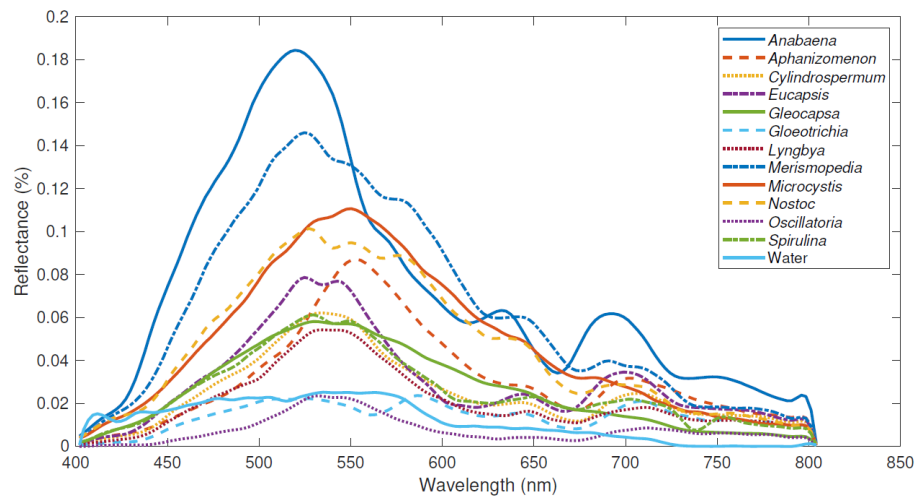
Lab-based spectral library of cyanobacterial endmembers



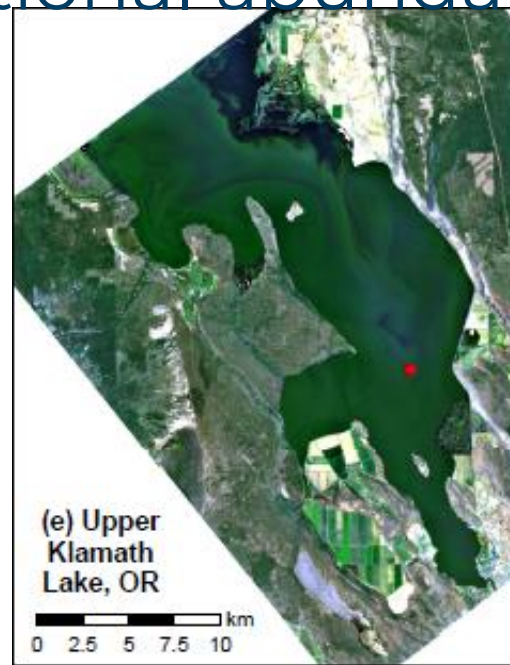
PROJECT SUMMARY

Spectral Mixture Analysis for Surveillance of Harmful Algal Blooms (SMASH): A framework for integrating hyperspectral images acquired in the lab and from space to not only detect the presence of an algal bloom but also identify which taxa are present and their fractional abundances

Legleiter et al., 2022



Lab-based spectral library of cyanobacterial endmembers



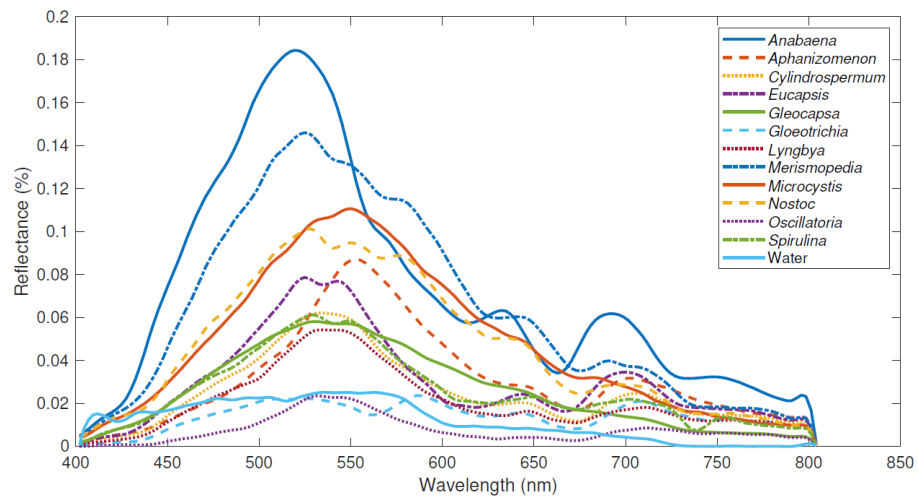
Hyperspectral satellite image



PROJECT SUMMARY

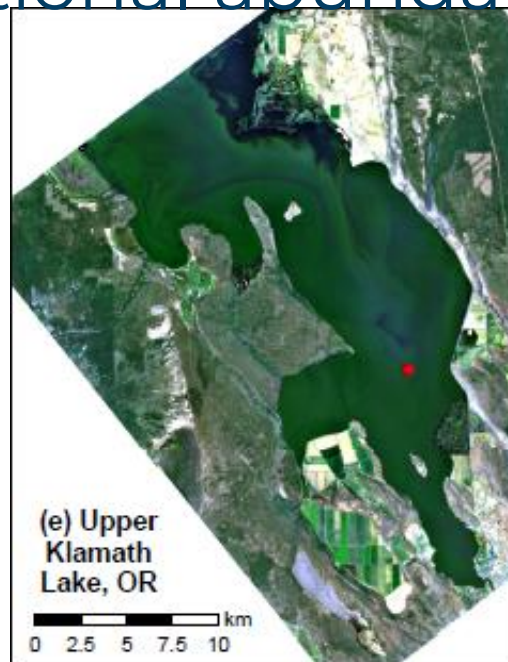
Spectral Mixture Analysis for Surveillance of Harmful Algal Blooms (SMASH): A framework for integrating hyperspectral images acquired in the lab and from space to not only detect the presence of an algal bloom but also identify which taxa are present and their fractional abundances

Legleiter et al., 2022

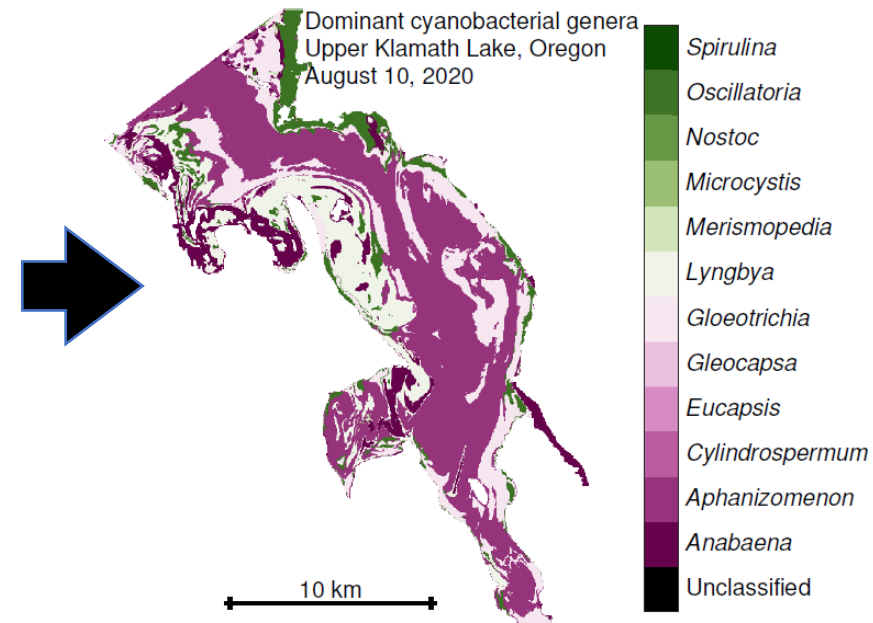


Lab-based spectral library of cyanobacterial endmembers

+



Hyperspectral satellite image

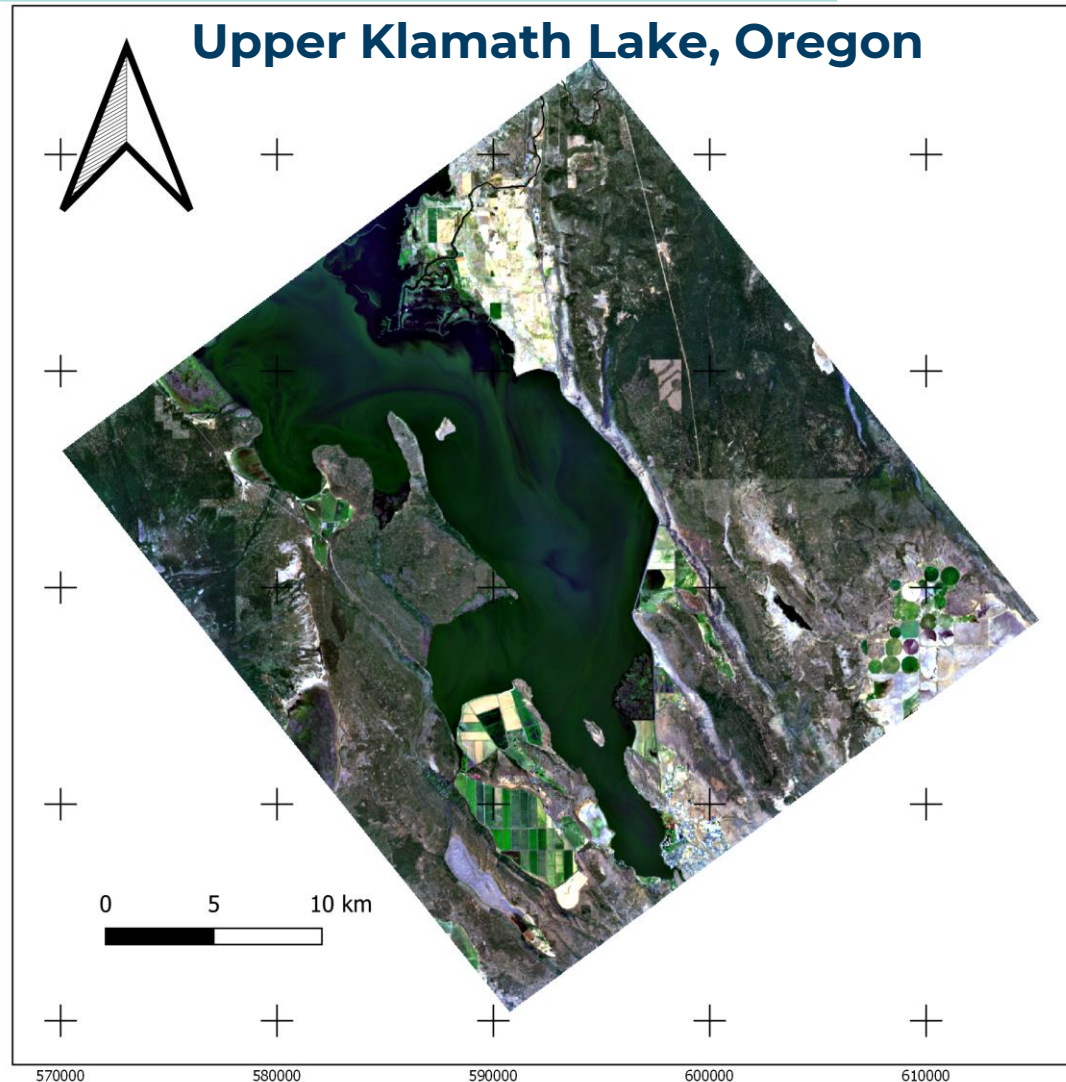


Map of cyanobacteria genera

MAJOR TAKEAWAYS

SMASH application:

- Hyperspectral image



MAJOR TAKEAWAYS

SMASH application:

- Hyperspectral image
- First mask water, ...

UK20200810 contrast-stretched RGB image
R: 650 nm, G: 550.3 nm, B: 470.7 nm

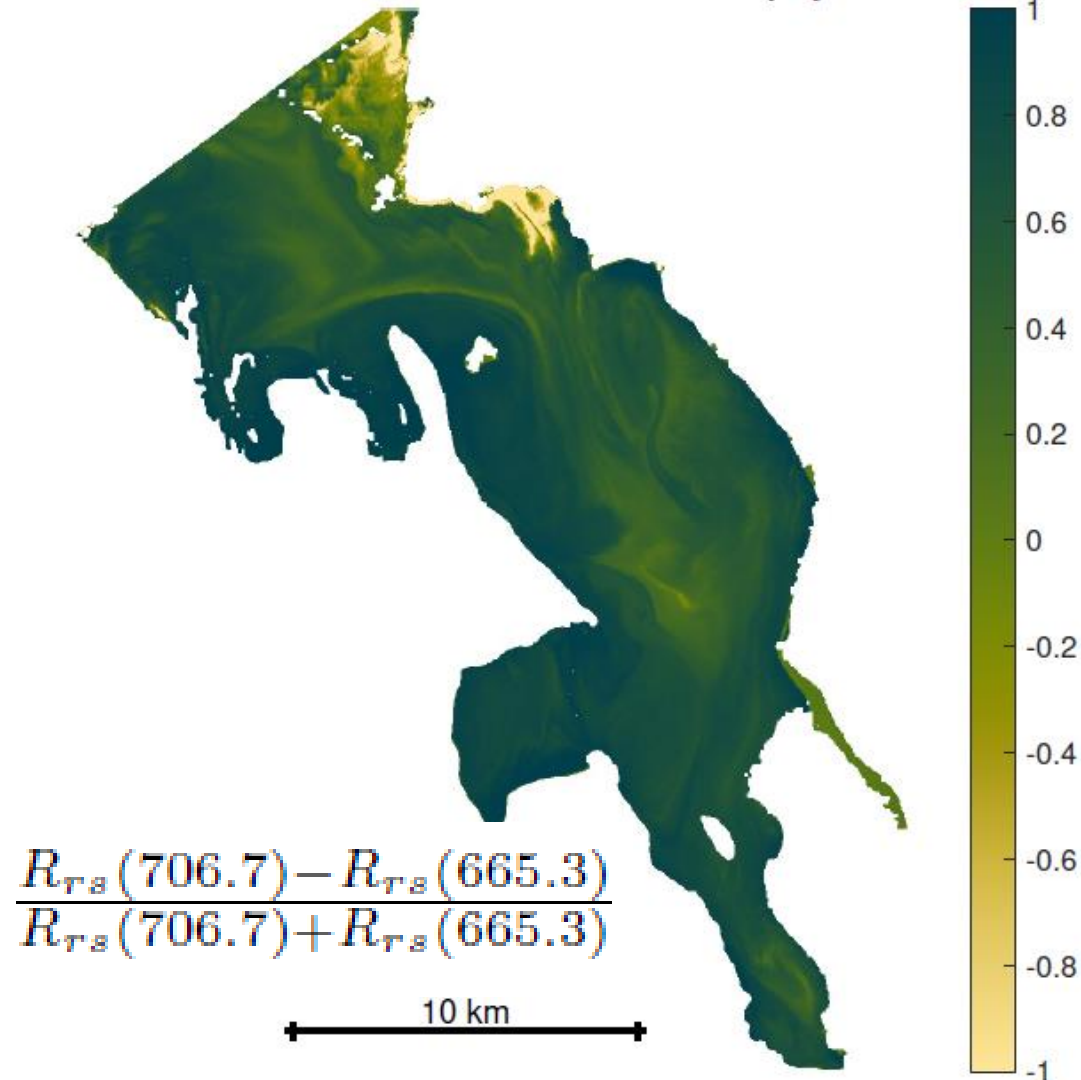


MAJOR TAKEAWAYS

SMASH application:

- Hyperspectral image
- First mask water, ...
- ..., then check for chlorophyll, ...

UK20200810: Normalized Difference Chlorophyll Index

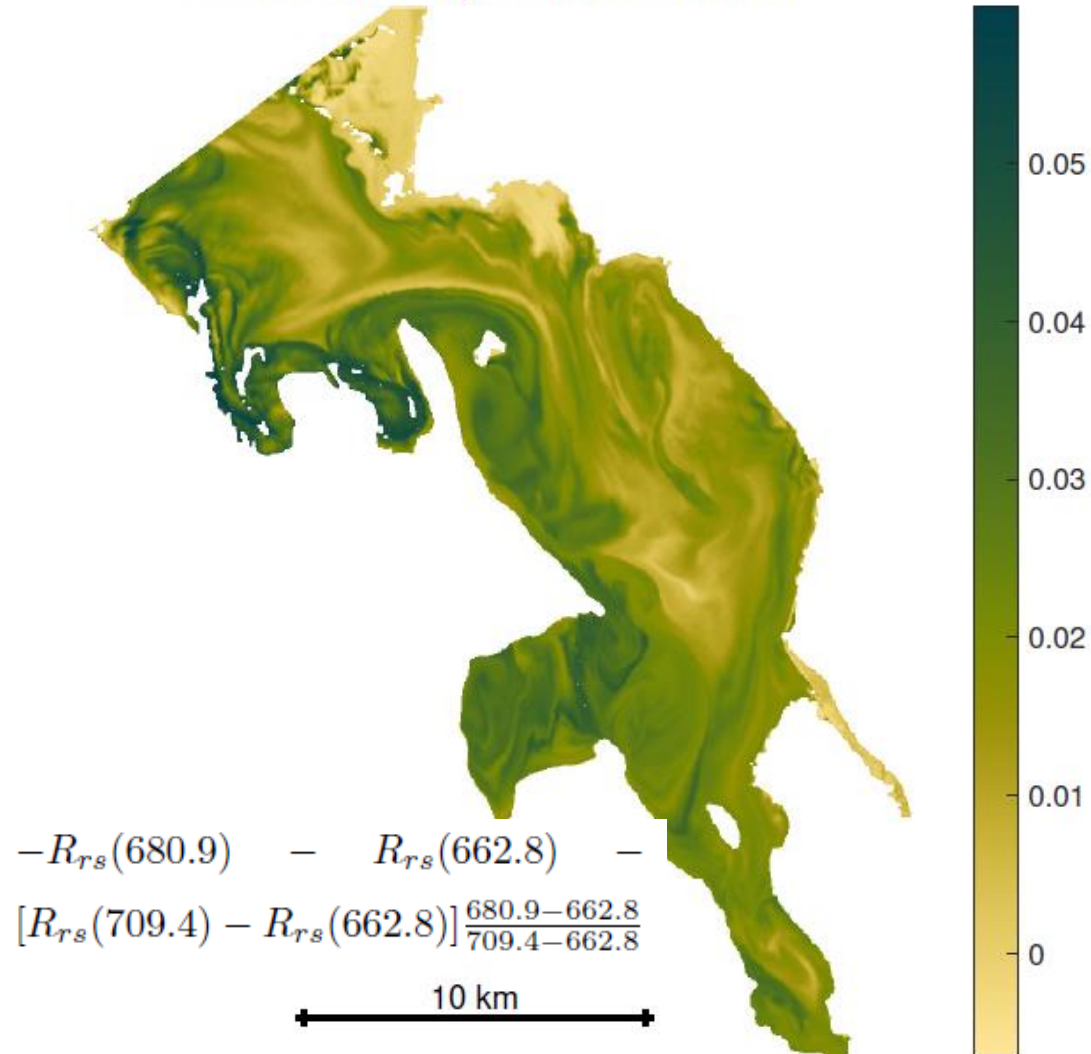


MAJOR TAKEAWAYS

SMASH application:

- Hyperspectral image
- First mask water, ...
- ..., then check for chlorophyll, ...
- ... get a bit more specific with a cyanobacterial index, and ...

UK20200810: Cyanobacterial Index

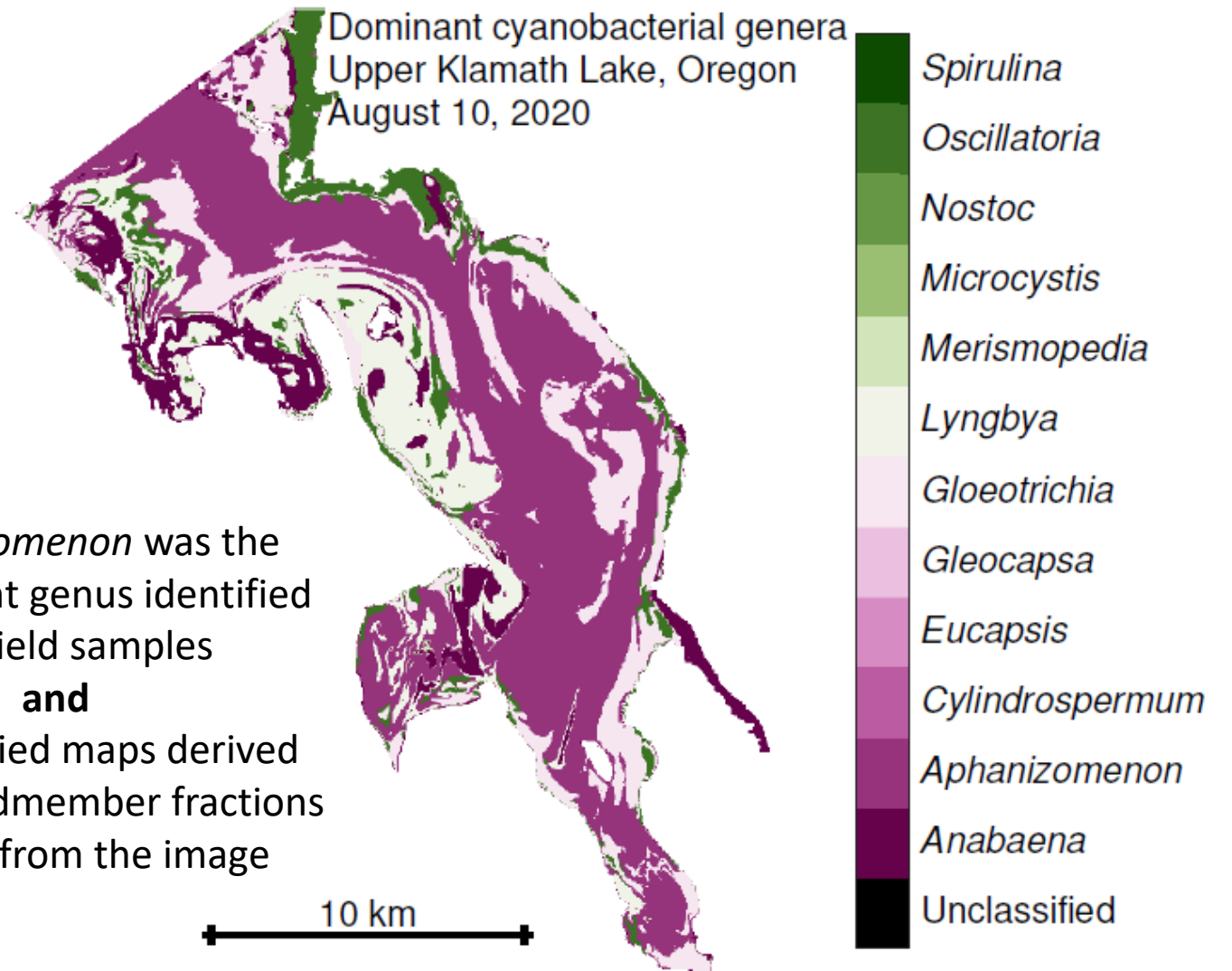


MAJOR TAKEAWAYS

SMASH application:

- Hyperspectral image
- First mask water, ...
- ..., then check for chlorophyll, ...
- ... get a bit more specific with a cyanobacterial index, and ...
- ... then use SMASH to identify which particular genera are present and where

Aphanizomenon was the dominant genus identified in algal field samples
and
in classified maps derived from endmember fractions inferred from the image



ADDITIONAL RELEVANT INFO

What about other taxa?

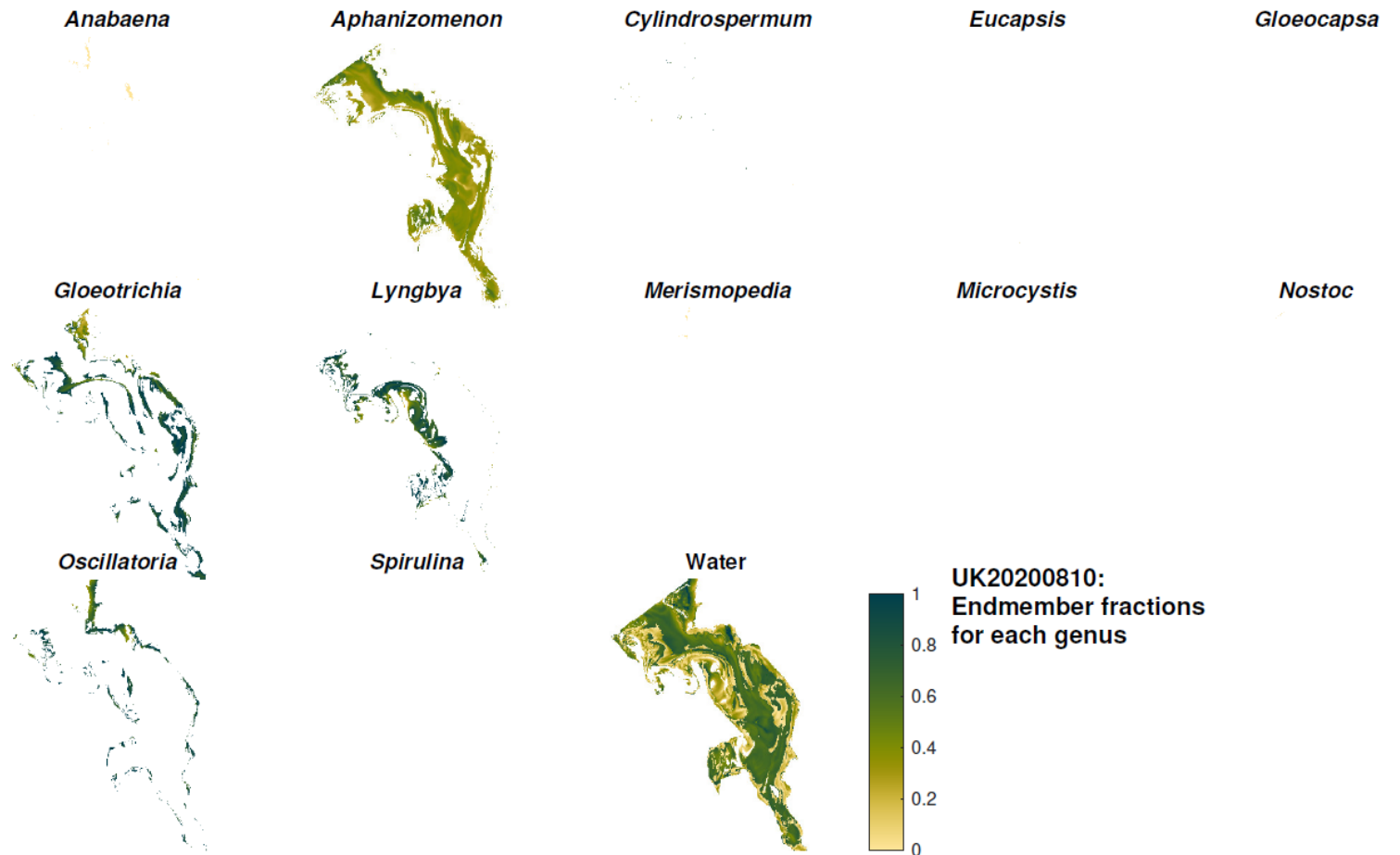
- Multiple endmember spectral mixture analysis (MESMA) provides estimated fractional abundances for each endmember in each pixel



ADDITIONAL RELEVANT INFO

What about other taxa?

- Multiple endmember spectral mixture analysis (MESMA) provides estimated fractional abundances for each endmember in each pixel
- Four genera account for most of the non-negligible fractions: *Aphanizomenon*, *Gloeotrichia*, *Lyngbya*, and *Oscillatoria*

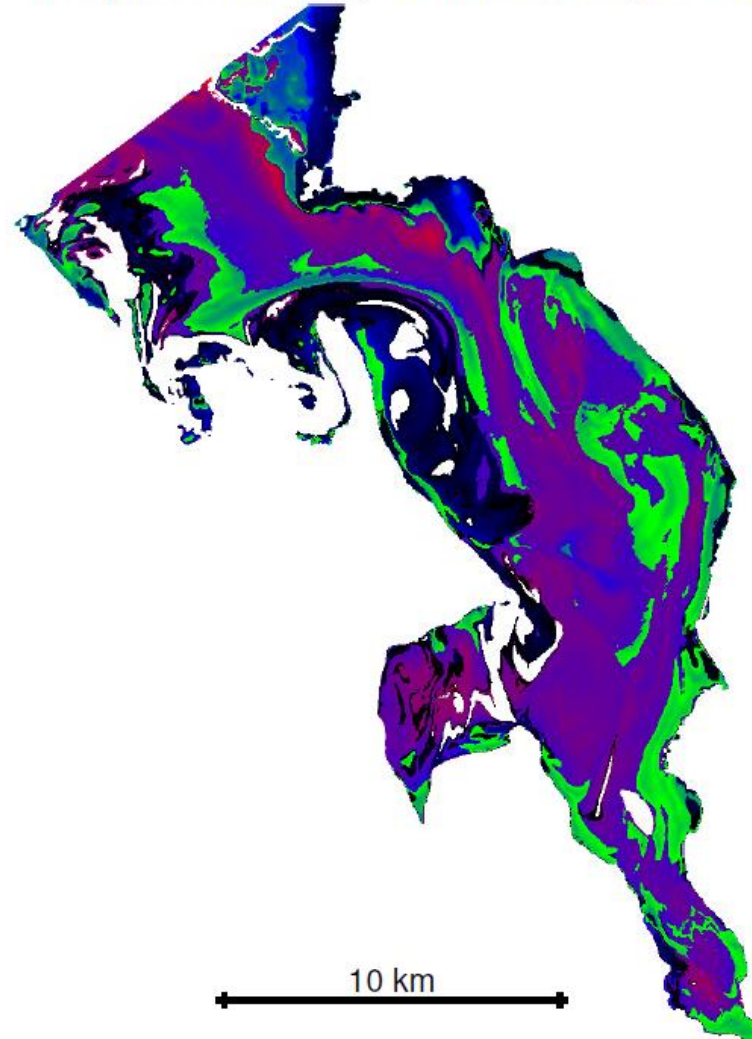


ADDITIONAL RELEVANT INFO

What about other taxa?

- Multiple endmember spectral mixture analysis (MESMA) provides estimated fractional abundances for each endmember in each pixel
- Four genera account for most of the non-negligible fractions: *Aphanizomenon*, *Gloeotrichia*, *Lyngbya*, and *Oscillatoria*
- Fraction images can be combined into a color composite for visualization

UK20200810: Endmember fraction composite:
R: *Aphanizomenon*, G: *Gloeotrichia*, B: Water



RESEARCH PRIORITIES

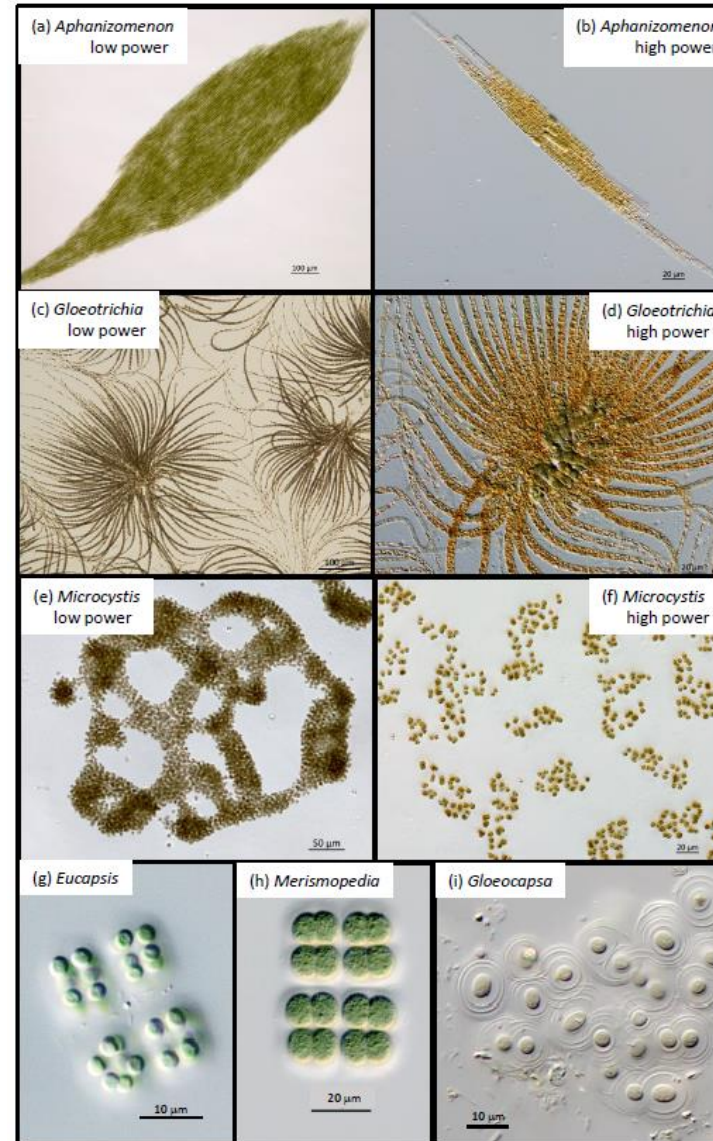
- Enhance blue-green algae monitoring, including time series (longitudinal) as another data point
- Improve blue-green algae field identification
- Determine if and what role environmental conditions have on cyanotoxin levels
- Understand sensor limitations



NEW DATA GAPS

Augment spectral library

First input to SMASH is a spectral library of algal endmembers, so further work is needed to grow the current library by collecting additional field samples to analyze under microscope



Example microscope images for 6 of the 12 genera included in the spectral library, under low or high power as indicated. Planktonic filamentous cyanobacteria include *Aphanizomenon* (a and b) and *Gloeotrichia* (c and d). *Microcystis* (e and f) is a planktonic coccoid cyanobacteria. (g) *Eucapsis*, (h) *Merismopedia*, and (i) *Gloeocapsa* are coccoid cyanobacteria occurring in planktonic or benthic forms.

NEW DATA GAPS

Augment spectral library

First input to SMASH is a spectral library of algal endmembers, so further work is needed to grow the current library by collecting additional field samples to analyze under microscope

Develop end-user software

Ongoing effort to provide a flexible tool to facilitate the application of SMASH

The screenshot displays the SMASH (Spectral Mixture Analysis for Surveillance of Harmful Algal Blooms) software interface. The window title is "SMASH: Spectral Mixture Analysis for Surveillance of Harmful Algal Blooms".

Select input data

Select directory, then load an image, a library, and a water spectrum

Select input data directory | Load *.mat data file from previous session

Hyperspectral image input

Select sensor type: DESIS
Select GeoTIFF image file
Reflectance scale factor: 10000
Site: UK | Date: 20200810
Spectral subset min wvl (nm): 400
Spectral subset max wvl (nm): 800
Create spectral subset
Create rectangular spatial subset

Spectral library input

Select spectral library file
Reflectance scale factor: 1
Add water endmembers to library
Sensor response: DESIS
Convolve spectra to sensor
Savitzky-Golay filter settings
n: 2 | p: 3 | Length: 7
Apply filter to spectral library

Data directory: C:\Users\cjl\OneDrive - DOI\HABS\SMASH\UKL\UK20200810
Image file: DESIS-HSI-L2A-DT0485743928_009-20200810T185658-V0210-S
Library file: HABlabSpecFullDataNoToly.csv
Water file: WaterExtractedFromImage

Data preparation

Image pre-processing

Calculate NDWI
Select masking method
 Automated threshold
 Interactive threshold
 Digitize polygon
 Import shapefile
Create mask

Image filtering

Spectral: Savitzky-Golay settings
n: 2 | p: 3 | Length: 7
Spatial: Wiener smoothing
Window: 3 | Apply filters
Calculate spectral indices

Spectral library selection

Launch spectral library viewer

Class	Plot	Bold
Anabaena	<input checked="" type="checkbox"/>	<input type="checkbox"/>
Aphanizomenon	<input checked="" type="checkbox"/>	<input type="checkbox"/>
Cylindrospermum	<input checked="" type="checkbox"/>	<input type="checkbox"/>
Eucapsis	<input checked="" type="checkbox"/>	<input type="checkbox"/>
Gleocapsa	<input checked="" type="checkbox"/>	<input type="checkbox"/>
Gleotrichia	<input checked="" type="checkbox"/>	<input type="checkbox"/>
Lyngbya	<input checked="" type="checkbox"/>	<input type="checkbox"/>
Merismopedia	<input checked="" type="checkbox"/>	<input type="checkbox"/>
Microcystis	<input checked="" type="checkbox"/>	<input type="checkbox"/>

Export spectral library to file

Display panel controls

Band: 402 | View grayscale | R: 749.7 | G: 650 | B: 550.3 | View RGB | View library

30-Apr-2023 06:11:01: Selected band at 650 nm as green for color display
30-Apr-2023 06:11:06: Selected band at 550.3 nm as blue for color display
30-Apr-2023 06:11:08: Displayed specified image in app window
30-Apr-2023 06:11:08: RGB display of R = 749.7 nm, G = 650 nm, B = 550.3 nm

Save SMASH output

Clear intermediate data fields from memory | Save SMASH session to *.mat data file

The main display area shows a map of a coastal region with a color-coded overlay representing the spectral mixture analysis results. The map axes are Northing (m) and Easting (m), both scaled by $\times 10^5$. The title of the map is $\times 10^6$ UK20200810: R = 749.7 nm, G = 650 nm, B = 550.3 nm.

ACKNOWLEDGEMENTS

Co-authors on paper introducing the SMASH framework:

- Tyler King, USGS Idaho Water Science Center
- Kurt Carpenter, USGS Oregon Water Science Center
- Natalie Hall, USGS MD-DE-DC Water Science Center
- Adam Mumford, USGS Laboratory & Analytical Sciences Division
- Terry Slonecker, USGS National Civil Application Center
- Jennifer Graham, USGS New York Water Science Center
- Victoria Stengel, USGS Oklahoma-Texas Water Science Center
- Nancy Simon, USGS Laboratory & Analytical Sciences Division
- Barry Rosen, Florida Gulf Coast University

Citation:

Legleiter, C. J., King, T. V., Carpenter, K. D., Hall, N. C., Mumford, A. C., Slonecker, T., Graham, J. L., Stengel, V. G., Simon, N., & Rosen, B. H. (2022). Spectral mixture analysis for surveillance of harmful algal blooms (SMASH): A field-, laboratory-, and satellite-based approach to identifying cyanobacteria genera from remotely sensed data. *Remote Sensing of Environment*, 279, 113089.

<https://doi.org/https://doi.org/10.1016/j.rse.2022.113089>

