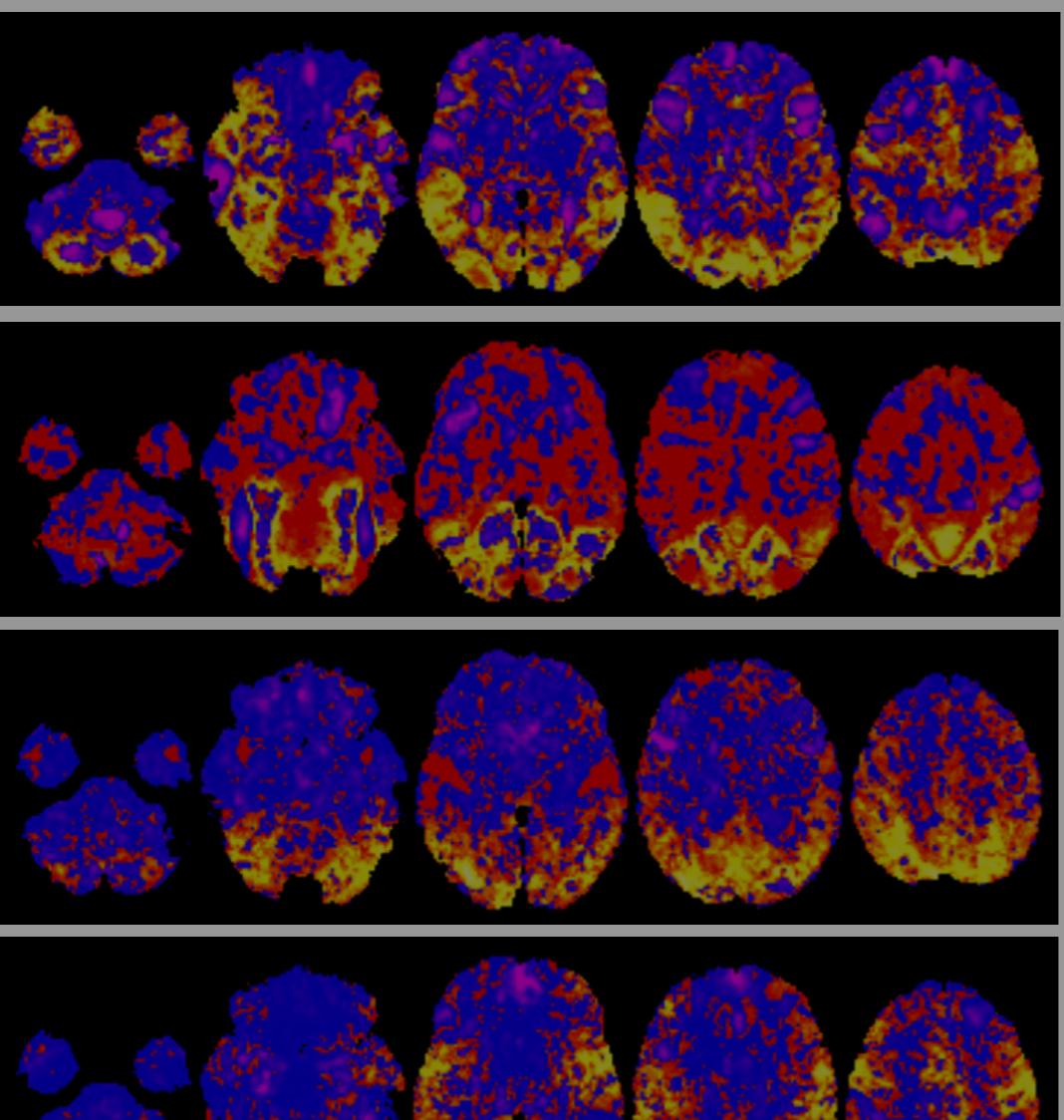
 **BioImage Suite** [Web](#)  
fast & portable image analysis



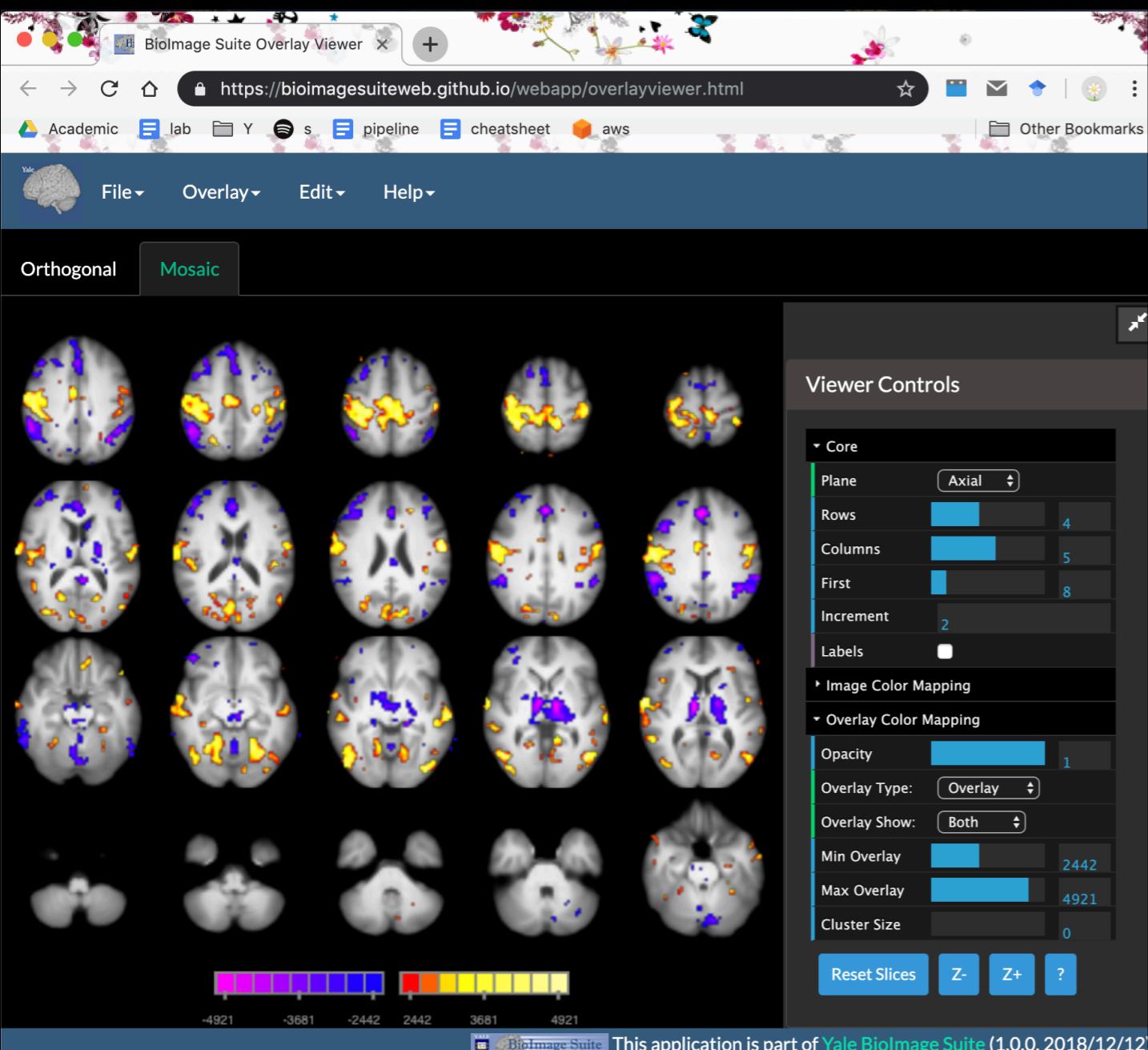
# INTRODUCING BIOIMAGE SUITE WEB

STEPHANIE NOBLE  
YALE UNIVERSITY

# OVERVIEW



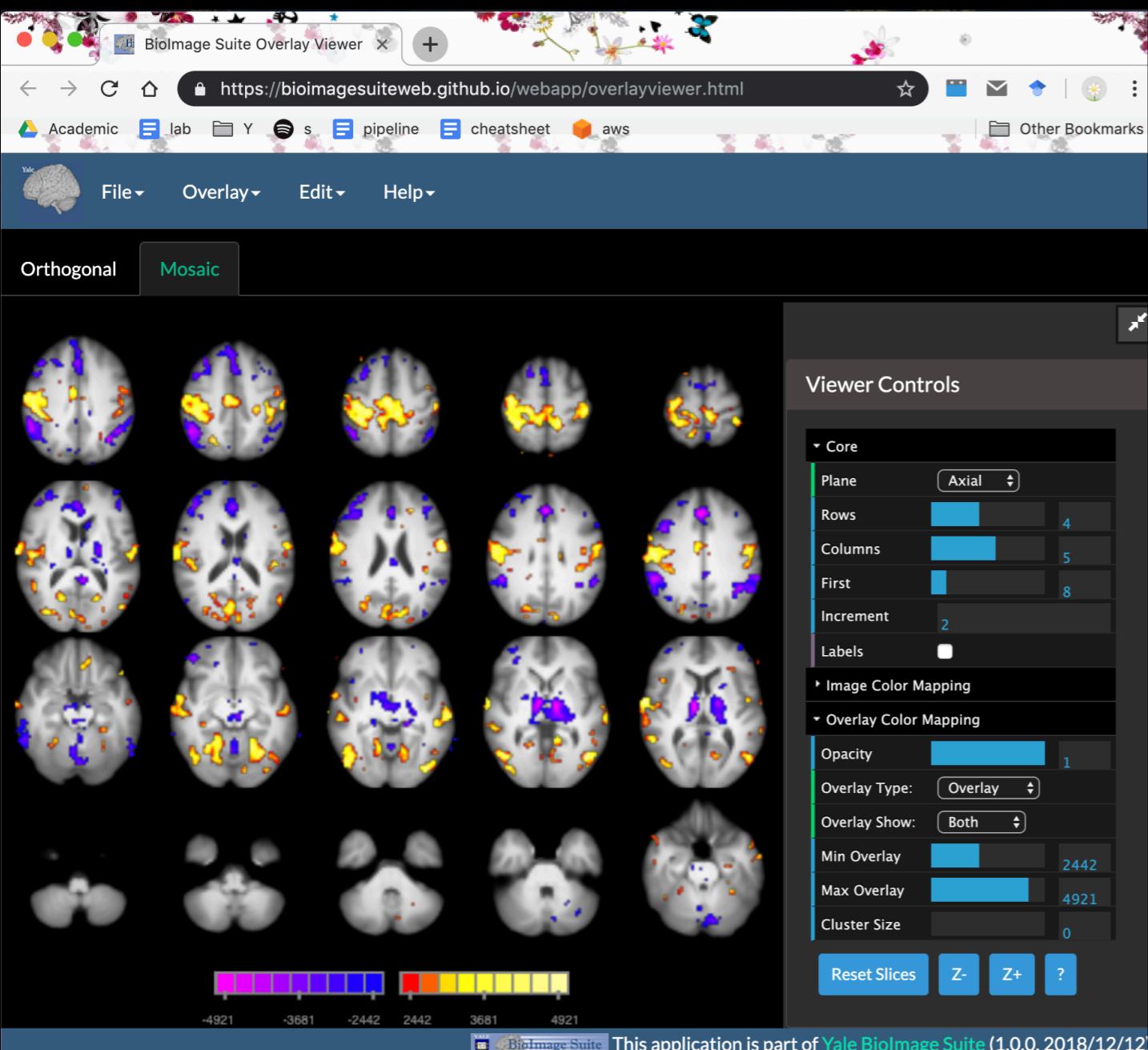
# OVERVIEW



- Web-based application



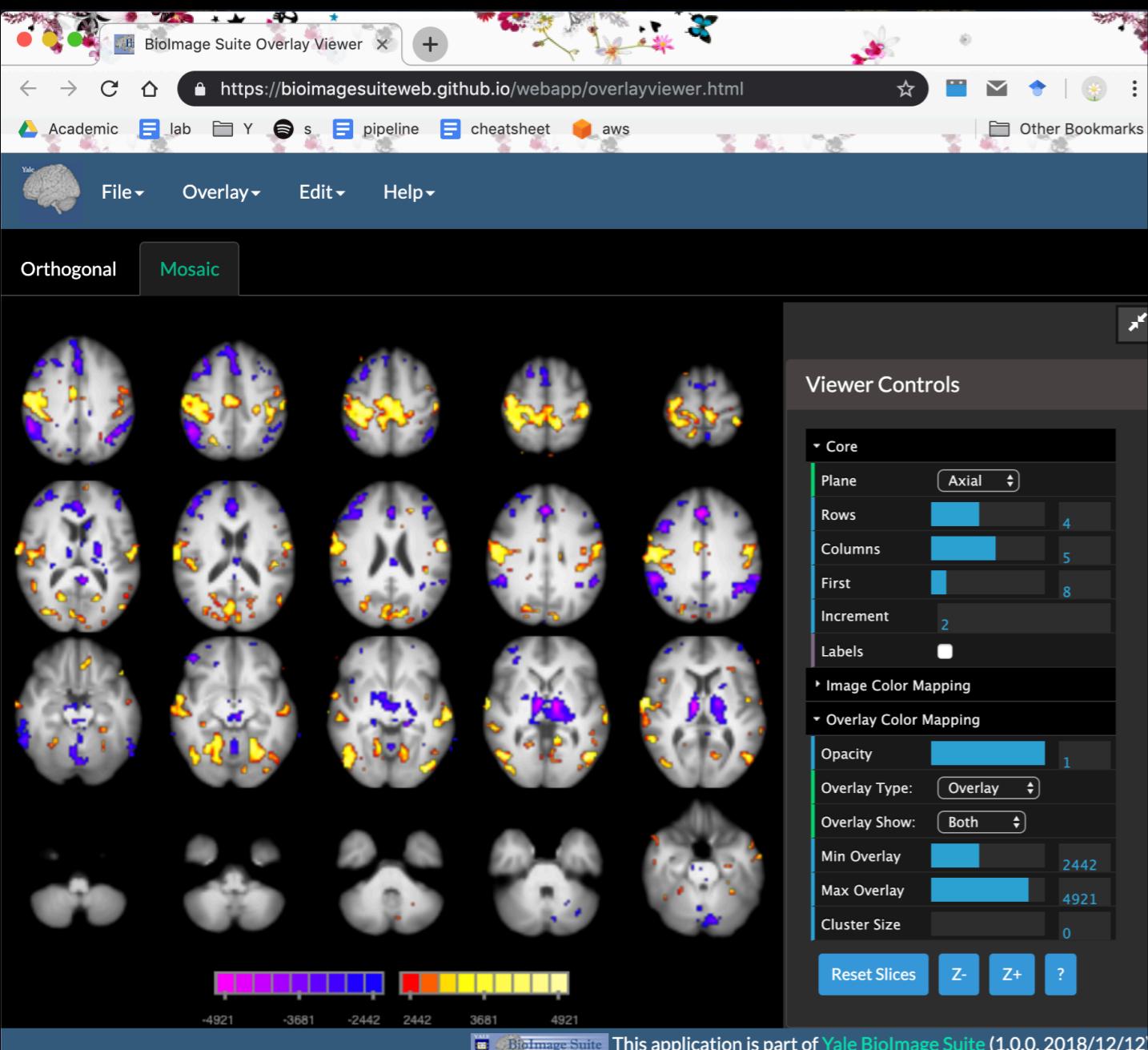
# OVERVIEW



- Web-based application
- Easy-to-use yet powerful



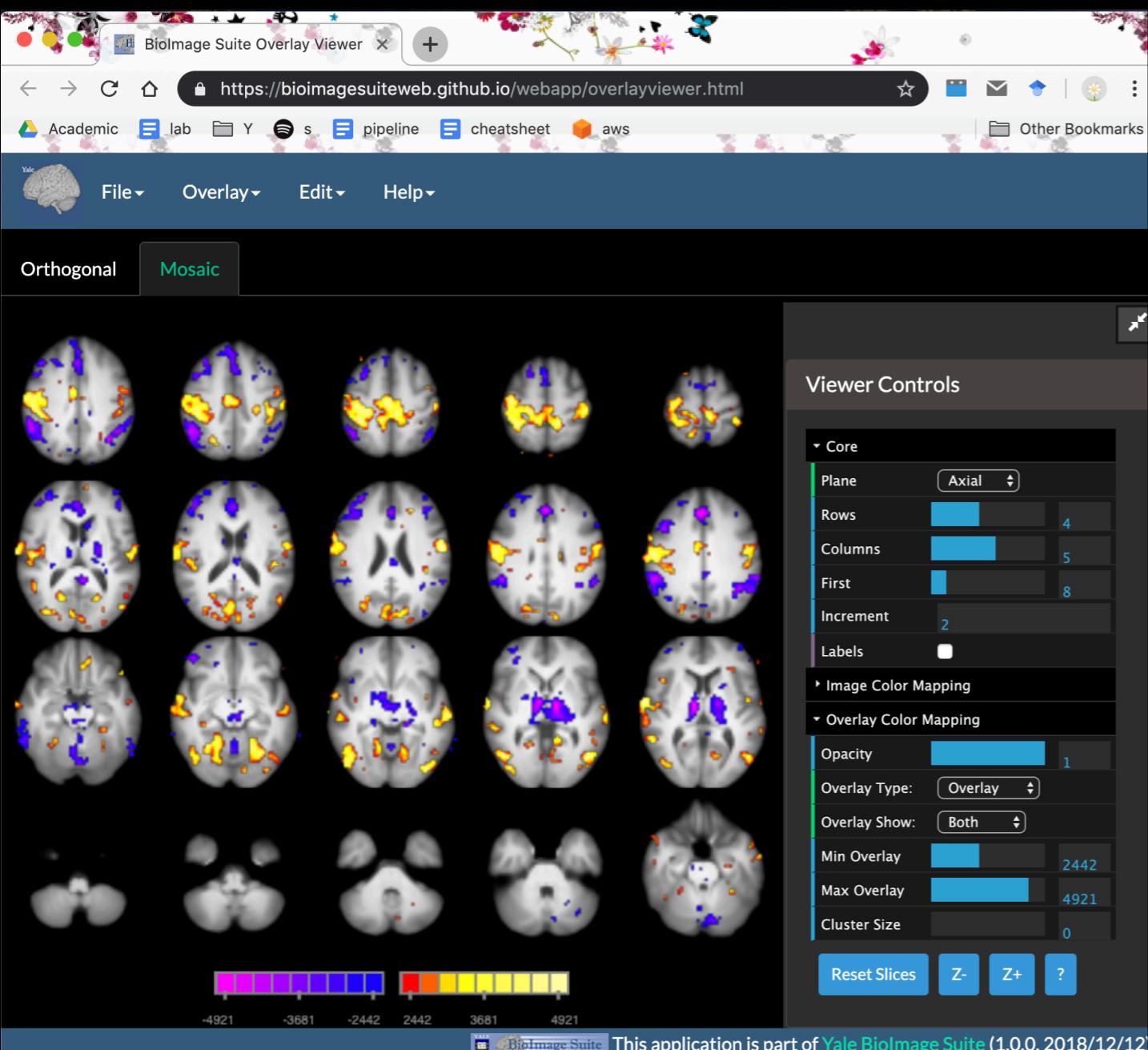
# OVERVIEW



- Web-based application
- Easy-to-use yet powerful
- No installation!



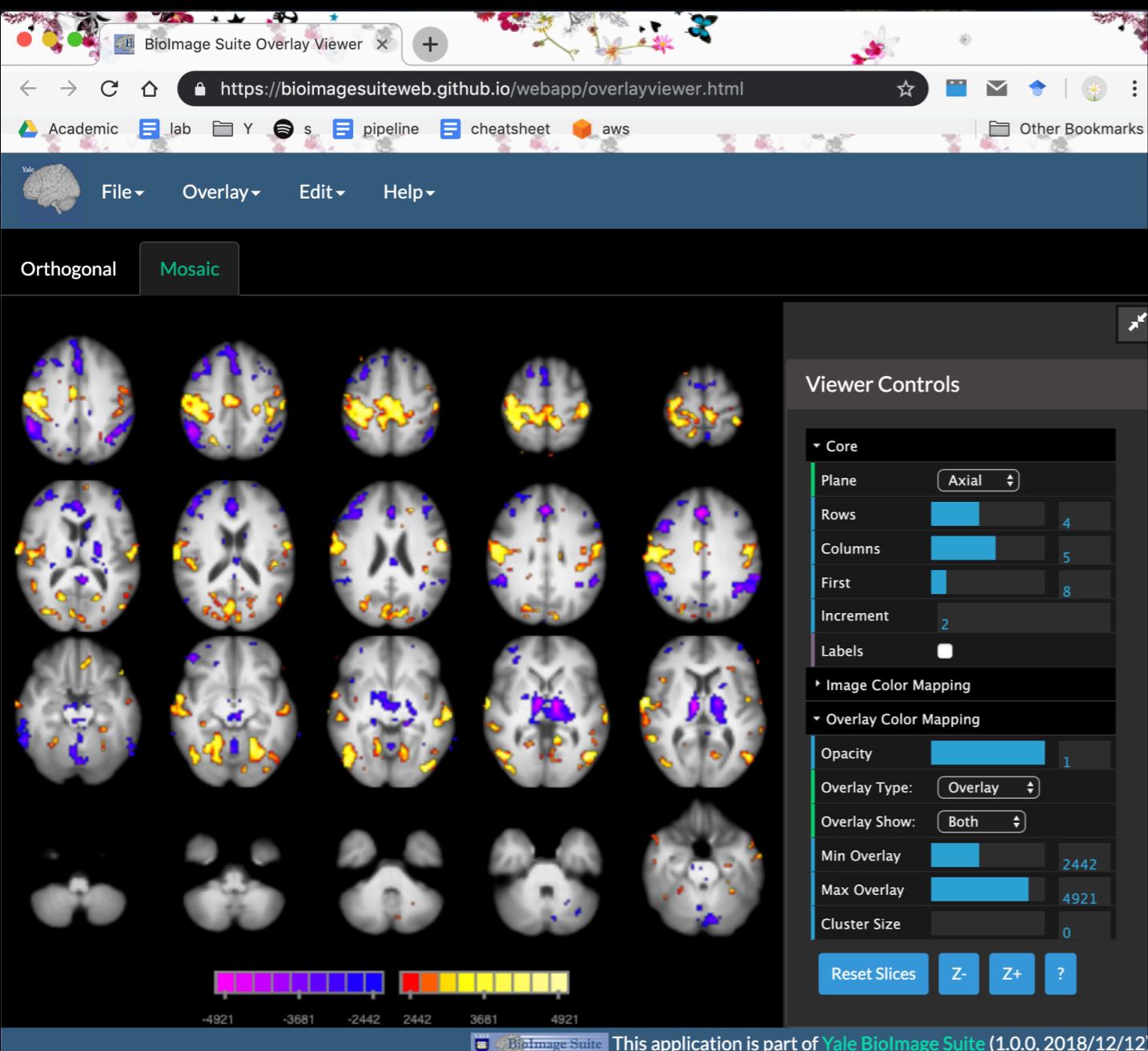
# OVERVIEW



- Web-based application
- Easy-to-use yet powerful
- No installation!
- No servers! All local processing



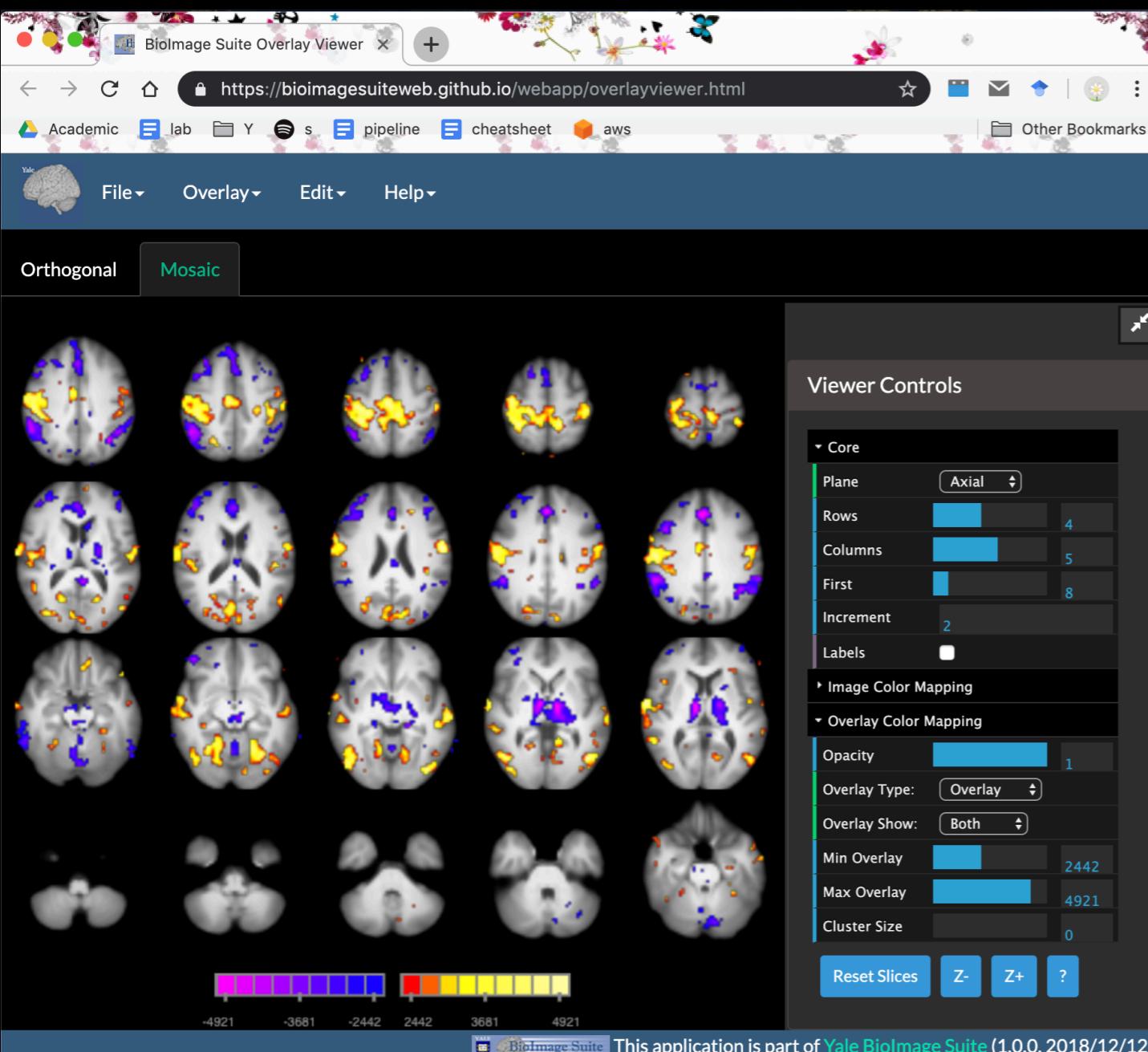
# OVERVIEW



- Web-based application
- Easy-to-use yet powerful
- No installation!
- No servers! All local processing
- Novel architecture & features



# OVERVIEW



- Web-based application
- Easy-to-use yet powerful
- No installation!
- No servers! All local processing
- Novel architecture & features

[Introduction video](#)

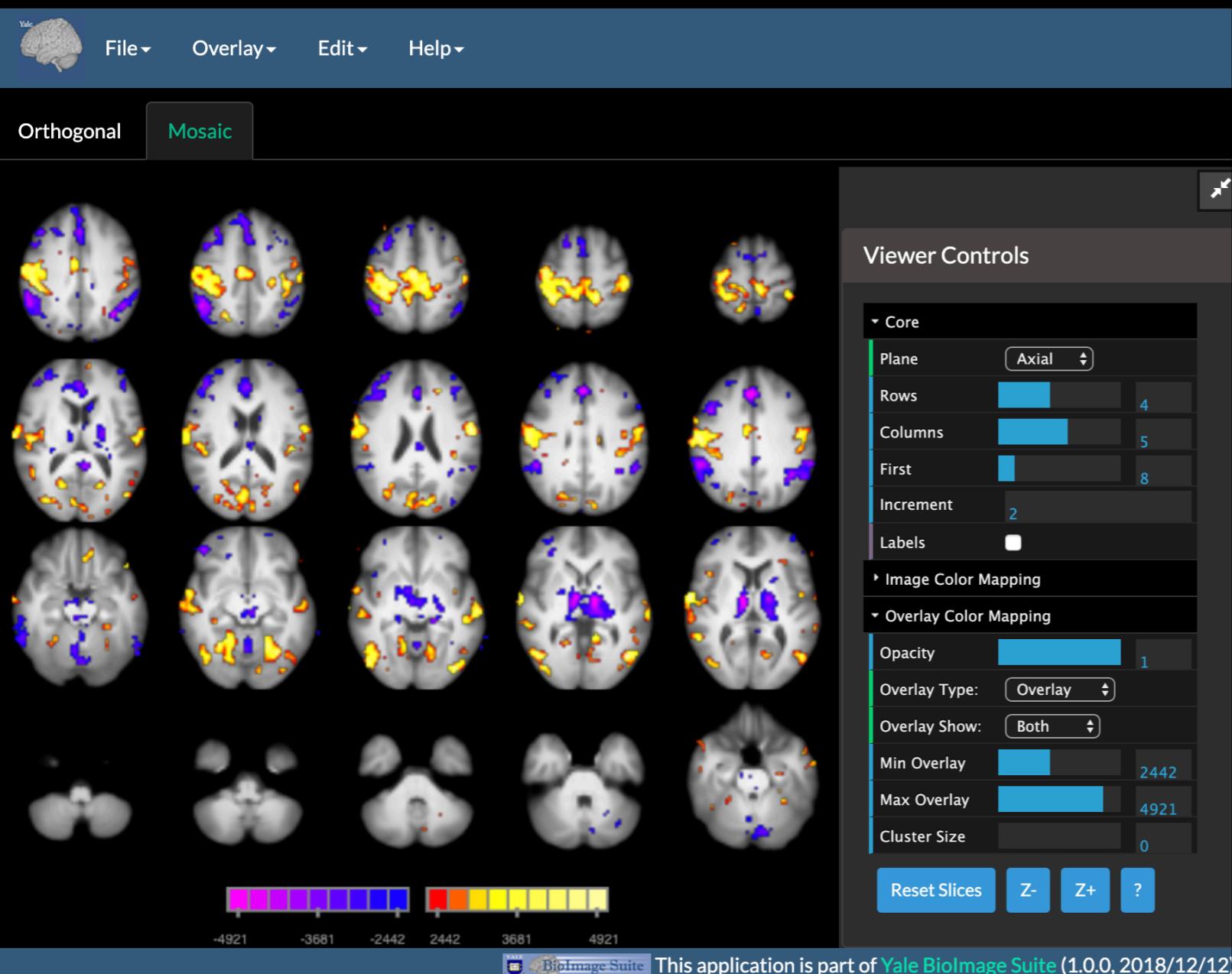


Follow along in the app:



# OVERLAY VIEWER

## Overlay Viewer



BioImage Suite

bioimagesuite.org

This application is part of Yale BioImage Suite (1.0.0, 2018/12/12)

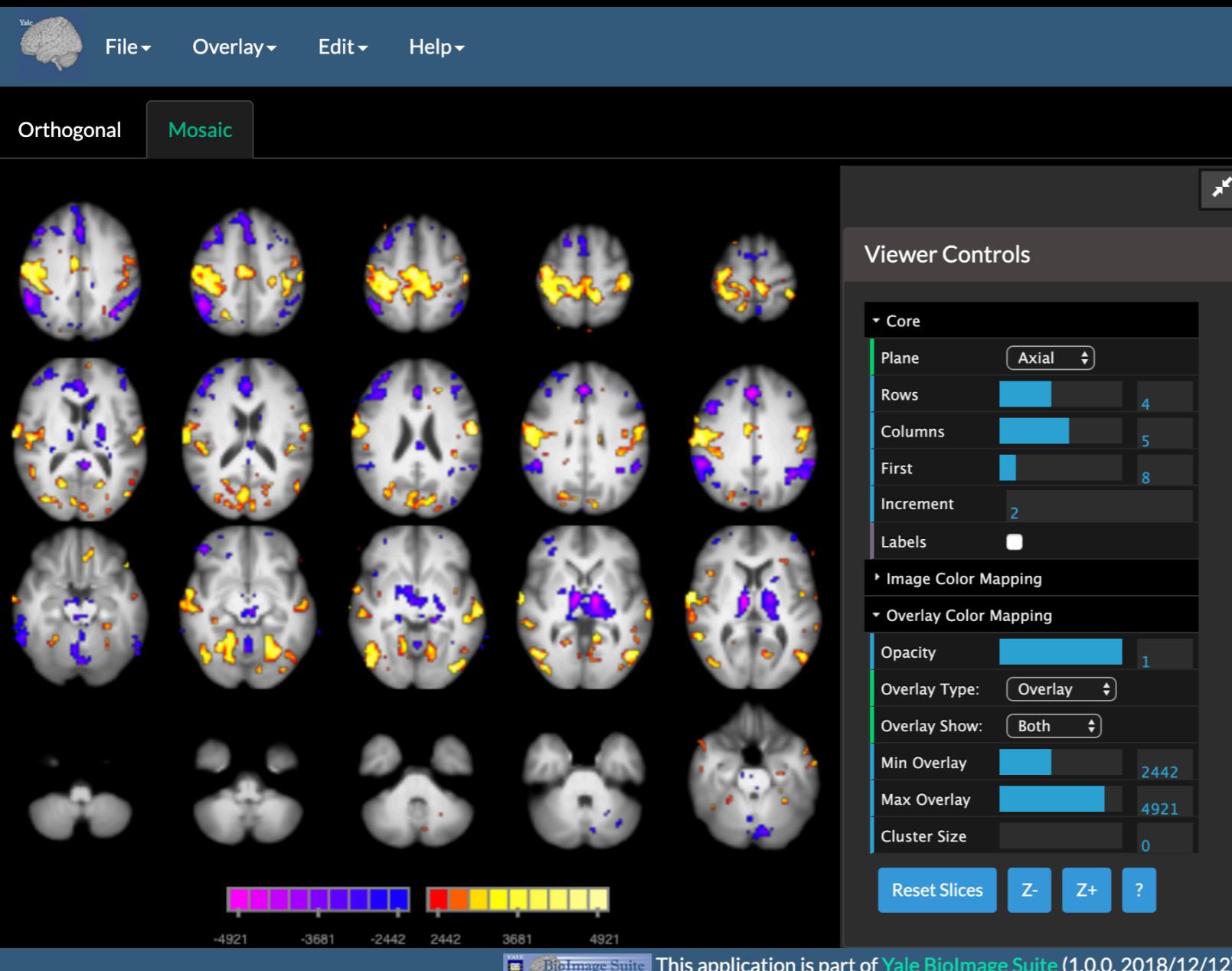


Follow along in the app:



# OVERLAY VIEWER

## Overlay Viewer



Directions

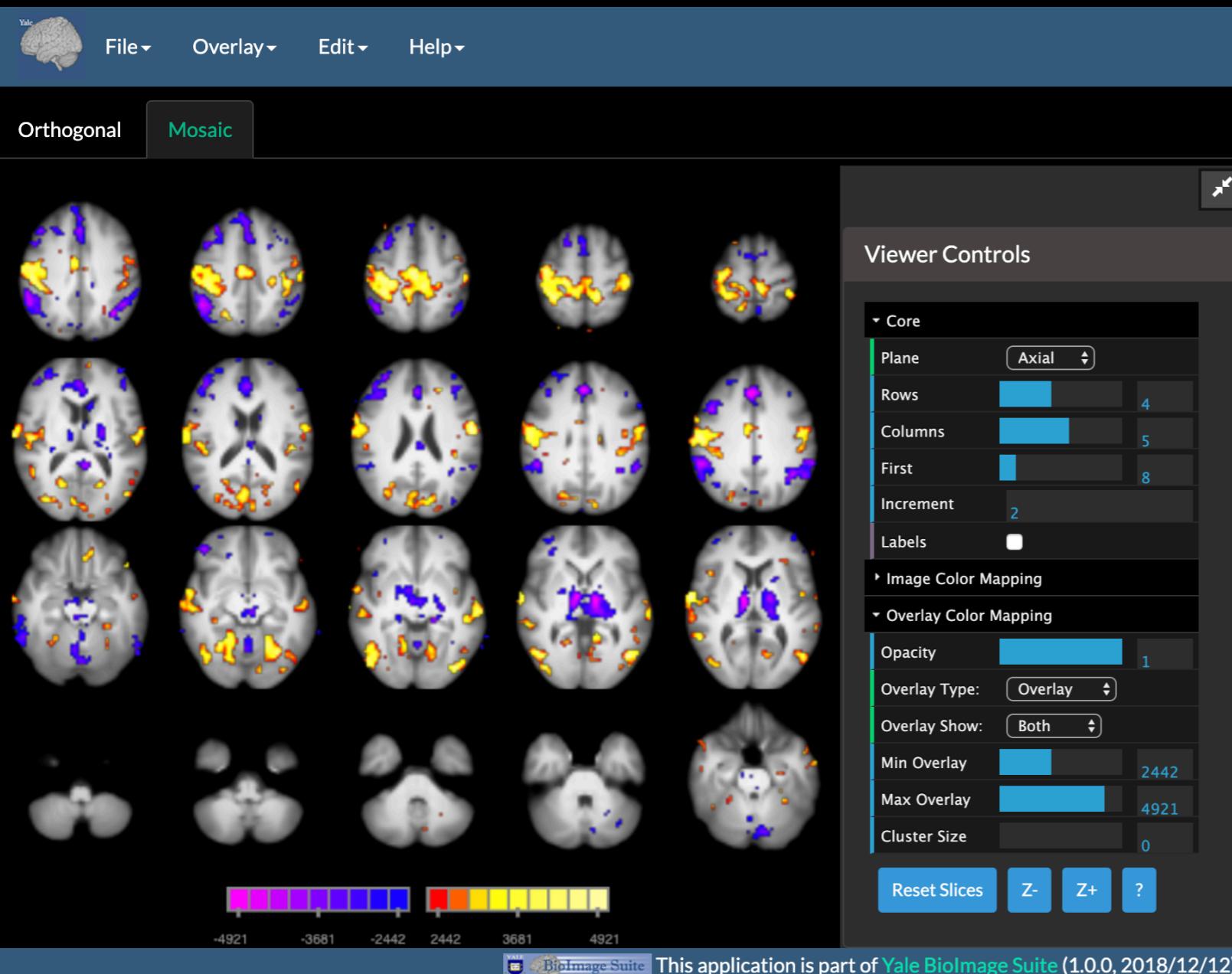
[www.bioimagesuite.org](http://www.bioimagesuite.org)



[www.bioimagesuite.org](http://www.bioimagesuite.org)

# OVERLAY VIEWER

## Overlay Viewer



## Directions

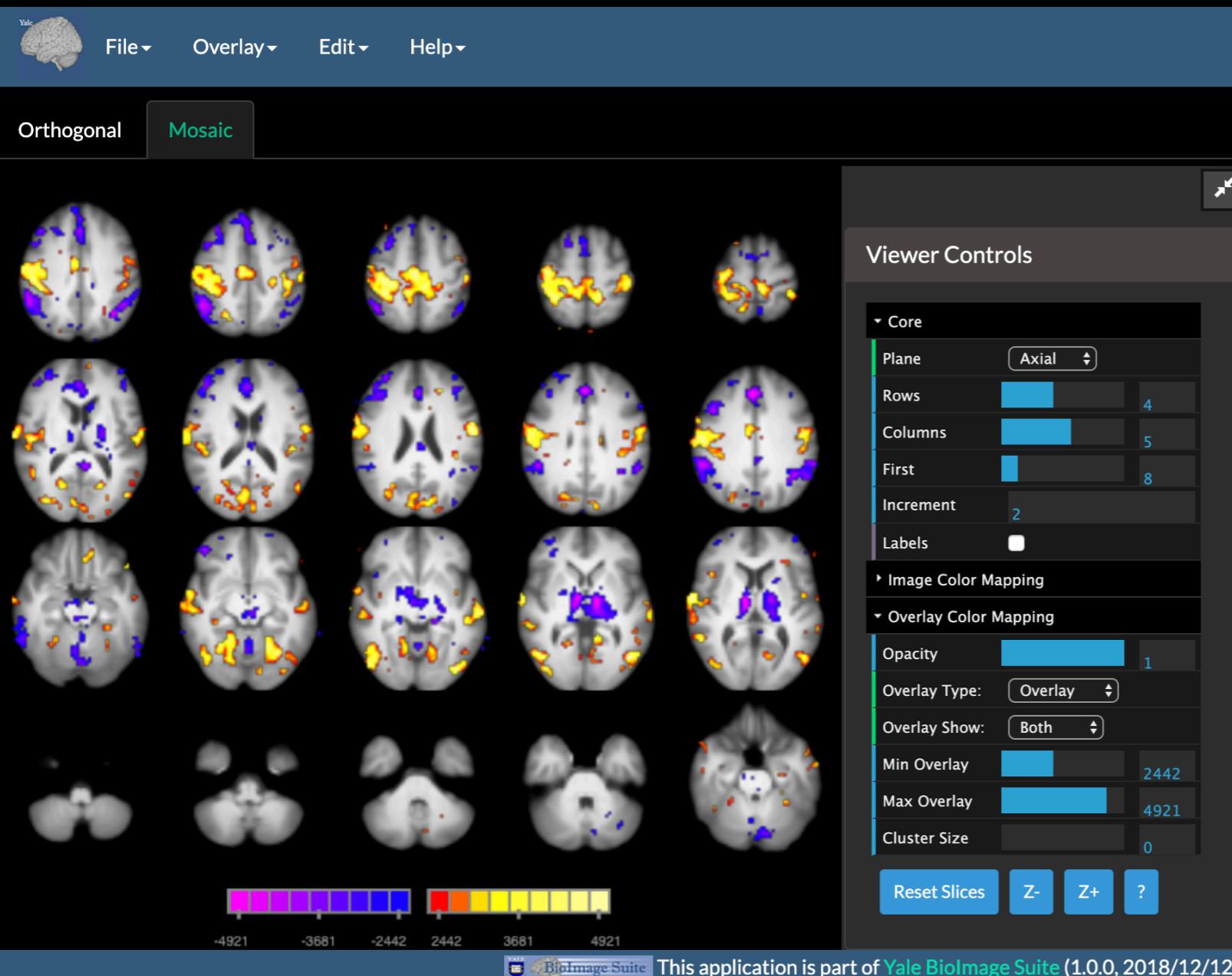
1. Applications > Overlay Viewer




[www.bioimagesuite.org](http://www.bioimagesuite.org)

# OVERLAY VIEWER

## Overlay Viewer



## Directions

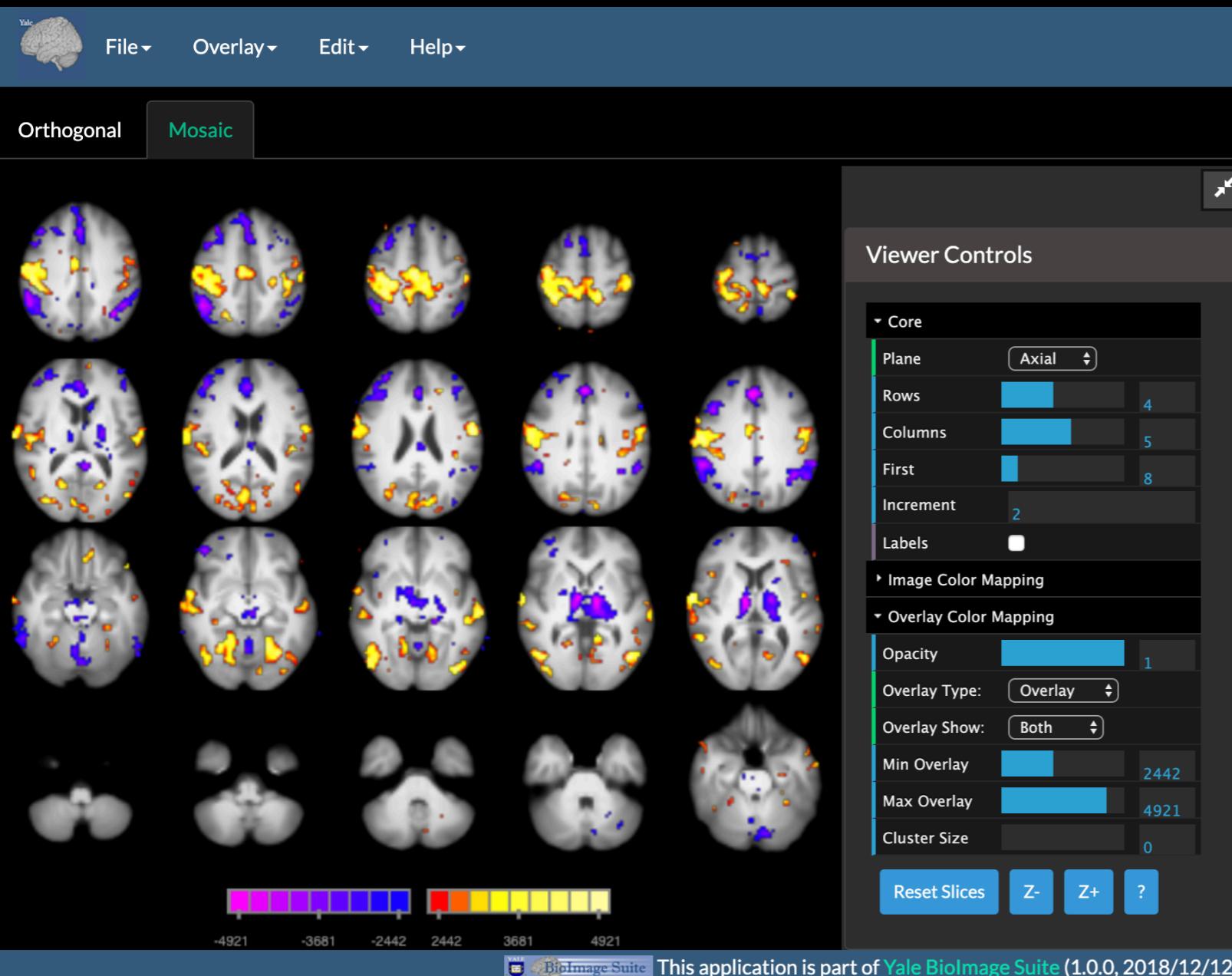
1. Applications > Overlay Viewer
2. Load Image and Overlay Data




[www.bioimagesuite.org](http://www.bioimagesuite.org)

# OVERLAY VIEWER

## Overlay Viewer



## Directions

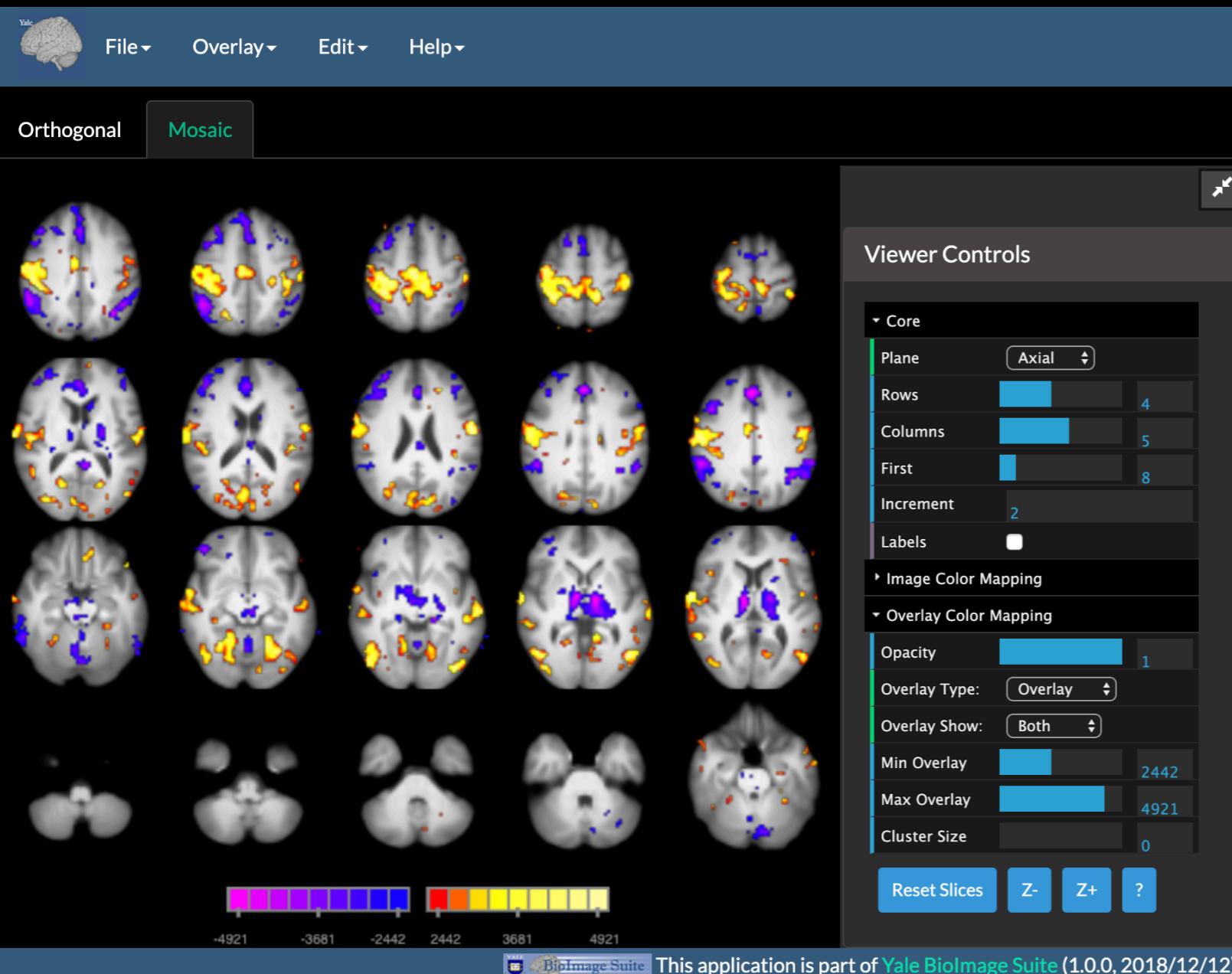
1. Applications > Overlay Viewer
2. Load Image and Overlay Data
  1. For Demo: Help > Load Sample Data




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# OVERLAY VIEWER

## Overlay Viewer



## Directions

1. Applications > Overlay Viewer
2. Load Image and Overlay Data
  1. For Demo: Help > Load Sample Data
3. Play with Viewer Controls: Image Colors, Orthogonal v. Mosaic, etc.

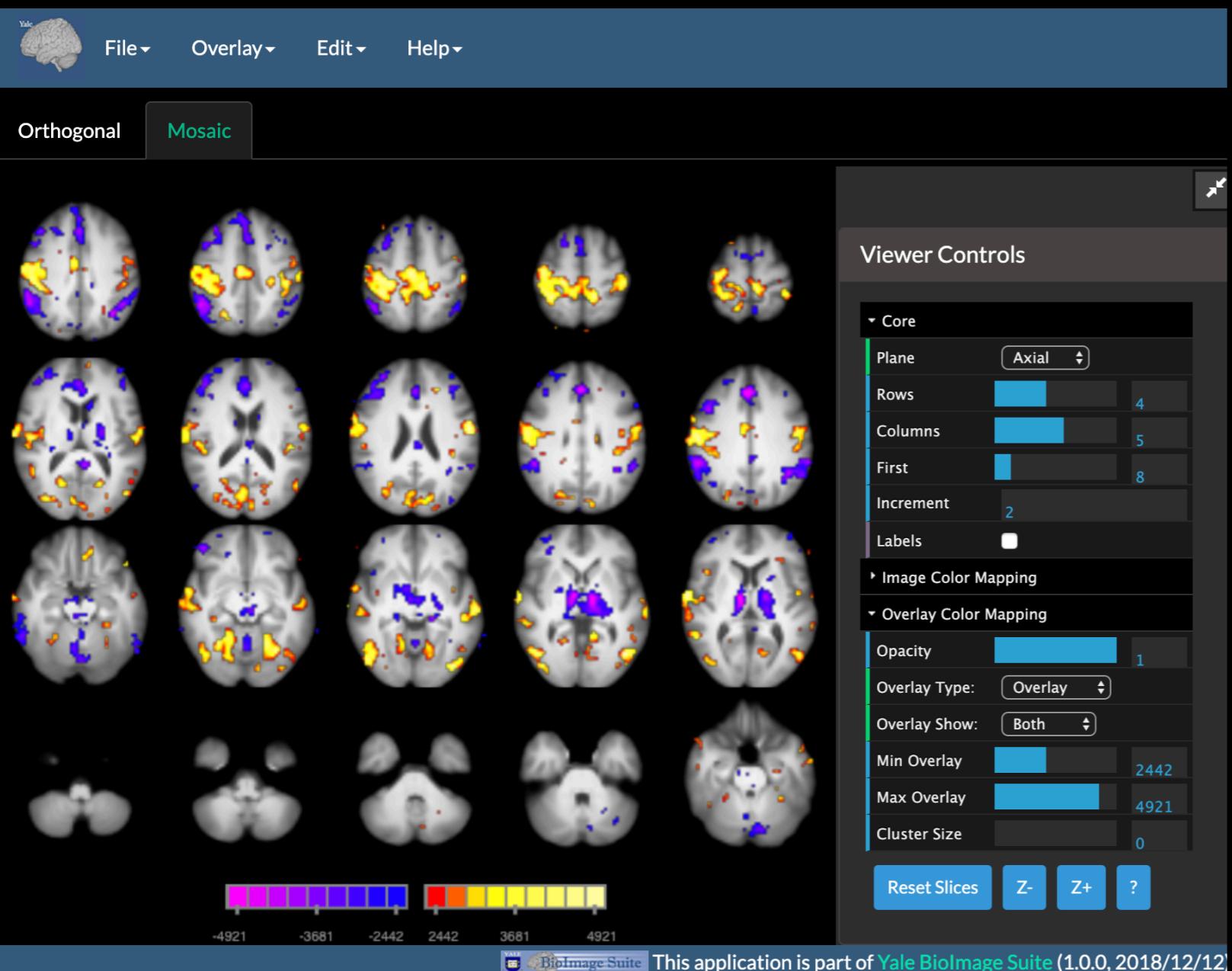


Follow along in the app:



# LIVE FIGURES!

## Overlay Viewer



Follow along in the app:

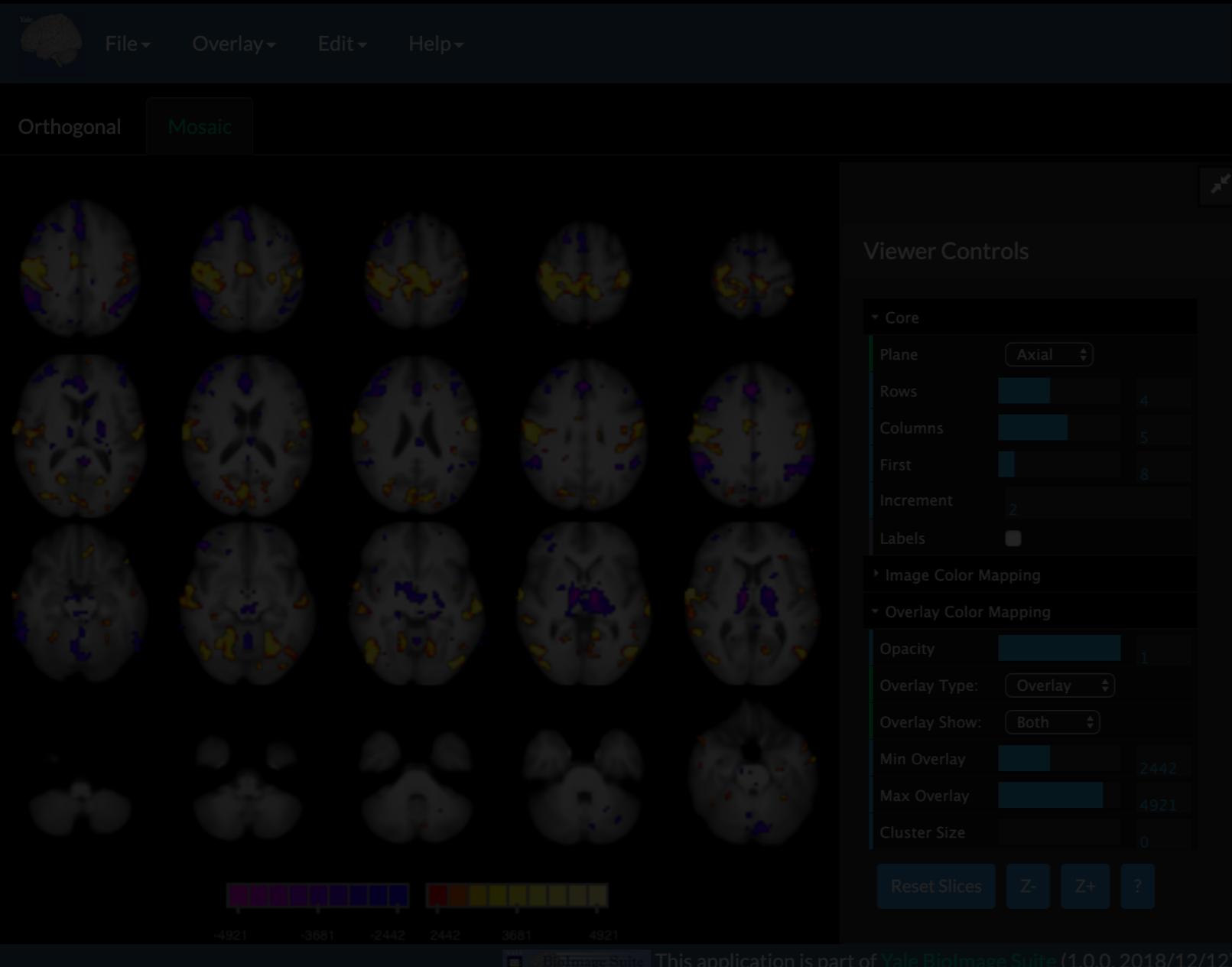


[www.bioimagesuite.org](http://www.bioimagesuite.org)

# LIVE FIGURES! ↵

Full application state + data

Overlay Viewer



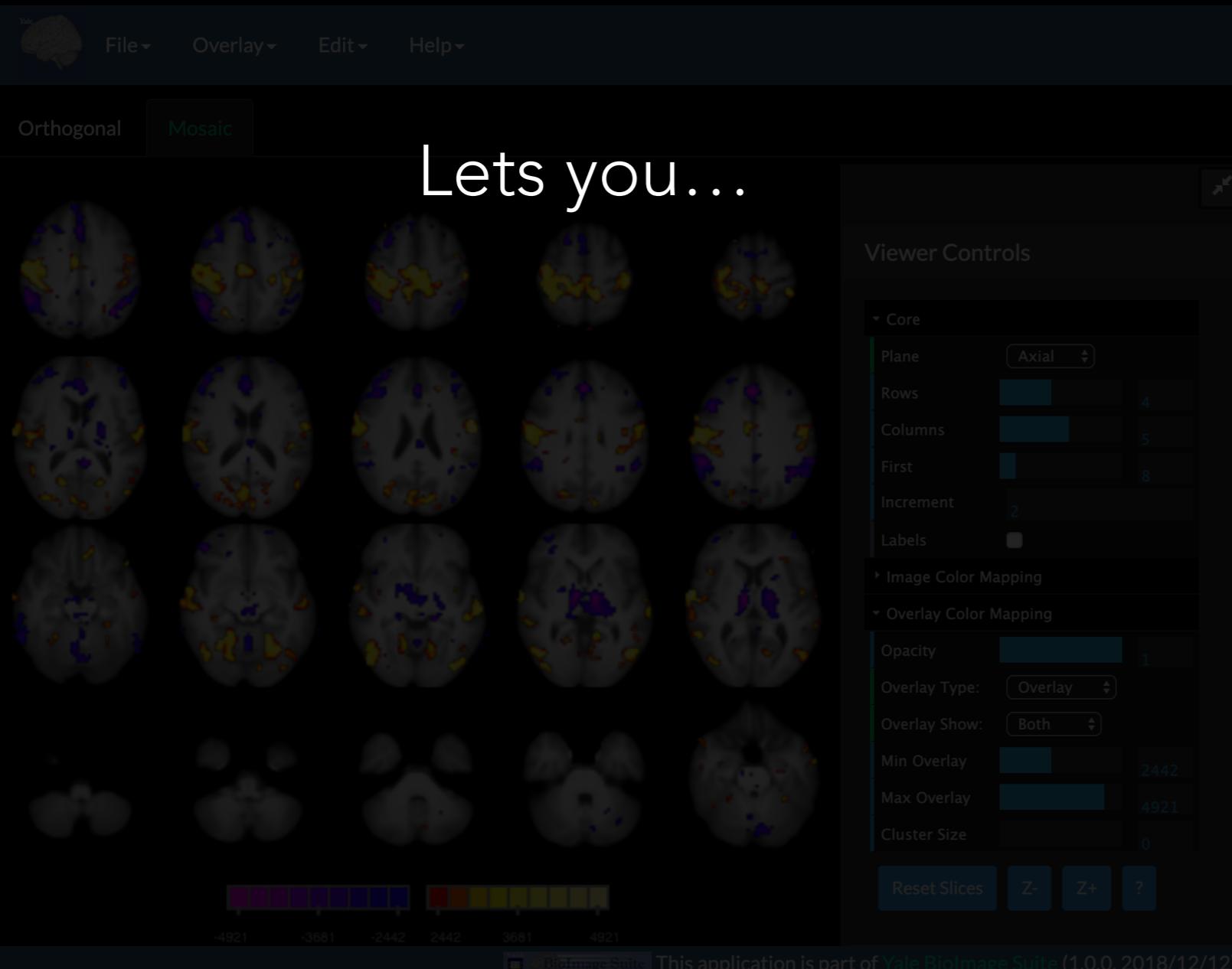
Follow along in the app:



# LIVE FIGURES! ↵

Full application state + data

Overlay Viewer

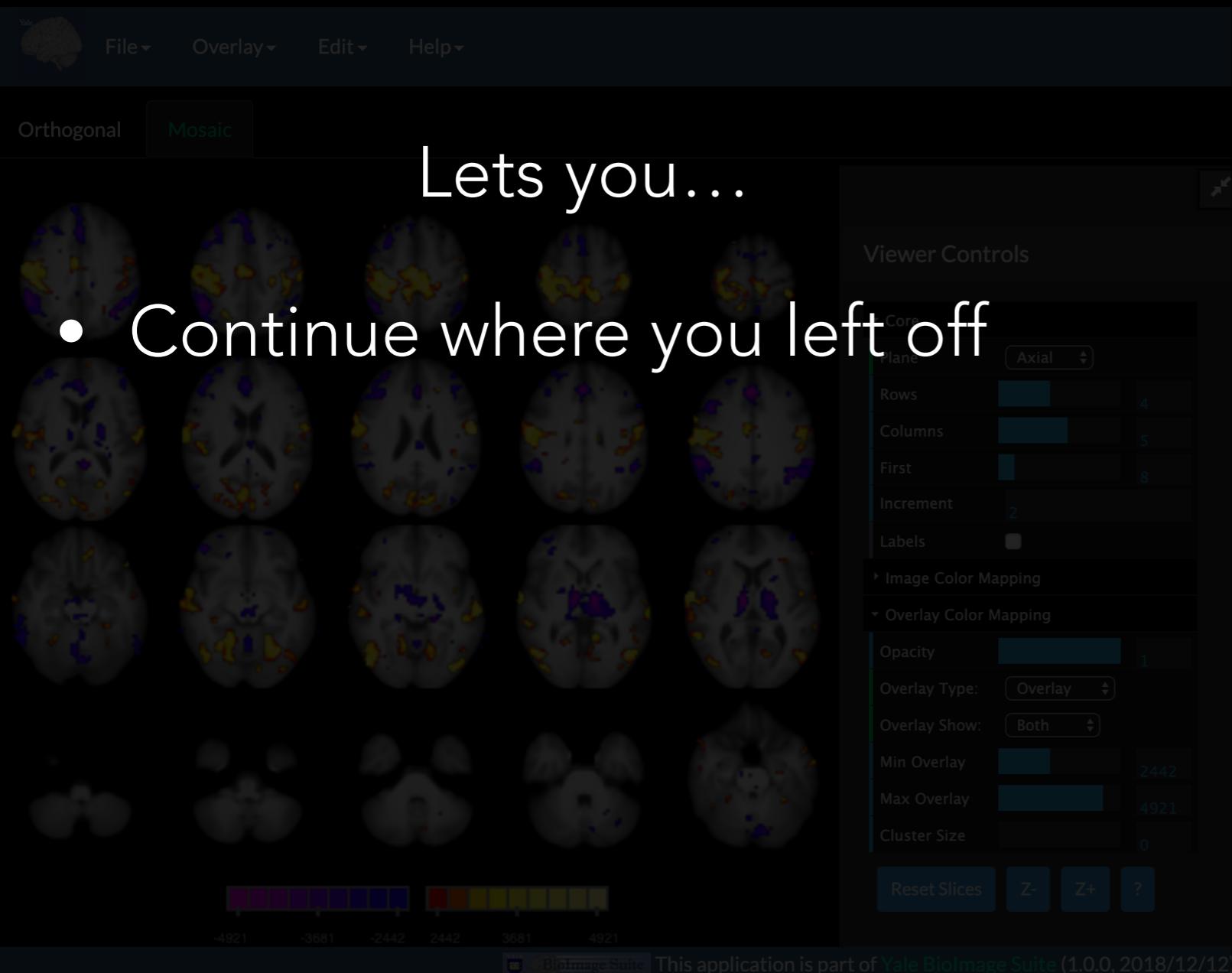




# LIVE FIGURES! ↵

Full application state + data

Overlay Viewer





# LIVE FIGURES! ↗

Full application state + data

Overlay Viewer

The screenshot shows the Overlay Viewer application interface. At the top, there's a menu bar with 'File', 'Overlay', 'Edit', and 'Help'. Below the menu, there are two tabs: 'Orthogonal' (selected) and 'Mosaic'. The main area displays a grid of brain slices, each showing a different overlay pattern. A large text box in the center says 'Lets you...'. To the right of the slices is a 'Viewer Controls' panel. This panel includes a dropdown for 'Plane' set to 'Axial', a section for 'Labels' with a 'Labels' button, and sections for 'Image Color Mapping' and 'Overlay Color Mapping'. Under 'Overlay Color Mapping', there are sliders for 'Opacity' (set to 1), 'Overlay Type' (set to 'Overlay'), 'Overlay Show' (set to 'Both'), and 'Cluster Size' (set to 0). There are also sliders for 'Min Overlay' (set to 2442) and 'Max Overlay' (set to 4921). At the bottom of the controls panel are buttons for 'Reset Slices', 'Z-', 'Z+', and '?'. At the very bottom of the screen, there's a footer bar with the BioImage Suite logo and the text 'This application is part of Yale BioImage Suite (1.0.0, 2018/12/12)'.

- Continue where you left off
- Share with others (collaborators, publications, etc.)





[www.bioimagesuite.org](http://www.bioimagesuite.org)

# LIVE FIGURES! ↗

Full application state + data

Overlay Viewer

The screenshot shows a dark-themed application window titled "Overlay Viewer". At the top, there's a menu bar with "File", "Overlay", "Edit", and "Help". Below the menu, there are two tabs: "Orthogonal" and "Mosaic", with "Mosaic" currently selected. The main area displays a grid of several brain slices, each showing a different overlay pattern. To the right of the slices is a "Viewer Controls" panel. This panel includes a dropdown for "Plane" set to "Axial", a section for "Labels" with a dropdown for "Core", and sections for "Image Color Mapping" and "Overlay Color Mapping". Under "Overlay Color Mapping", there are sliders for "Opacity" (set to 1), "Overlay Type" (set to "Overlay"), and "Overlay Show" (set to "Both"). There are also sections for "Max Overlay" (set to 2442) and "Cluster Size" (set to 0). At the bottom of the controls panel are buttons for "Get Slices", "Z+", and "?". The footer of the application window contains the text "BioImage Suite" and "This application is part of Yale BioImage Suite (1.0.0, 2018/12/12)".

Lets you...

- Continue where you left off
- Share with others (collaborators, publications, etc.)
  - now they too can dynamically change views, thresholds, etc.





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# LIVE FIGURES! ↗

Full application state + data

Overlay Viewer

The screenshot shows a grid of brain slices with various overlays. A central text box says "Lets you..." followed by a bulleted list. To the right is a "Viewer Controls" panel with settings like Plane (Axial), Rows (4), Columns (5), First (8), Increment (2), Labels, and Opacity (1). It also includes sections for Image Color Mapping and Overlay Color Mapping, with sliders for Min Overlay (2442) and Max Overlay (4921). At the bottom are buttons for Reset Slices, Z+, and ?.

- Continue where you left off
- Share with others (collaborators, publications, etc.)

—now they too can dynamically change views, thresholds, etc.

Yale BioImage Suite This application is part of Yale BioImage Suite (1.0.0, 2018/12/12)

Directions





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# LIVE FIGURES! ↗

Full application state + data

Overlay Viewer

The screenshot shows a grid of brain slices with various overlays. A central text box says "Lets you..." followed by a bulleted list: "• Continue where you left off" and "• Share with others (collaborators, publications, etc.)". Below this, another text box says "—now they too can dynamically change views, thresholds, etc." The application interface includes a menu bar with File, Overlay, Edit, and Help, and a toolbar with Orthogonal and Mosaic buttons. On the right, there's a "Viewer Controls" panel with settings like Plane (Axial), Rows (4), Columns (5), First (8), Increment, Labels, Image Color Mapping, Overlay Color Mapping, Opacity (set to 1), Overlay Type (Overlay), Overlay Show (Both), Min Overlay (2442), Max Overlay (4921), Cluster Size (0), and buttons for Reset Slices, Z+, and ?.

Directions

1. (Previous: open overlay app, load data, choose parameters)





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# LIVE FIGURES! ↵..

Full application state + data

Overlay Viewer

The screenshot shows a grid of brain slices with various overlays. A central text box says "Lets you..." followed by a bulleted list: "• Continue where you left off" and "• Share with others (collaborators, publications, etc.)". Below this, another text box says "—now they too can dynamically change views, thresholds, etc." A "Viewer Controls" panel on the right side of the interface includes settings for "Plane" (Axial), "Rows" (4), "Columns" (5), "First" (8), "Increment" (1), "Labels" (checkbox), "Image Color Mapping", "Overlay Color Mapping" (selected), "Opacity" (1), "Overlay Type" (Overlay), "Overlay Show" (Both), "Min Overlay" (2442), "Max Overlay" (4921), "Cluster Size" (0), and buttons for "Reset Slices", "Z+", and "?". At the bottom, there's a footer bar with the BioImage Suite logo and the text "This application is part of Yale BioImage Suite (1.0.0, 2018/12/12)".

Directions

1. (Previous: open overlay app, load data, choose parameters)
2. File > Save Application State





# LIVE FIGURES! ↵

Full application state + data

Overlay Viewer

The screenshot shows the Overlay Viewer application interface. At the top, there's a menu bar with 'File', 'Overlay', 'Edit', and 'Help'. Below the menu, there are two tabs: 'Orthogonal' and 'Mosaic', with 'Mosaic' currently selected. The main area displays a grid of brain slices, each showing a different overlay pattern. A large text overlay 'Lets you...' is positioned above the slices. To the right of the slices is a detailed 'Viewer Controls' panel. This panel includes settings for 'Core Plane' (set to 'Axial'), 'Rows' (4), 'Columns' (5), 'First Increment' (8), and 'Labels'. It also features sections for 'Image Color Mapping' and 'Overlay Color Mapping', with 'Opacity' set to 1. Under 'Overlay Type', it says 'Overlay' and 'Overlay Show' is set to 'Both'. There are also sliders for 'Min Overlay' (2442) and 'Max Overlay' (4921). The bottom of the panel has buttons for 'Reset Slices', 'Z+', and '?'. At the very bottom of the application window, there's a footer bar with the text 'BioImage Suite' and 'This application is part of Yale BioImage Suite (1.0.0, 2018/12/12)'.

Directions

1. (Previous: open overlay app, load data, choose parameters)
2. File > Save Application State
3. File > Load Application State (can drag and drop)





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# LIVE FIGURES! ↵

Full application state + data

Overlay Viewer

Orthogonal    Mosaic

File ▾    Overlay ▾    Edit ▾    Help ▾

Lets you...

- Continue where you left off
- Share with others (collaborators, publications, etc.)

—now they too can dynamically change views, thresholds, etc.

Viewer Controls

- Core Plane: Axial
- Rows: 4
- Columns: 5
- First Increment: 8
- Labels
- Image Color Mapping
- Overlay Color Mapping
- Opacity: 1
- Overlay Type: Overlay
- Overlay Show: Both
- Min Overlay: 2442
- Max Overlay: 4921
- Cluster Size: 0

Reset Slice Z+ ?

-4921 -3681 -2442 2442 3681 4921

BioImage Suite This application is part of Yale BioImage Suite (1.0.0, 2018/12/12)

Directions

1. (Previous: open overlay app, load data, choose parameters)
2. File > Save Application State
3. File > Load Application State (can drag and drop)

Try a Live Figure from the BISWeb GitHub:



TBD



Follow along in the app:



# CLUSTER REPORTER

## Overlay Viewer

Yale

File ▾ Overlay ▾ Edit ▾ Help ▾

Orthogonal Mosaic

Cluster Analyzer

#	Coordinates of Peak	Size (voxels)	Value At Peak
1	MNI: 66, -6, 6	1256	5720.294
2	MNI: 9, -12, 3	353	-5516.678
3	MNI: 54, -45, 39	263	-5096.590
4	MNI: 42, -66, -3	262	5764.263
5	MNI: 3, 33, 33	249	-5490.896
6	MNI: -33, -60, 42	179	-5405.376
7	MNI: -57, -9, 24	177	5157.129

Image: images/samplefunc.nii.gz dim=61,73,61,1,1, sp=3,3,0,1 orient=LPS type=float

Save Table

Coronal-ik Sagittal-jk Axial-ij

Viewer Controls

Core

- Mode: Slices
- I-Coord: 8
- J-Coord: 32
- K-Coord: 26
- Labels:
- Disable Mouse:

Image Color Mapping

Overlay Color Mapping

- Opacity: 1
- Overlay Type: Overlay
- Overlay Show: Both
- Min Overlay: 2882.1
- Max Overlay: 5188
- Cluster Size: 144

Reset Slices Z- Z+ ?

img (8,32,26) <6, 18, Ovr: 5720.29

BioImage Suite This application is part of Yale BioImage Suite (1.0.0.2018/12/12).



Follow along in the app:



# CLUSTER REPORTER

## Overlay Viewer

Yale

File ▾ Overlay ▾ Edit ▾ Help ▾

Orthogonal Mosaic

Cluster Analyzer

#	Coordinates of Peak	Size (voxels)	Value At Peak
1	MNI: 66, -6, 6	1256	5720.294
2	MNI: 9, -12, 3	353	-5516.678
3	MNI: 54, -45, 39	263	-5096.590
4	MNI: 42, -66, -3	262	5764.263
5	MNI: 3, 33, 33	249	-5490.896
6	MNI: -33, -60, 42	179	-5405.376
7	MNI: -57, -9, 24	177	5157.129

Image: images/samplefunc.nii.gz dim=61,73,61,1,1, sp=3,3,0,1 orient=LPS type=float

Save Table

Coronal-ik Sagittal-jk Axial-ij

Viewer Controls

- Core
  - Mode: Slices
  - I-Coord: 8
  - J-Coord: 32
  - K-Coord: 26
  - Labels:
  - Disable Mouse:
- Image Color Mapping
- Overlay Color Mapping
  - Opacity: 1
  - Overlay Type: Overlay
  - Overlay Show: Both
  - Min Overlay: 2882.1
  - Max Overlay: 5188
  - Cluster Size: 144

Reset Slices Z- Z+ ?

bioImage Suite This application is part of Yale BioImage Suite (1.0.0.2018/12/12).

Directions

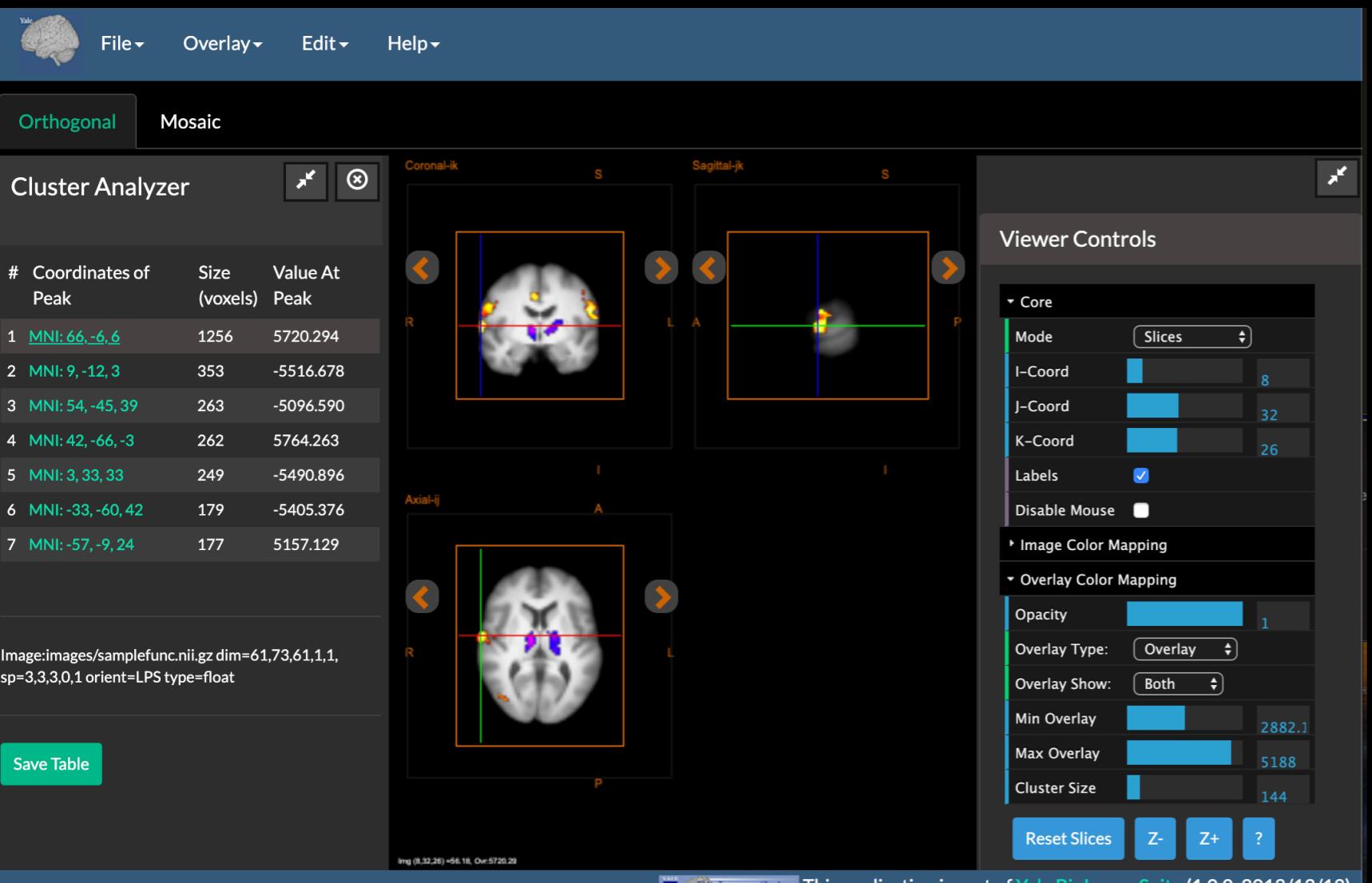
[www.bioimagesuite.org](http://www.bioimagesuite.org)




[www.bioimagesuite.org](http://www.bioimagesuite.org)

# CLUSTER REPORTER

## Overlay Viewer



## Directions

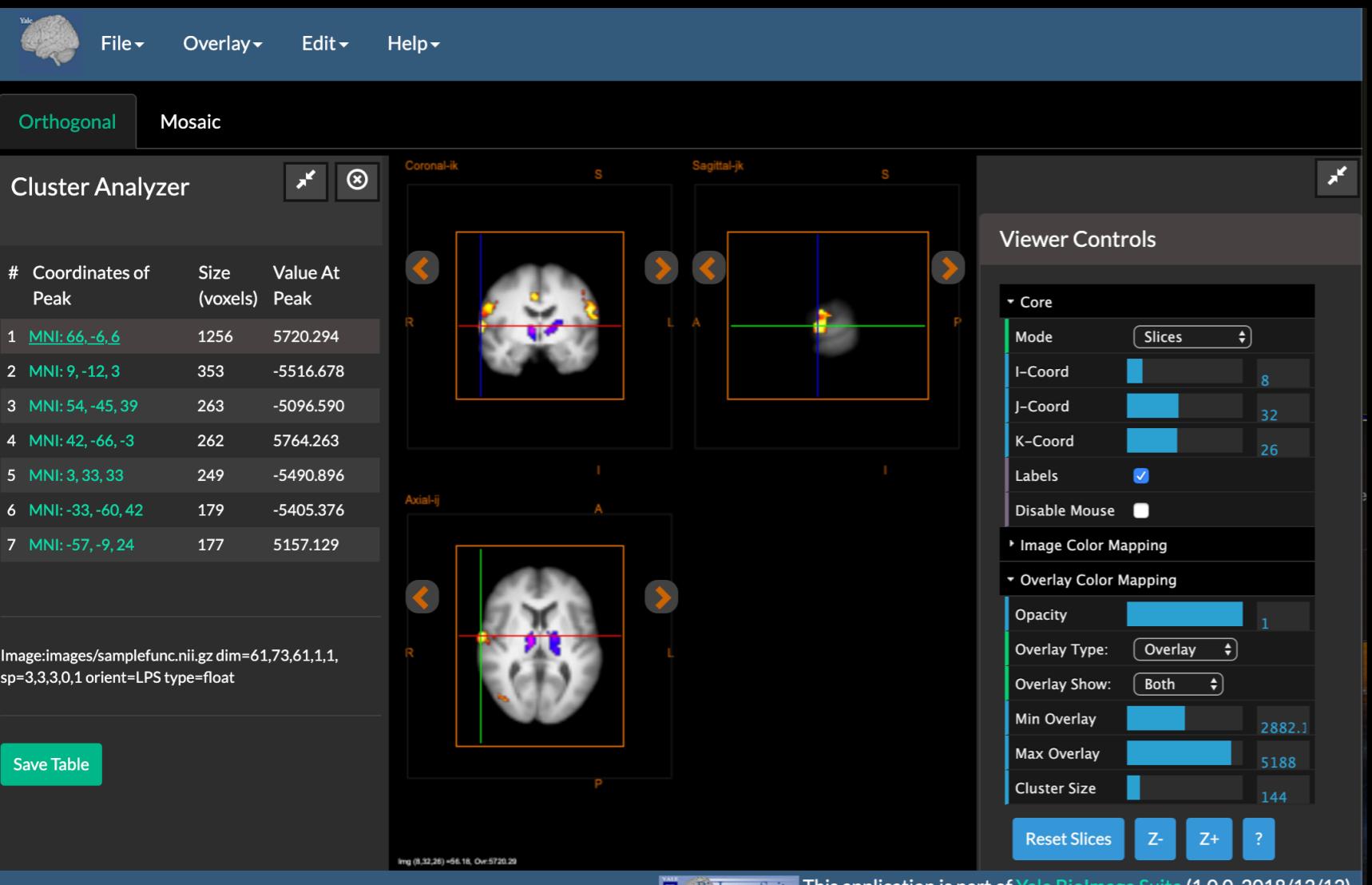
1. (Previous: open overlay app, load data, choose parameters)




[www.bioimagesuite.org](http://www.bioimagesuite.org)

# CLUSTER REPORTER

## Overlay Viewer



## Directions

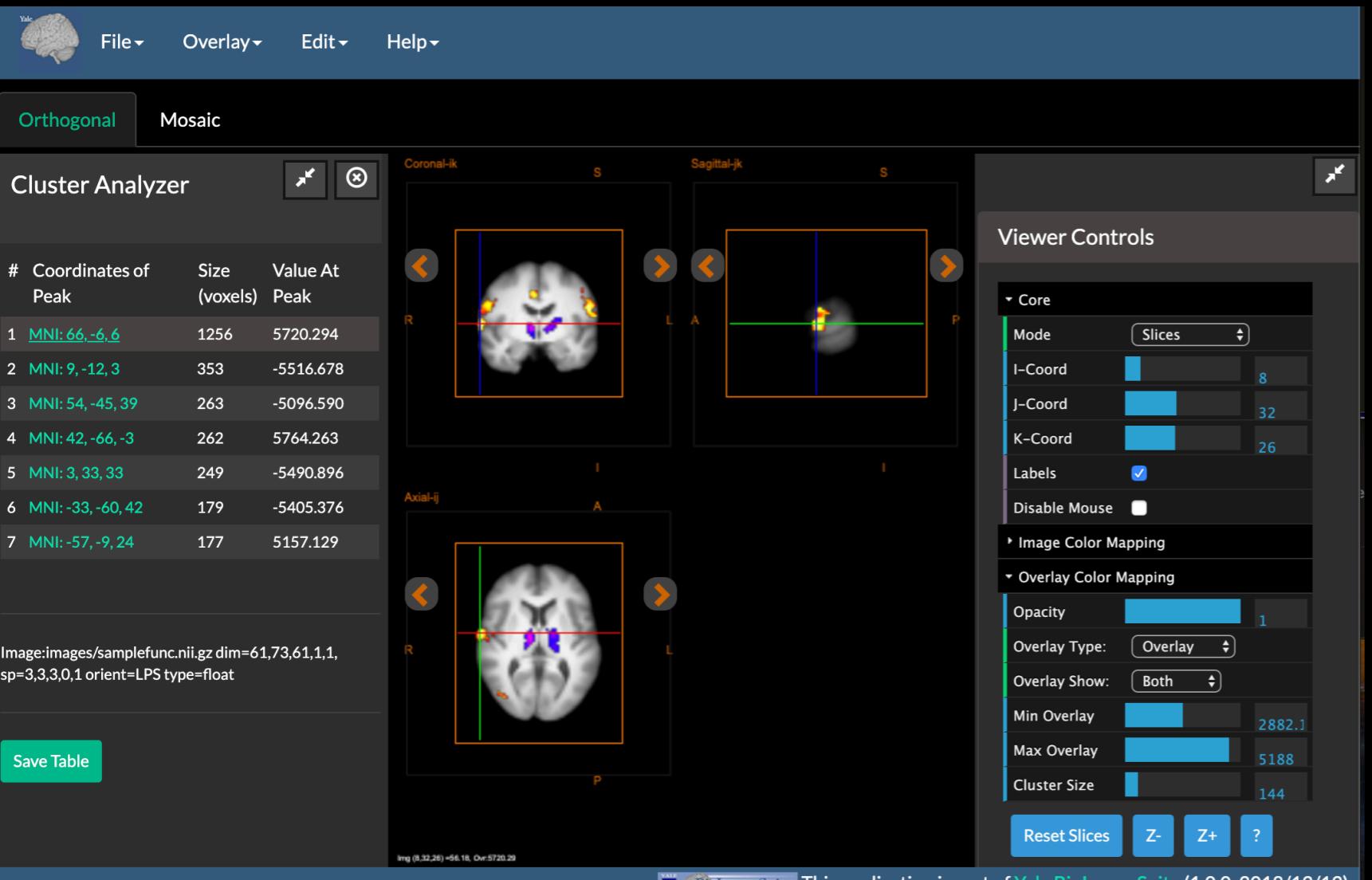
1. (Previous: open overlay app, load data, choose parameters)
2. Overlay Color Mapping > Cluster Size





# CLUSTER REPORTER

## Overlay Viewer



## Directions

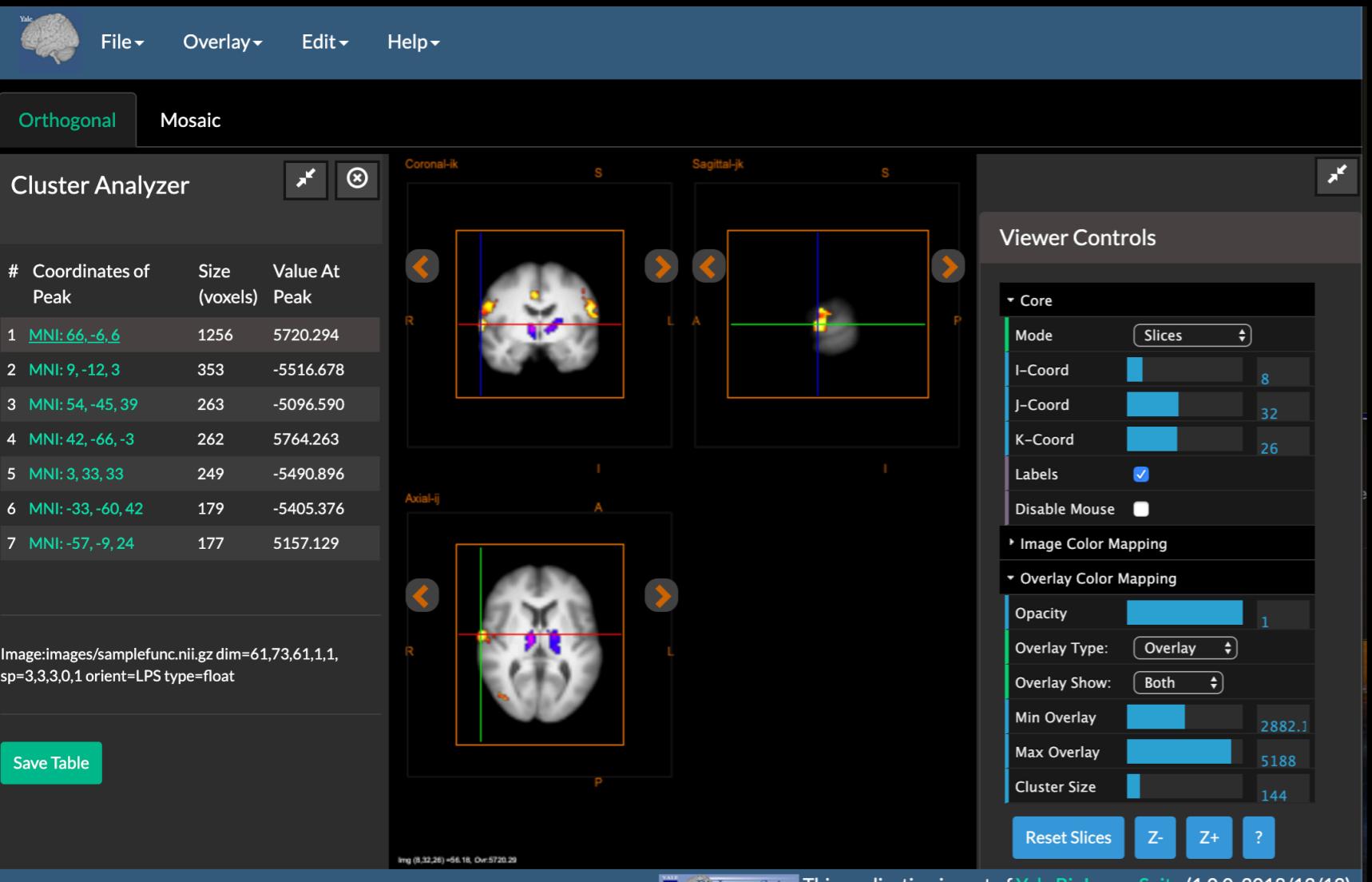
1. (Previous: open overlay app, load data, choose parameters)
2. Overlay Color Mapping > Cluster Size
3. Edit > Cluster Info Tool





# CLUSTER REPORTER

## Overlay Viewer



## Directions

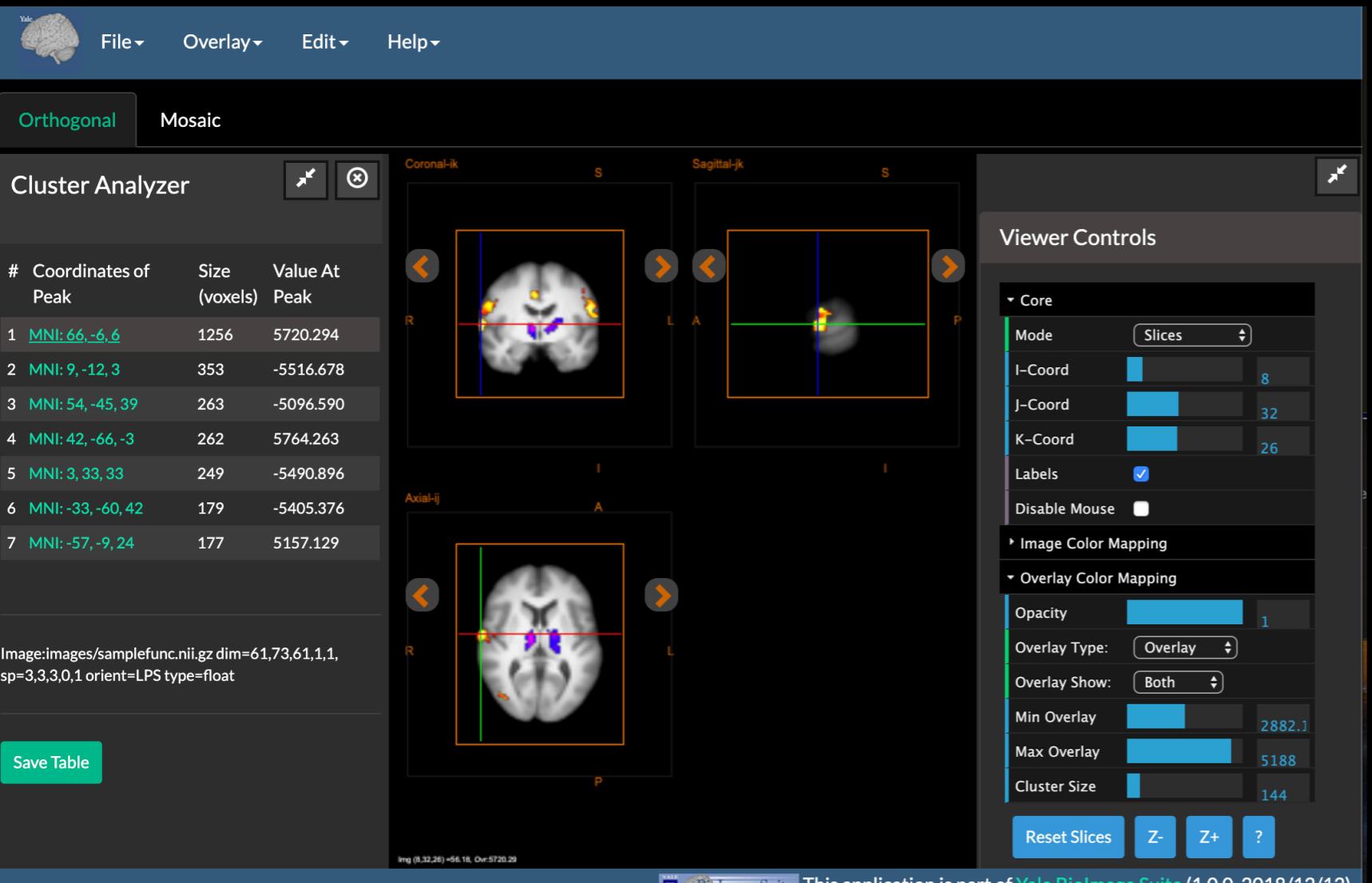
1. (Previous: open overlay app, load data, choose parameters)
2. Overlay Color Mapping > Cluster Size
3. Edit > Cluster Info Tool
4. Play with this





# CLUSTER REPORTER

## Overlay Viewer



## Directions

1. (Previous: open overlay app, load data, choose parameters)
2. Overlay Color Mapping > Cluster Size
3. Edit > Cluster Info Tool
4. Play with this

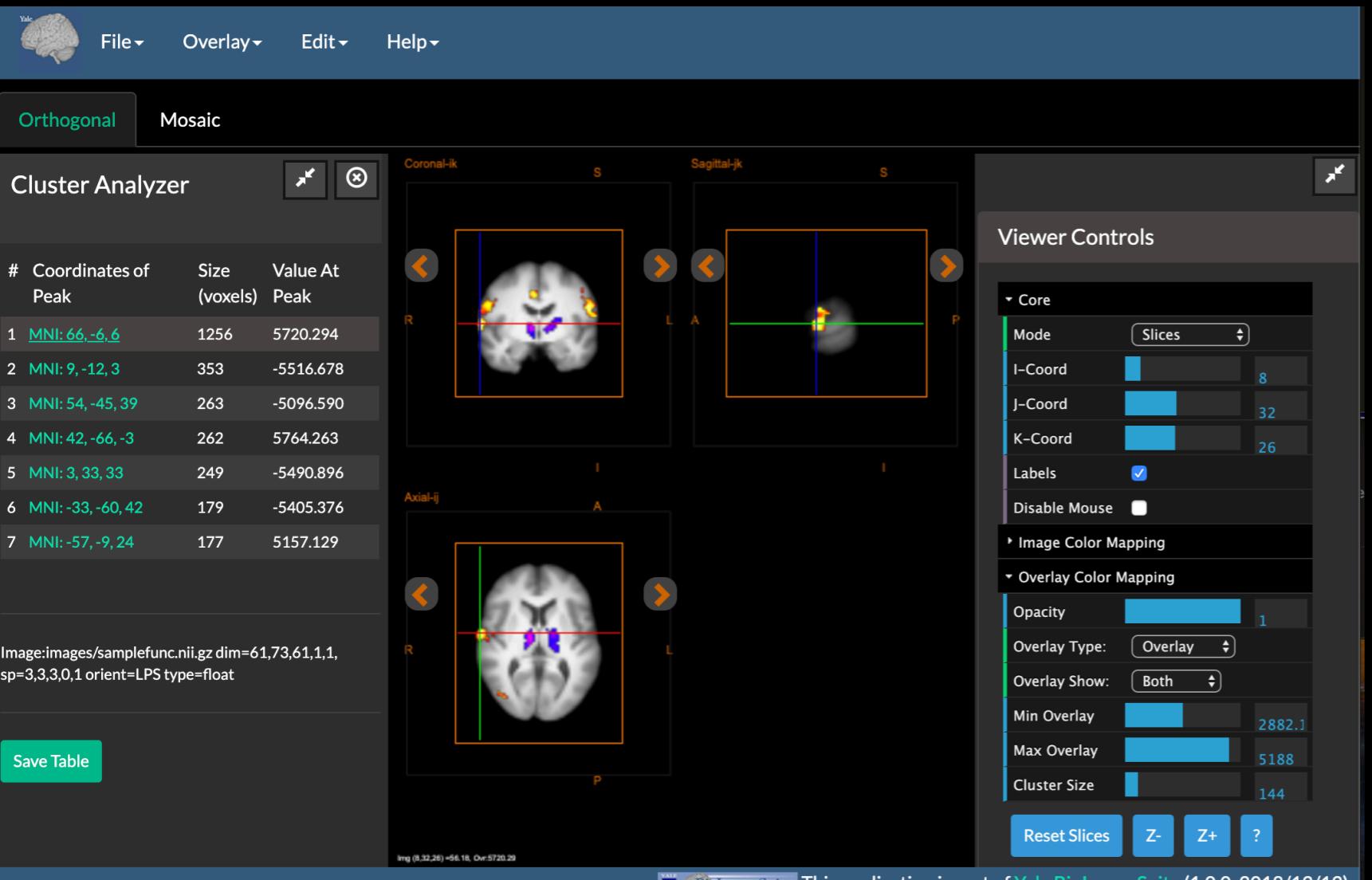
1. Go to Coordinates of Peak





# CLUSTER REPORTER

## Overlay Viewer



## Directions

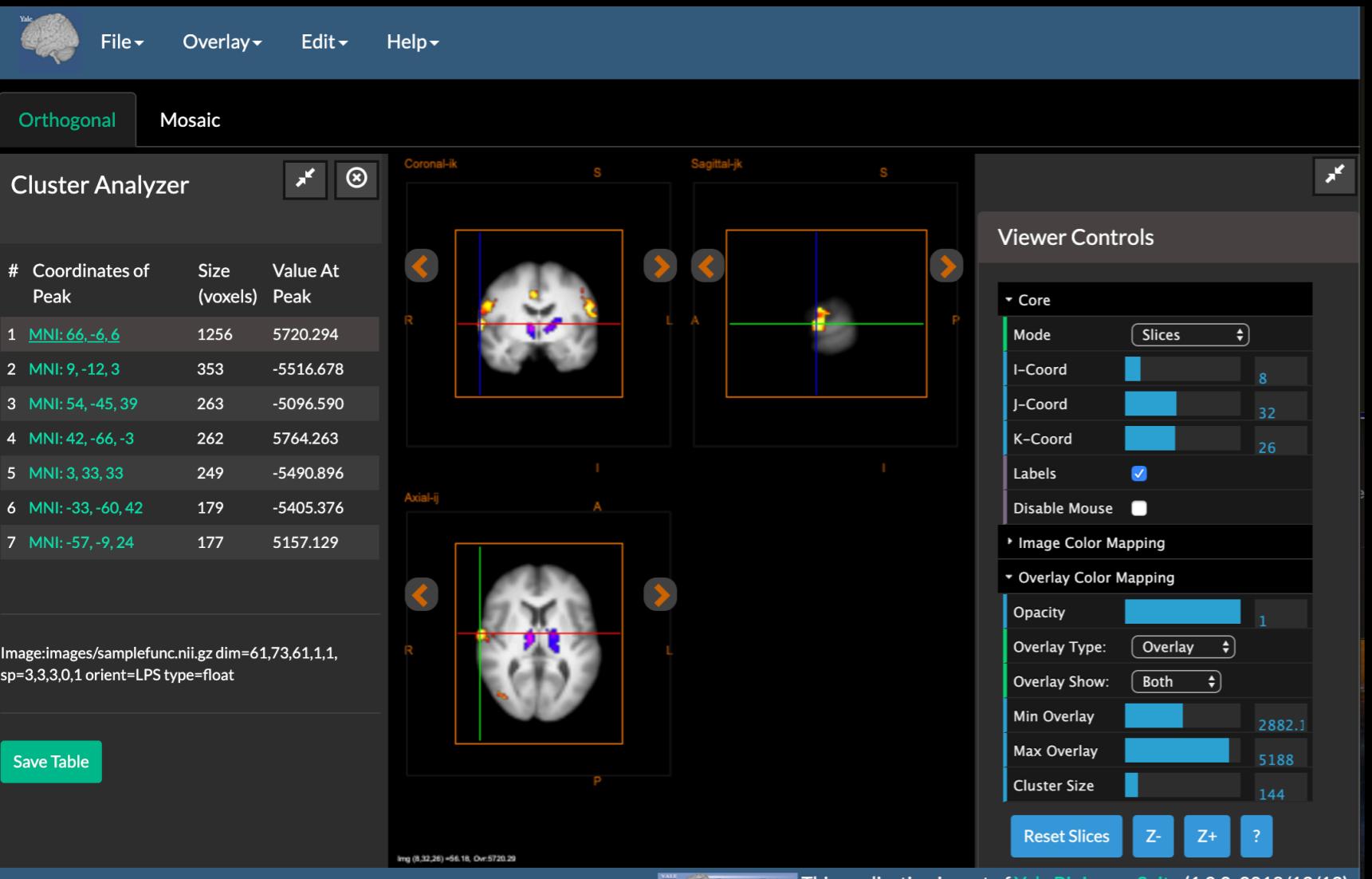
1. (Previous: open overlay app, load data, choose parameters)
2. Overlay Color Mapping > Cluster Size
3. Edit > Cluster Info Tool
4. Play with this
  1. Go to Coordinates of Peak
  2. Automatically updates for new Min Overlay and Cluster Size




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# CLUSTER REPORTER

## Overlay Viewer



## Directions

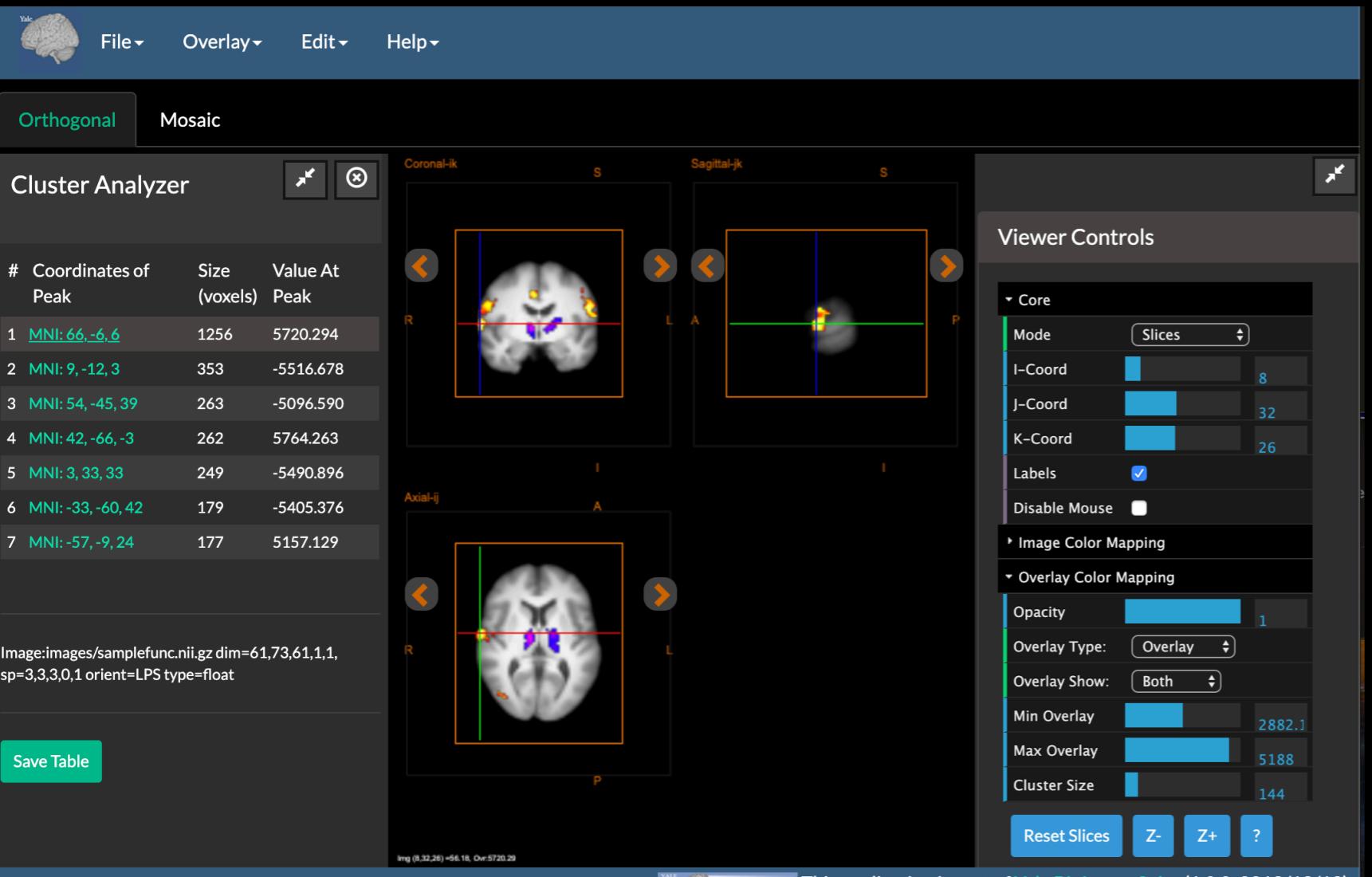
1. (Previous: open overlay app, load data, choose parameters)
2. Overlay Color Mapping > Cluster Size
3. Edit > Cluster Info Tool
4. Play with this
  1. Go to Coordinates of Peak
  2. Automatically updates for new Min Overlay and Cluster Size
  3. Can click peak coordinates




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# CLUSTER REPORTER

## Overlay Viewer



## Directions

1. (Previous: open overlay app, load data, choose parameters)
2. Overlay Color Mapping > Cluster Size
3. Edit > Cluster Info Tool
4. Play with this
  1. Go to Coordinates of Peak
  2. Automatically updates for new Min Overlay and Cluster Size
  3. Can click peak coordinates
5. Cluster Analyzer > Save Table



Follow along in the app:



# IMAGE PROCESSING

[www.bioimagesuite.org](http://www.bioimagesuite.org)

## Orthogonal Viewer

The screenshot shows the Yale BioImage Suite Orthogonal Viewer interface. At the top, there is a menu bar with options: File, Overlay, Edit, Image Processing, Segmentation, and Help. Below the menu, there are three orthogonal slices of a brain:

- Coronal-ik:** Shows a transverse slice with a red crosshair. Orientation markers R (Right), S (Superior), and I (Inferior) are visible. Navigation arrows are present on the left and right sides.
- Sagittal-jk:** Shows a longitudinal slice with a green crosshair. Orientation markers L (Left), A (Anterior), and P (Posterior) are visible. Navigation arrows are present at the top and bottom.
- Axial-ij:** Shows a coronal slice with a green crosshair. Orientation markers A (Anterior), I (Inferior), and P (Posterior) are visible. Navigation arrows are present on the left and right sides.

To the right of the slices is the **Viewer Controls** panel, which includes the following settings:

- Core:**
  - Mode: Slices
  - I-Coord: 90
  - J-Coord: 108
  - K-Coord: 90
  - Labels:
  - Disable Mouse:
- Image Color Mapping**
- Overlay Color Mapping**
- Buttons: Reset Slices, Z-, Z+, ?

Below the controls is the **Viewer Snapshot** section, which includes:

- Scale: x3
- Checkboxes: White Bkgd, Crop
- Button: Take Snapshot

At the bottom left, there is a status message: **Img (90,108,90) =0**. At the very bottom, there is a footer bar with the text: **BioImage Suite This application is part of Yale BioImage Suite (1.0.0, 2018/12/12)**.




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# IMAGE PROCESSING

## Orthogonal Viewer

## Directions

Yale

File ▾ Overlay ▾ Edit ▾ Image Processing ▾ Segmentation ▾ Help ▾

Coronal-ik      Sagittal-jk      Axial-ij

S      S      I

R      L      A      P

R      L      A      P

Img (90,108,90) = 0

BioImage Suite This application is part of Yale BioImage Suite (1.0.0, 2018/12/12)

The screenshot shows the Orthogonal Viewer interface with three main panels: Coronal, Sagittal, and Axial. Each panel displays a grayscale brain image with anatomical axes (Sagittal, Coronal, Axial) and spatial markers (R, L, A, P). The Coronal and Sagittal panels have orange outlines, while the Axial panel has a green outline. Navigation arrows are located between the panels. To the right is a 'Viewer Controls' sidebar with sections for 'Core' (Mode: Slices, I-Coord: 90, J-Coord: 108, K-Coord: 90, Labels checked, Disable Mouse unchecked), 'Image Color Mapping', and 'Overlay Color Mapping'. It also includes buttons for 'Reset Slices', 'Z-', 'Z+', and '?'. Below this is a 'Viewer Snapshot' section with 'Scale: x3', 'White Bkgd' (unchecked), 'Crop' (checked), and a 'Take Snapshot' button.



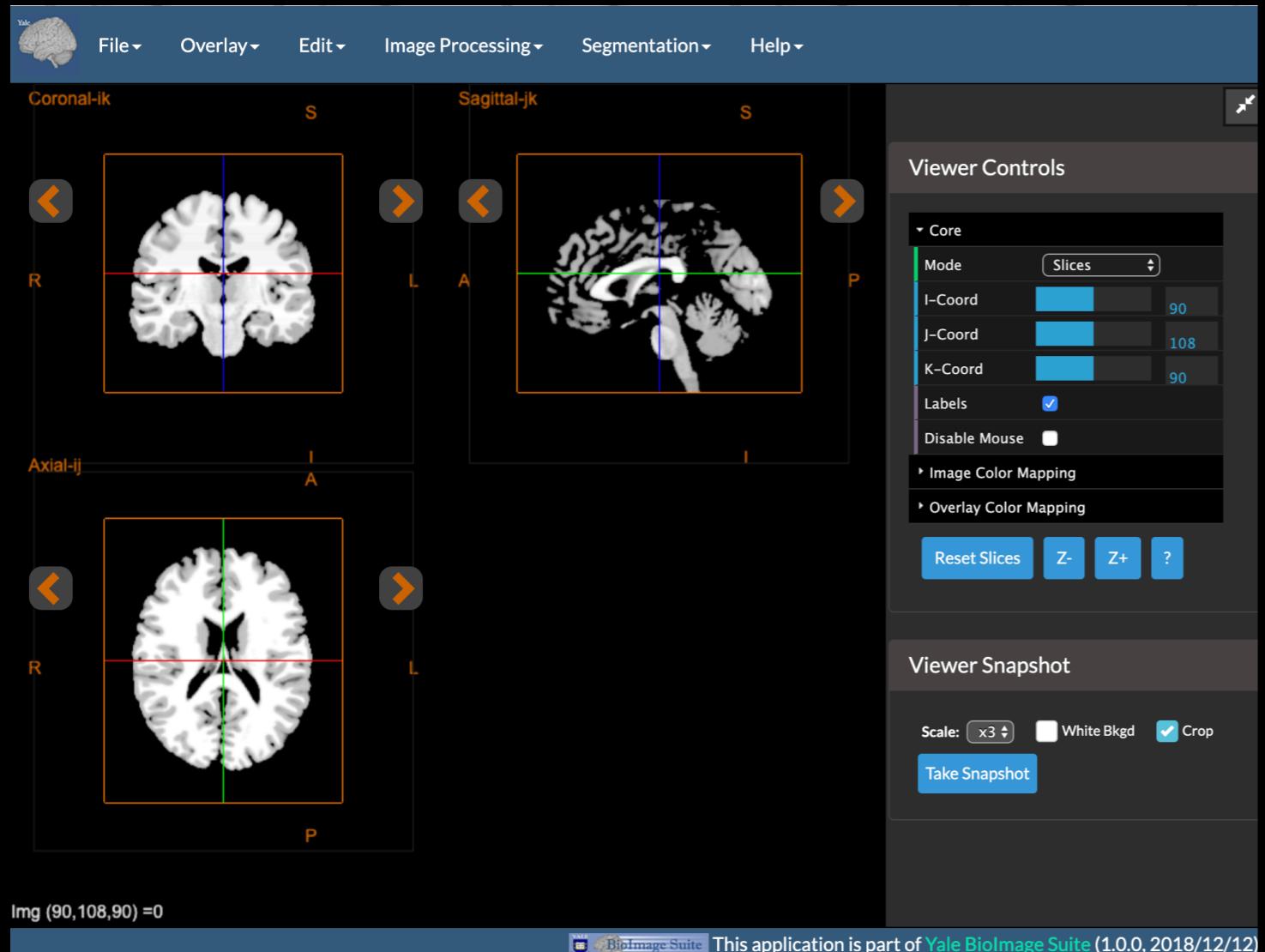

[www.bioimagesuite.org](http://www.bioimagesuite.org)

# IMAGE PROCESSING

## Orthogonal Viewer

## Directions

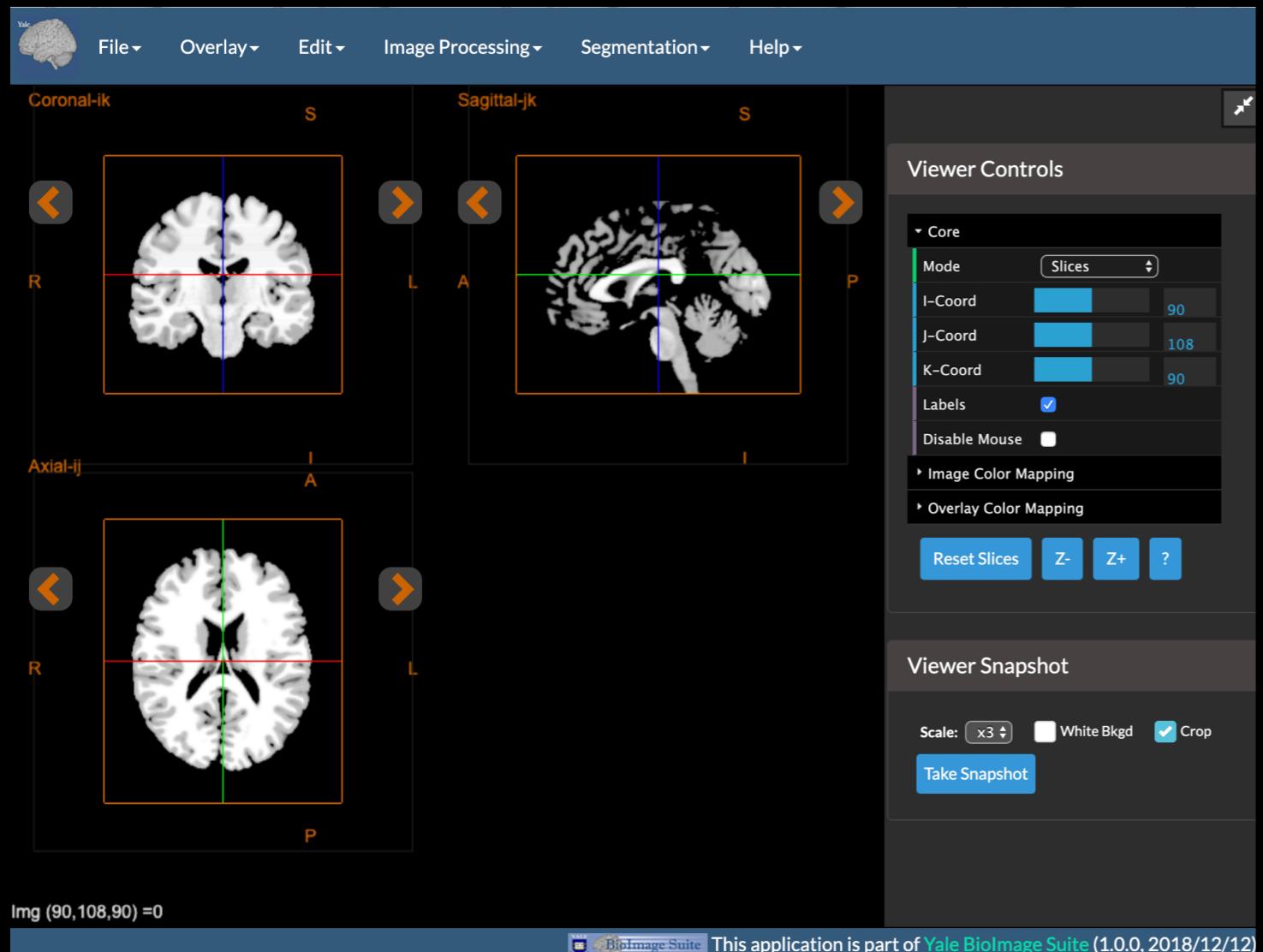
1. Applications > Orthogonal Viewer




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# IMAGE PROCESSING

## Orthogonal Viewer



## Directions

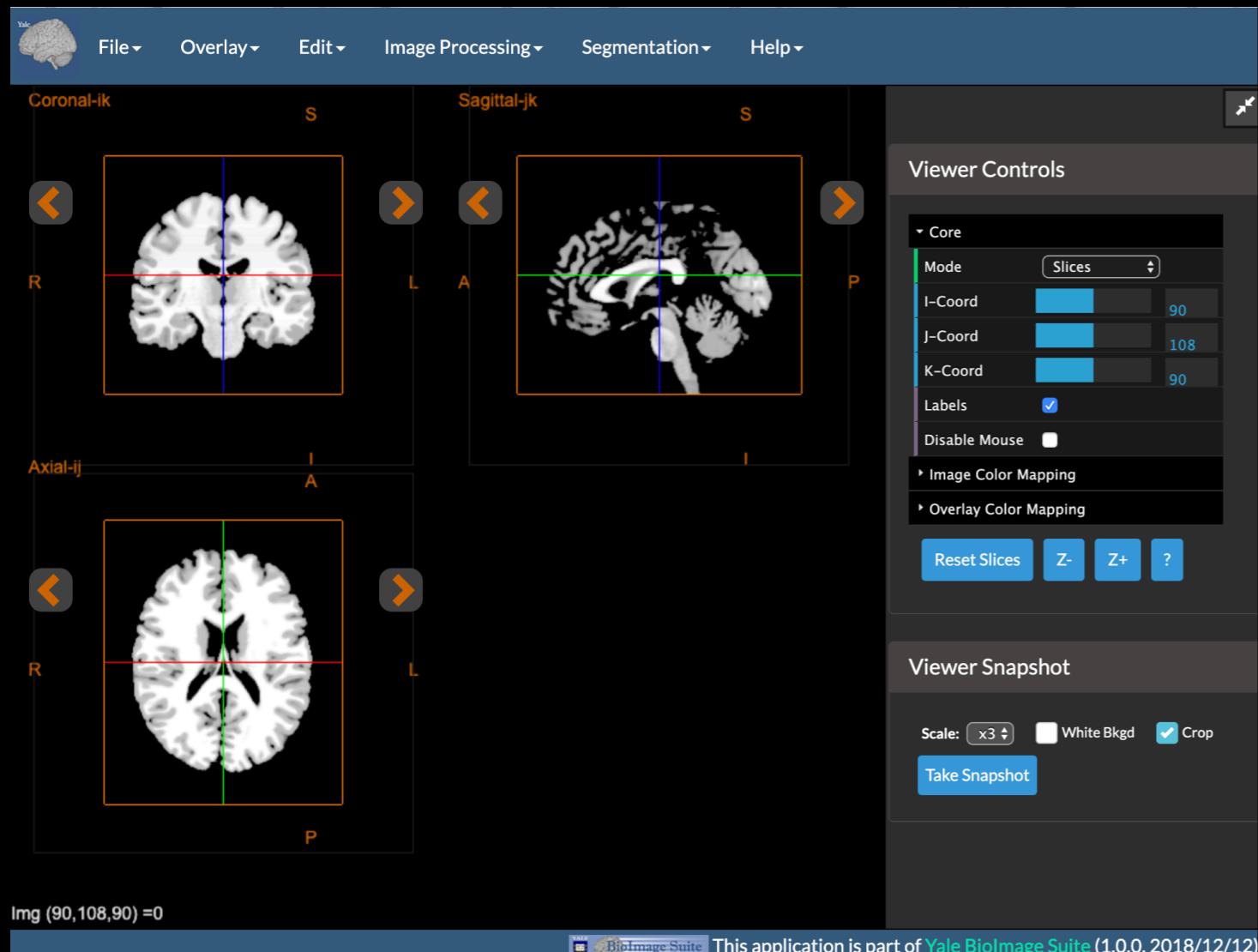
1. Applications > Orthogonal Viewer
2. Load Image and/or Overlay Data




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# IMAGE PROCESSING

## Orthogonal Viewer



## Directions

1. Applications > Orthogonal Viewer
2. Load Image and/or Overlay Data
  1. For Demo: File > Load MNI T1 (1mm)

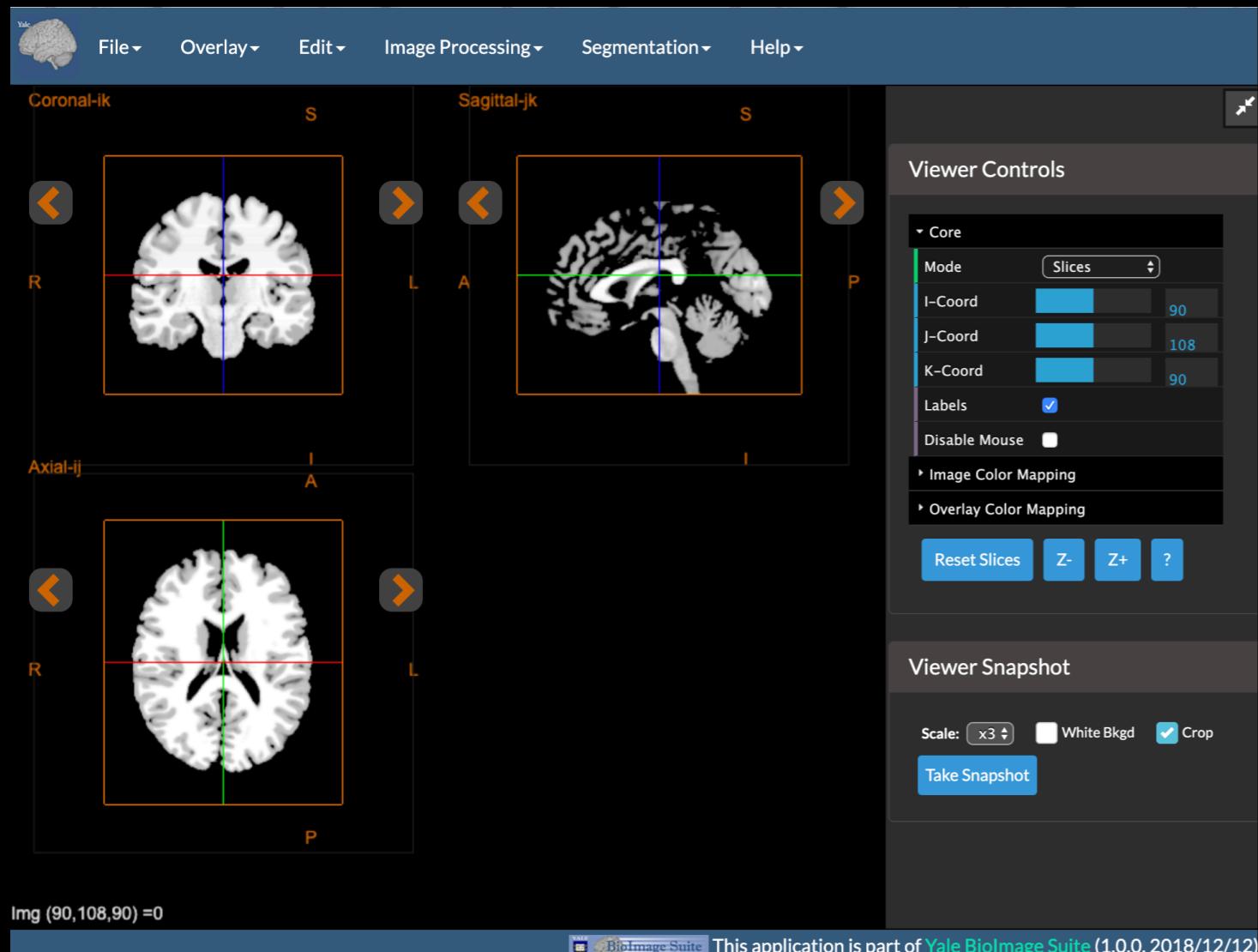




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# IMAGE PROCESSING

## Orthogonal Viewer



## Directions

1. Applications > Orthogonal Viewer
2. Load Image and/or Overlay Data
  1. For Demo: File > Load MNI T1 (1mm)
3. Some example operations for demo

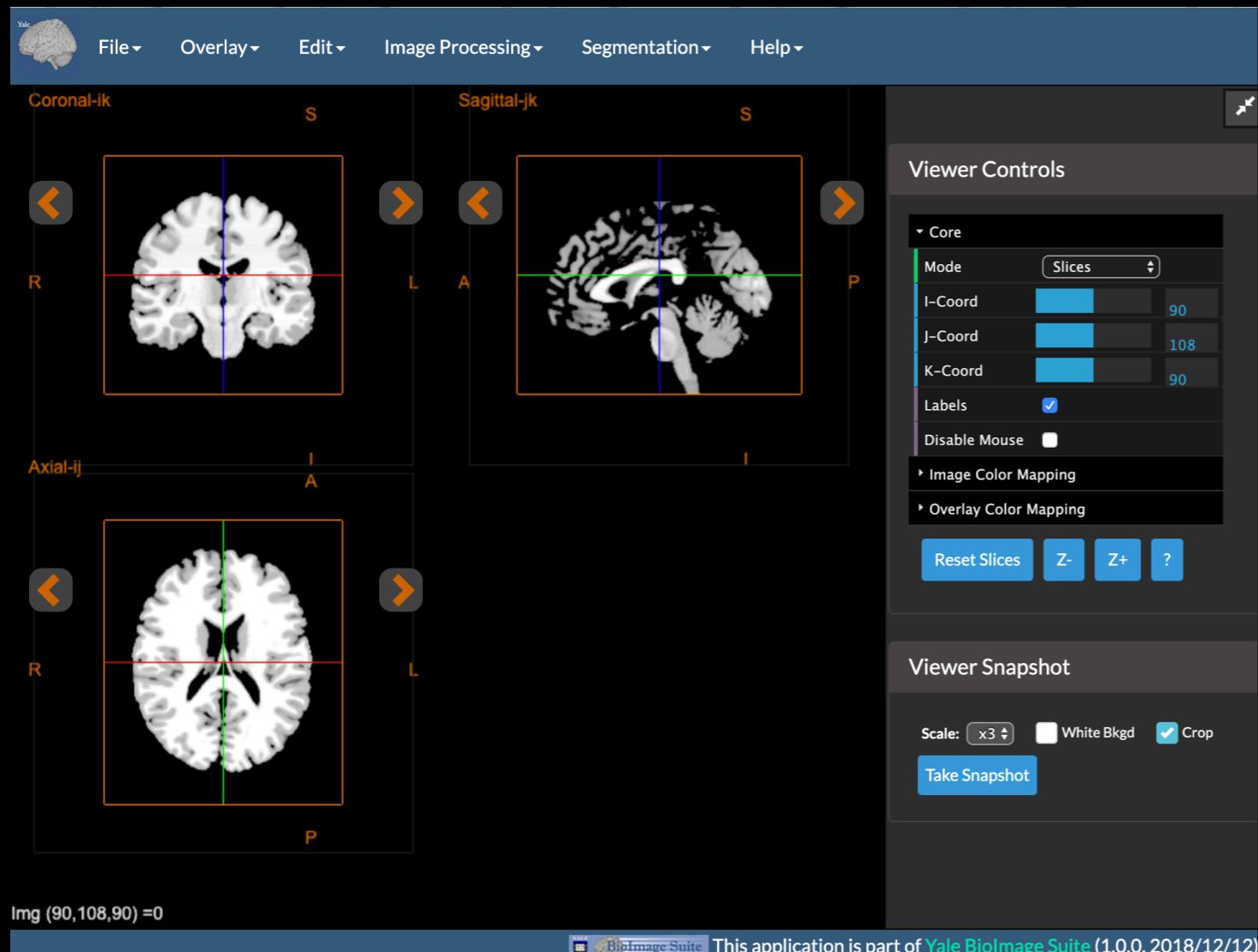




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# IMAGE PROCESSING

## Orthogonal Viewer



## Directions

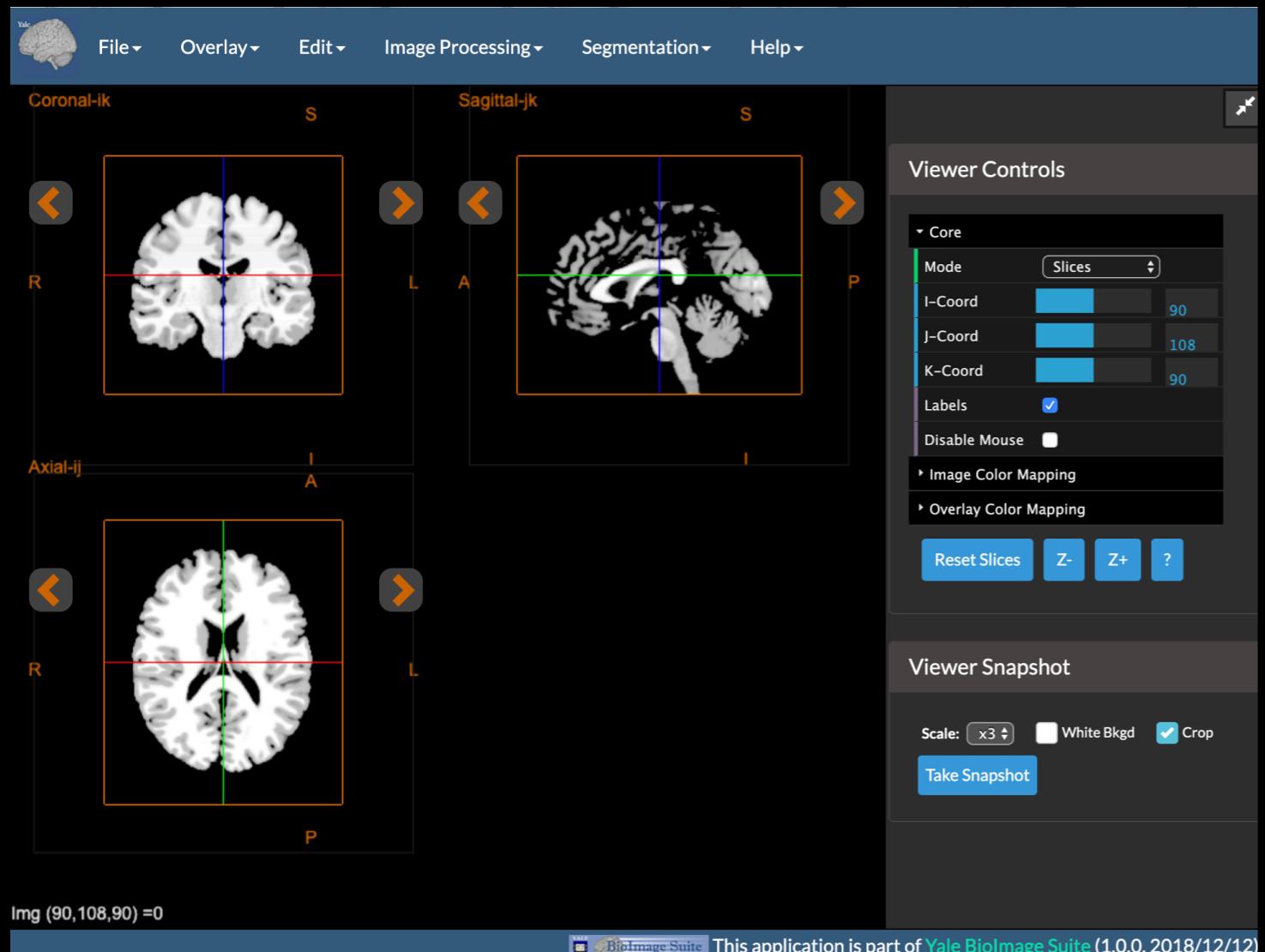
1. Applications > Orthogonal Viewer
2. Load Image and/or Overlay Data
  1. For Demo: File > Load MNI T1 (1mm)
3. Some example operations for demo
  1. **Image Processing > Smooth Image**




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# IMAGE PROCESSING

## Orthogonal Viewer



## Directions

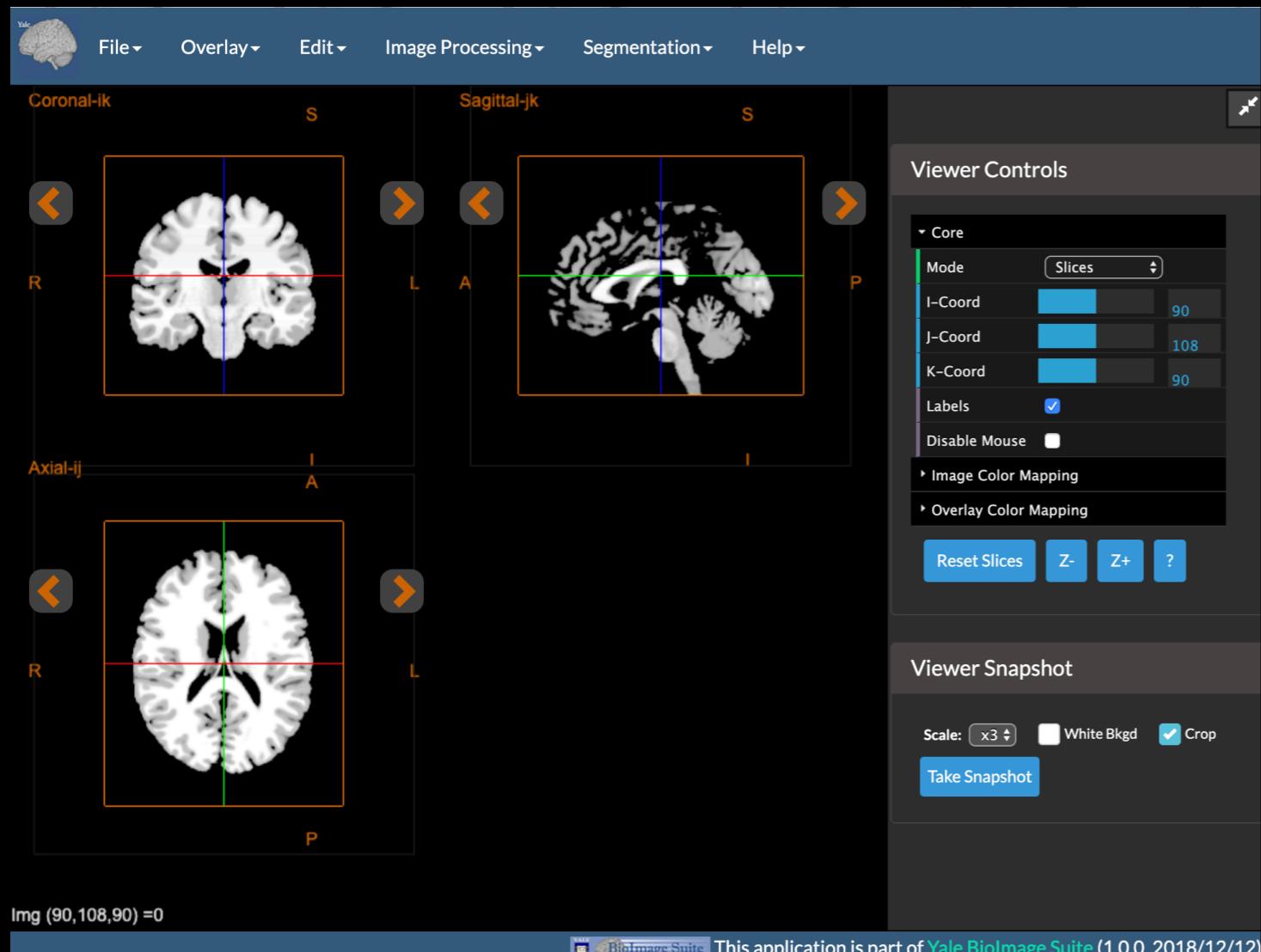
1. Applications > Orthogonal Viewer
2. Load Image and/or Overlay Data
  1. For Demo: File > Load MNI T1 (1mm)
3. Some example operations for demo
  1. **Image Processing > Smooth Image**
    1. Sigma = 5mm




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# IMAGE PROCESSING

## Orthogonal Viewer



## Directions

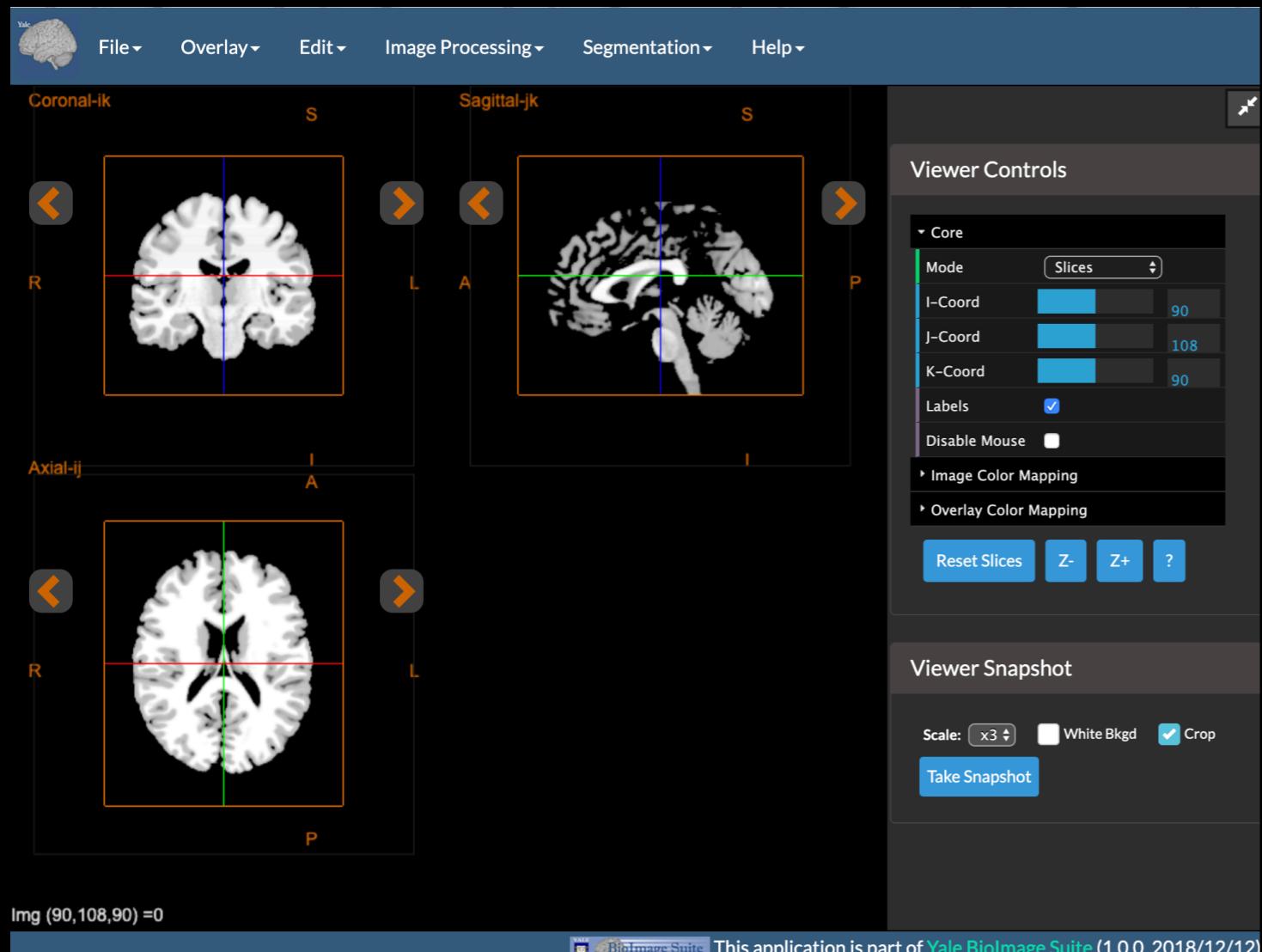
1. Applications > Orthogonal Viewer
2. Load Image and/or Overlay Data
  1. For Demo: File > Load MNI T1 (1mm)
3. Some example operations for demo
  1. **Image Processing > Smooth Image**
    1. Sigma = 5mm
    2. Click "Smooth"




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# IMAGE PROCESSING

## Orthogonal Viewer



## Directions

1. Applications > Orthogonal Viewer
2. Load Image and/or Overlay Data
  1. For Demo: File > Load MNI T1 (1mm)
3. Some example operations for demo
  1. **Image Processing > Smooth Image**
    1. Sigma = 5mm
    2. Click "Smooth"
    3. File > Save Image (for next step)

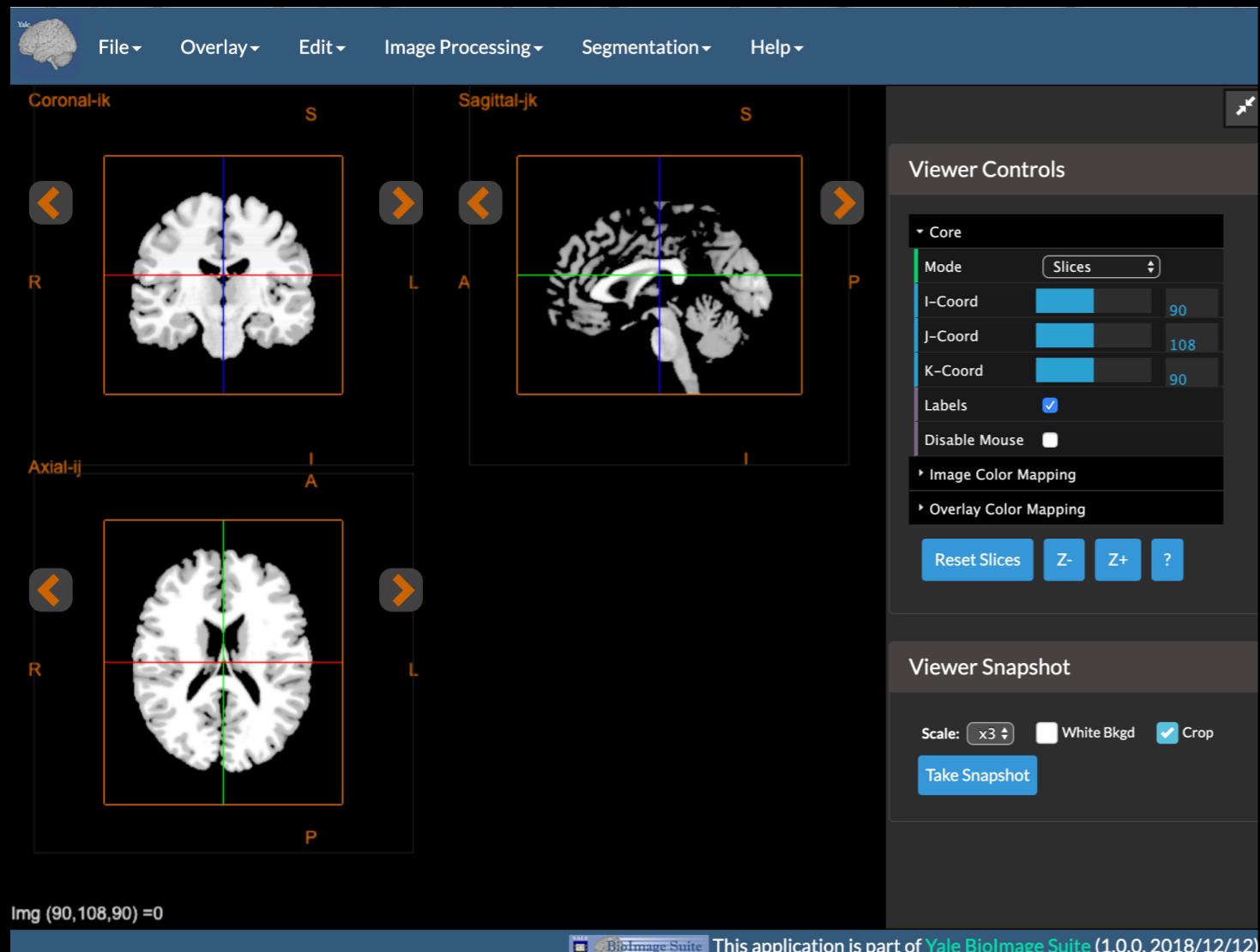




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# IMAGE PROCESSING

## Orthogonal Viewer



## Directions

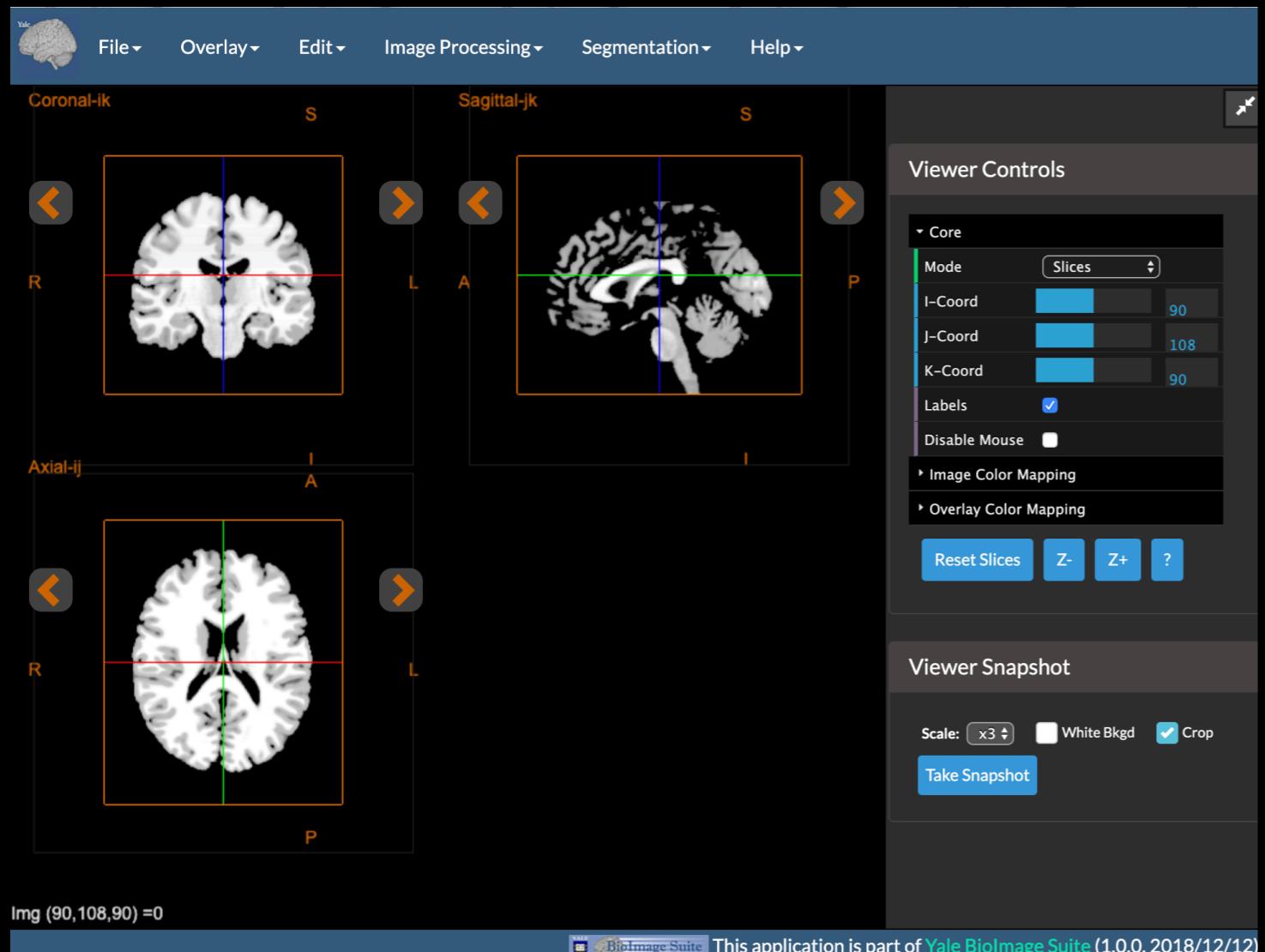
1. Applications > Orthogonal Viewer
2. Load Image and/or Overlay Data
  1. For Demo: File > Load MNI T1 (1mm)
3. Some example operations for demo
  - 1. Image Processing > Smooth Image**
    1. Sigma = 5mm
    2. Click "Smooth"
    3. File > Save Image (for next step)
  - 2. Image Processing > Combine Images**




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# IMAGE PROCESSING

## Orthogonal Viewer



## Directions

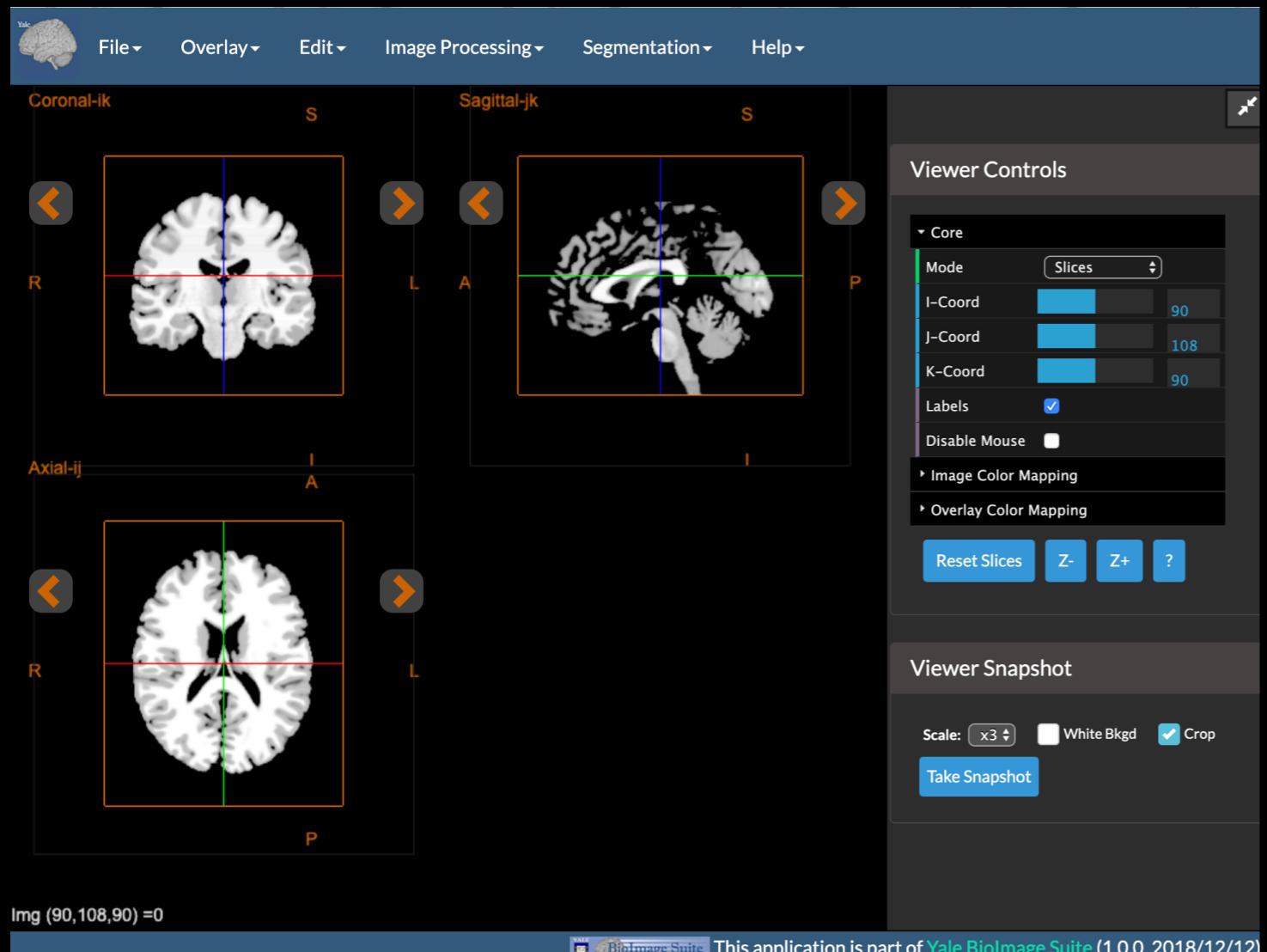
1. Applications > Orthogonal Viewer
2. Load Image and/or Overlay Data
  1. For Demo: File > Load MNI T1 (1mm)
3. Some example operations for demo
  - 1. Image Processing > Smooth Image**
    1. Sigma = 5mm
    2. Click "Smooth"
    3. File > Save Image (for next step)
  - 2. Image Processing > Combine Images**
    1. File > Load MNI T1 (1mm)




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# IMAGE PROCESSING

## Orthogonal Viewer



## Directions

1. Applications > Orthogonal Viewer
2. Load Image and/or Overlay Data
  1. For Demo: File > Load MNI T1 (1mm)
3. Some example operations for demo
  - 1. Image Processing > Smooth Image**
    1. Sigma = 5mm
    2. Click "Smooth"
    3. File > Save Image (for next step)
  - 2. Image Processing > Combine Images**
    1. File > Load MNI T1 (1mm)
    2. Overlay > Load Overlay (load smoothed image from above)

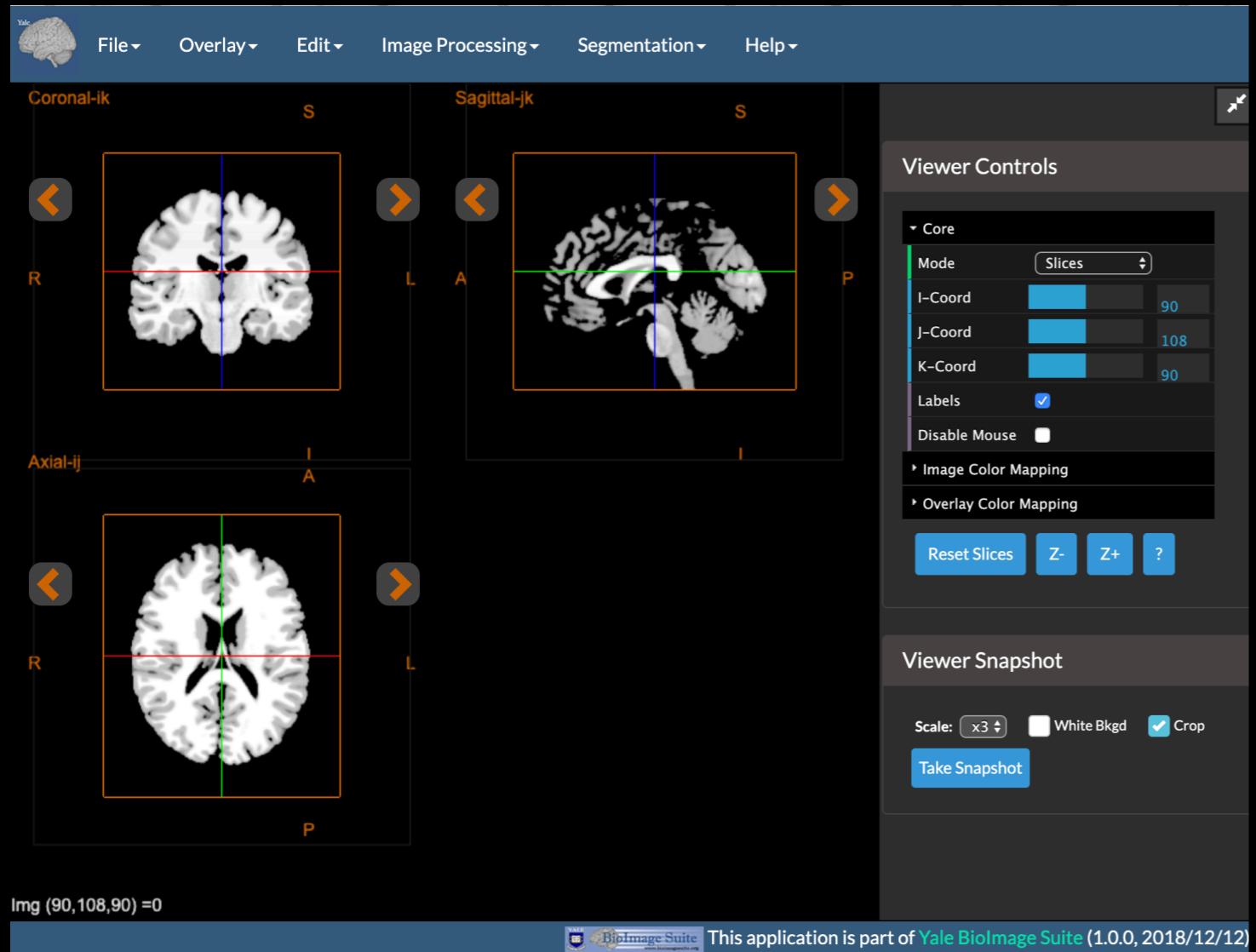




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# IMAGE PROCESSING

## Orthogonal Viewer



## Directions

1. Applications > Orthogonal Viewer
2. Load Image and/or Overlay Data
  1. For Demo: File > Load MNI T1 (1mm)
3. Some example operations for demo
  - 1. Image Processing > Smooth Image**
    1. Sigma = 5mm
    2. Click "Smooth"
    3. File > Save Image (for next step)
  - 2. Image Processing > Combine Images**
    1. File > Load MNI T1 (1mm)
    2. Overlay > Load Overlay (load smoothed image from above)
    3. Input 1: Image, Input 2: Overlay

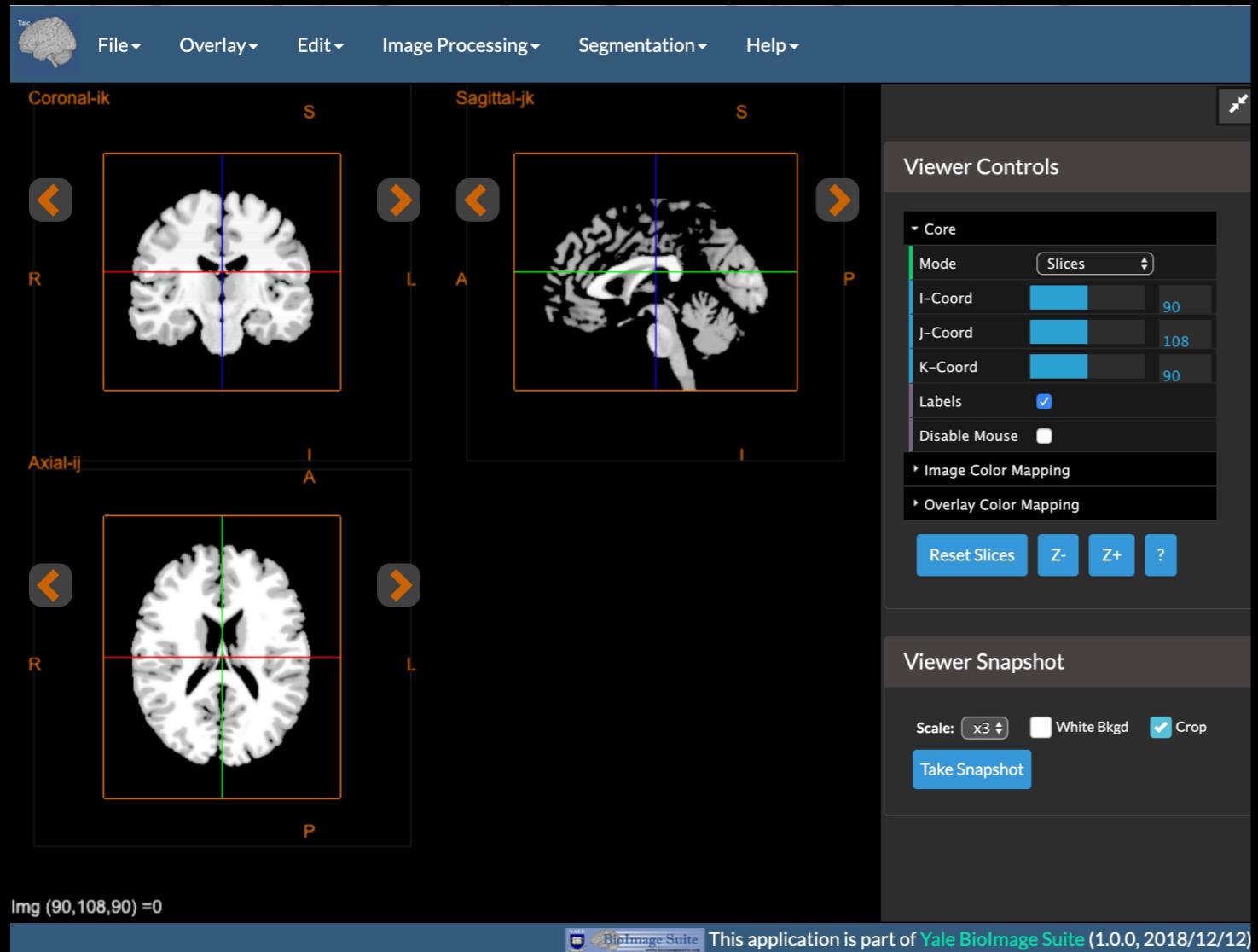




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# IMAGE PROCESSING

## Orthogonal Viewer



## Directions

1. Applications > Orthogonal Viewer
2. Load Image and/or Overlay Data
  1. For Demo: File > Load MNI T1 (1mm)
3. Some example operations for demo
  - 1. Image Processing > Smooth Image**
    1. Sigma = 5mm
    2. Click "Smooth"
    3. File > Save Image (for next step)
  - 2. Image Processing > Combine Images**
    1. File > Load MNI T1 (1mm)
    2. Overlay > Load Overlay (load smoothed image from above)
    3. Input 1: Image, Input 2: Overlay
    4. Operation: Subtract

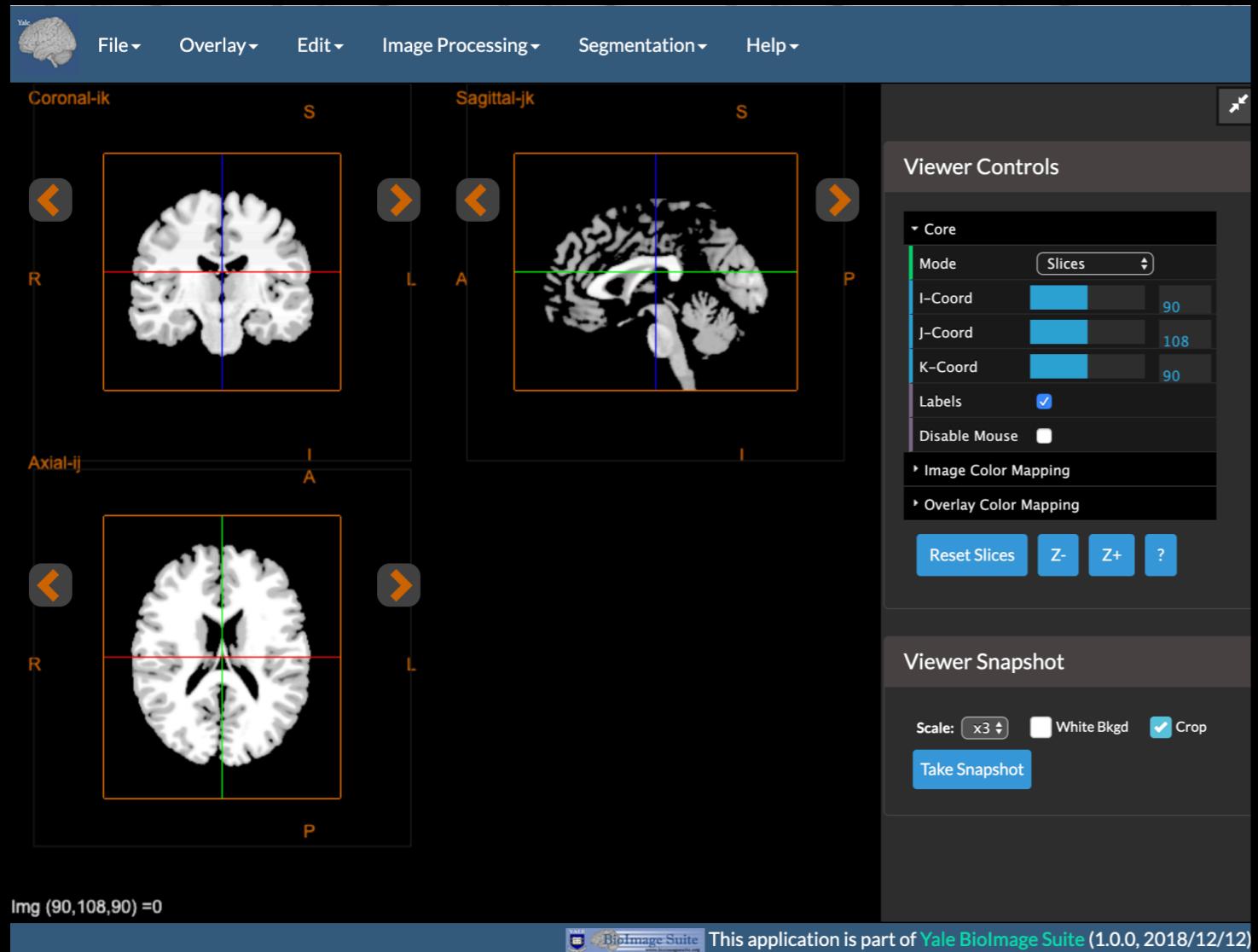




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# IMAGE PROCESSING

## Orthogonal Viewer



## Directions

1. Applications > Orthogonal Viewer
2. Load Image and/or Overlay Data
  1. For Demo: File > Load MNI T1 (1mm)
3. Some example operations for demo
  - 1. Image Processing > Smooth Image**
    1. Sigma = 5mm
    2. Click "Smooth"
    3. File > Save Image (for next step)
  - 2. Image Processing > Combine Images**
    1. File > Load MNI T1 (1mm)
    2. Overlay > Load Overlay (load smoothed image from above)
    3. Input 1: Image, Input 2: Overlay
    4. Operation: Subtract
    5. Click "Execute"

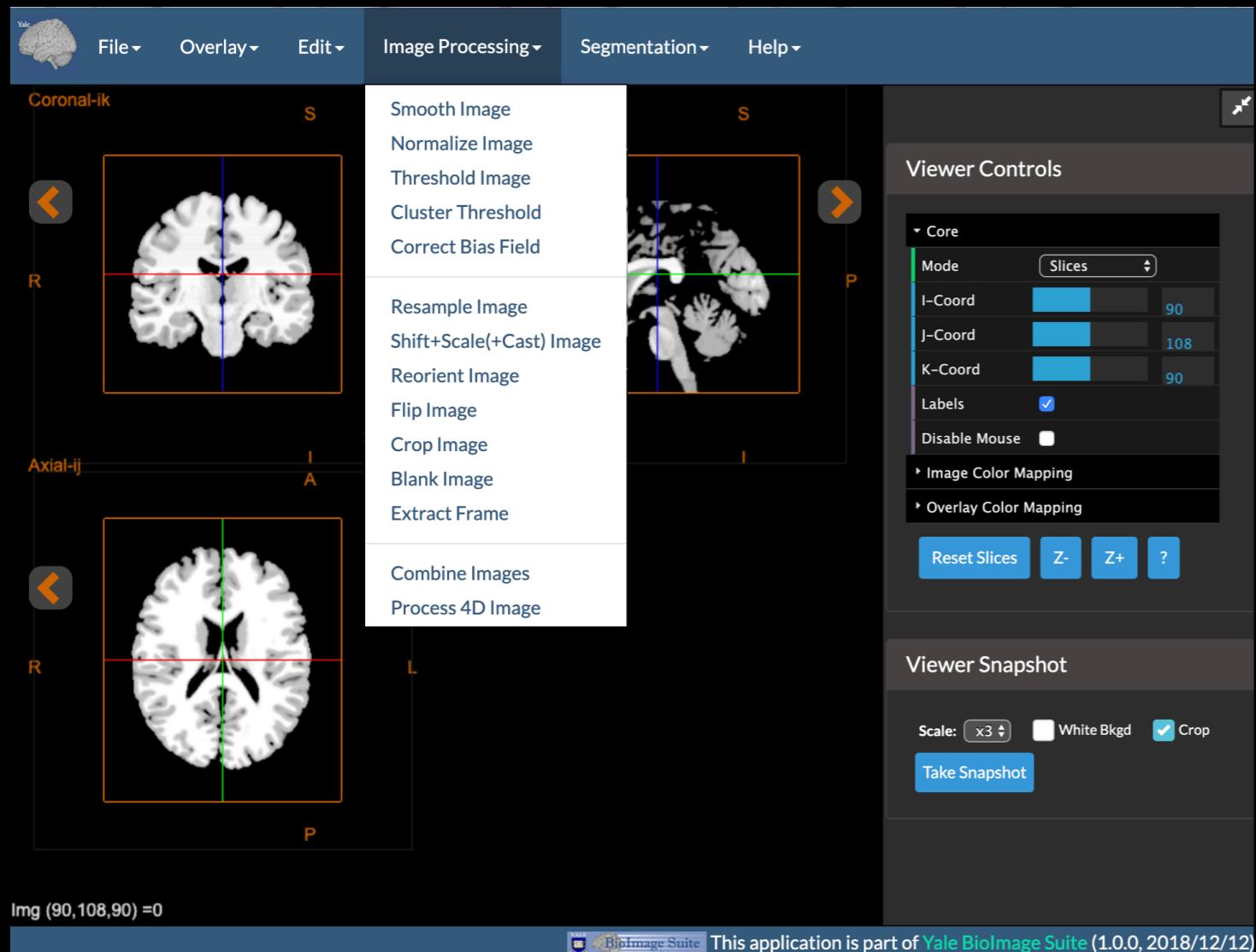




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# IMAGE PROCESSING

## Orthogonal Viewer



## Directions

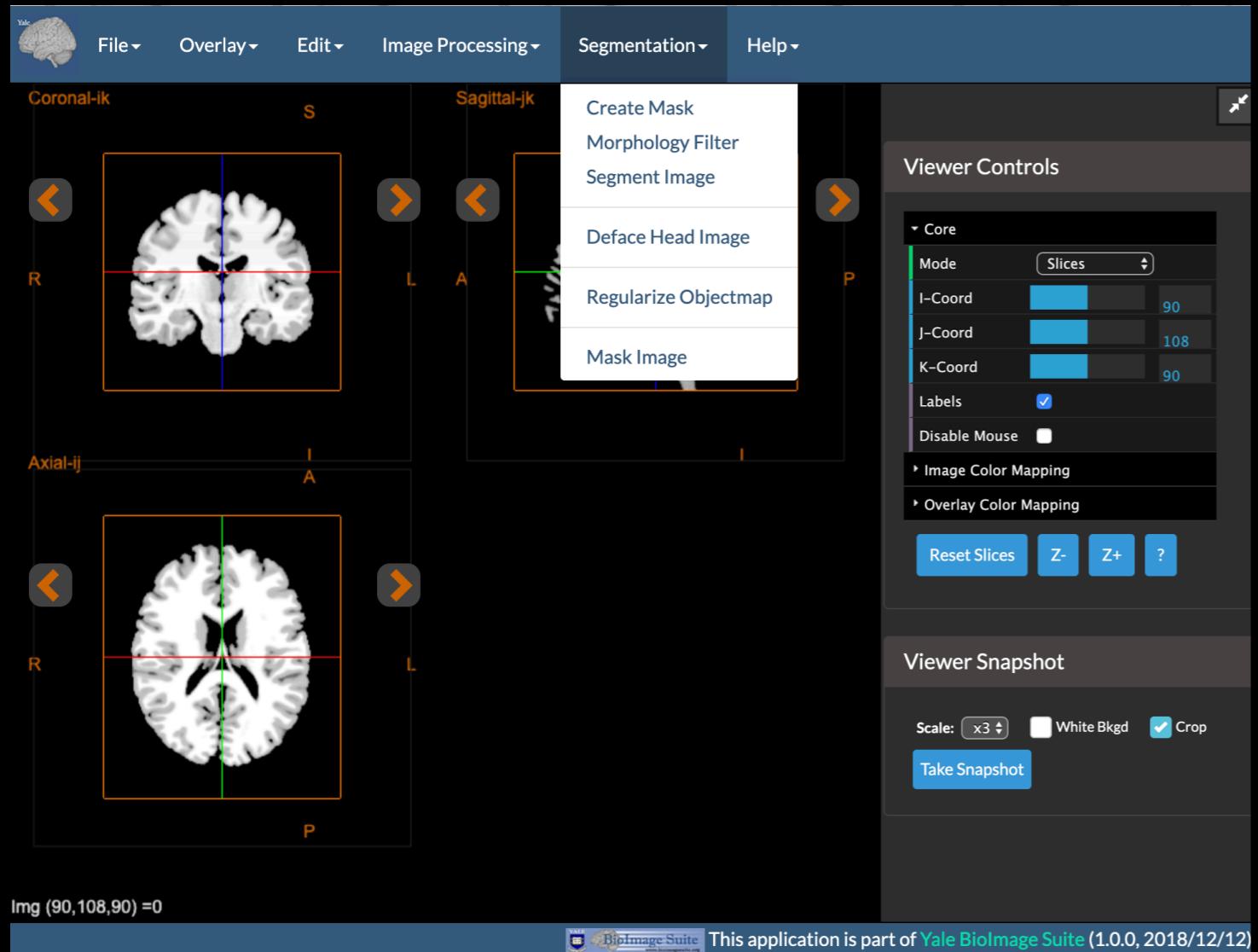
1. Applications > Orthogonal Viewer
2. Load Image and/or Overlay Data
  1. For Demo: File > Load MNI T1 (1mm)
3. Some example operations for demo
  - 1. Image Processing > Smooth Image**
    1. Sigma = 5mm
    2. Click "Smooth"
    3. File > Save Image (for next step)
  - 2. Image Processing > Combine Images**
    1. File > Load MNI T1 (1mm)
    2. Overlay > Load Overlay (load smoothed image from above)
    3. Input 1: Image, Input 2: Overlay
    4. Operation: Subtract
    5. Click "Execute"




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# IMAGE PROCESSING

## Orthogonal Viewer



## Directions

1. Applications > Orthogonal Viewer
2. Load Image and/or Overlay Data
  1. For Demo: File > Load MNI T1 (1mm)
3. Some example operations for demo
  - 1. Image Processing > Smooth Image**
    1. Sigma = 5mm
    2. Click "Smooth"
    3. File > Save Image (for next step)
  - 2. Image Processing > Combine Images**
    1. File > Load MNI T1 (1mm)
    2. Overlay > Load Overlay (load smoothed image from above)
    3. Input 1: Image, Input 2: Overlay
    4. Operation: Subtract
    5. Click "Execute"

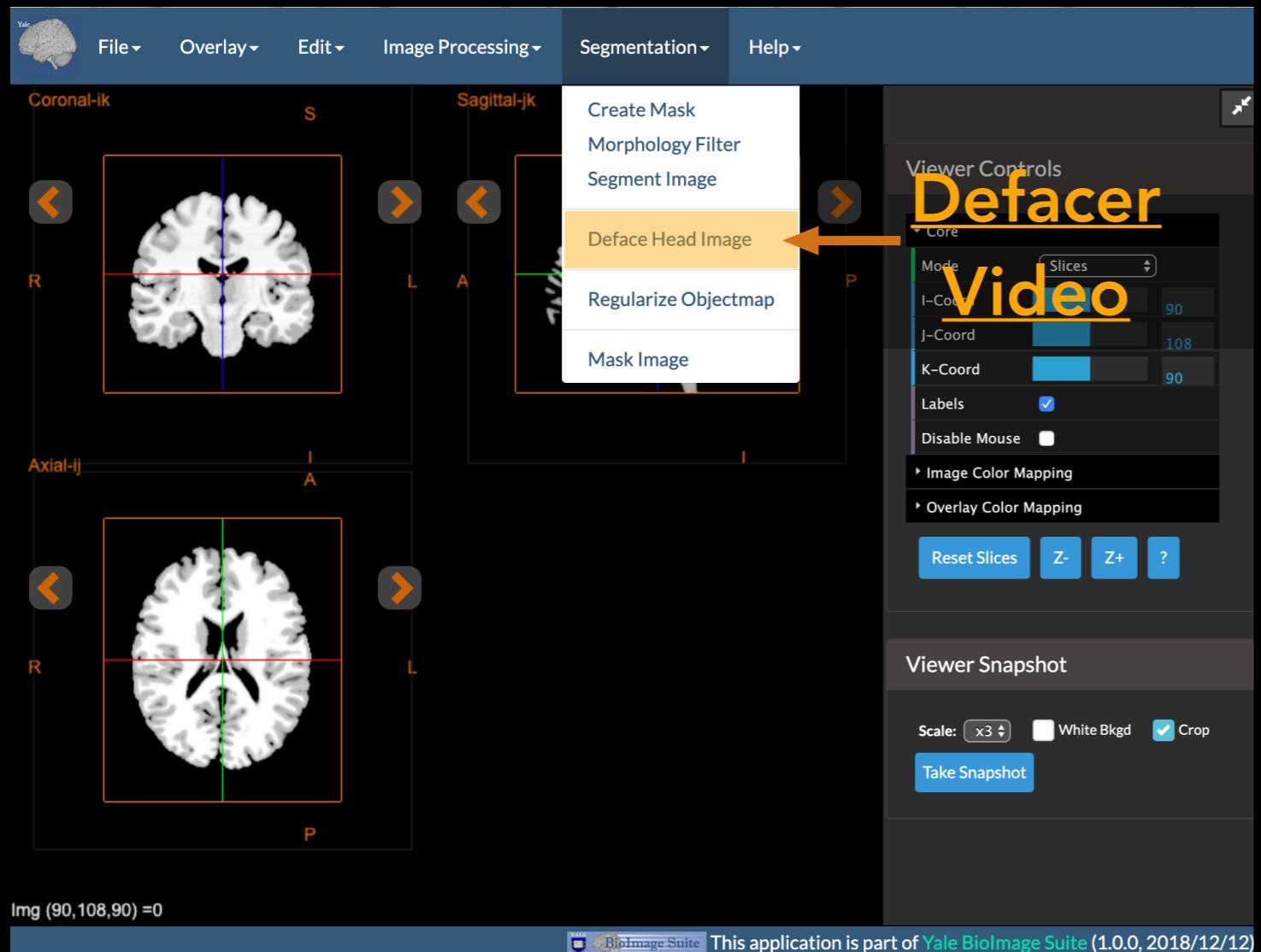




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# IMAGE PROCESSING

## Orthogonal Viewer



## Directions

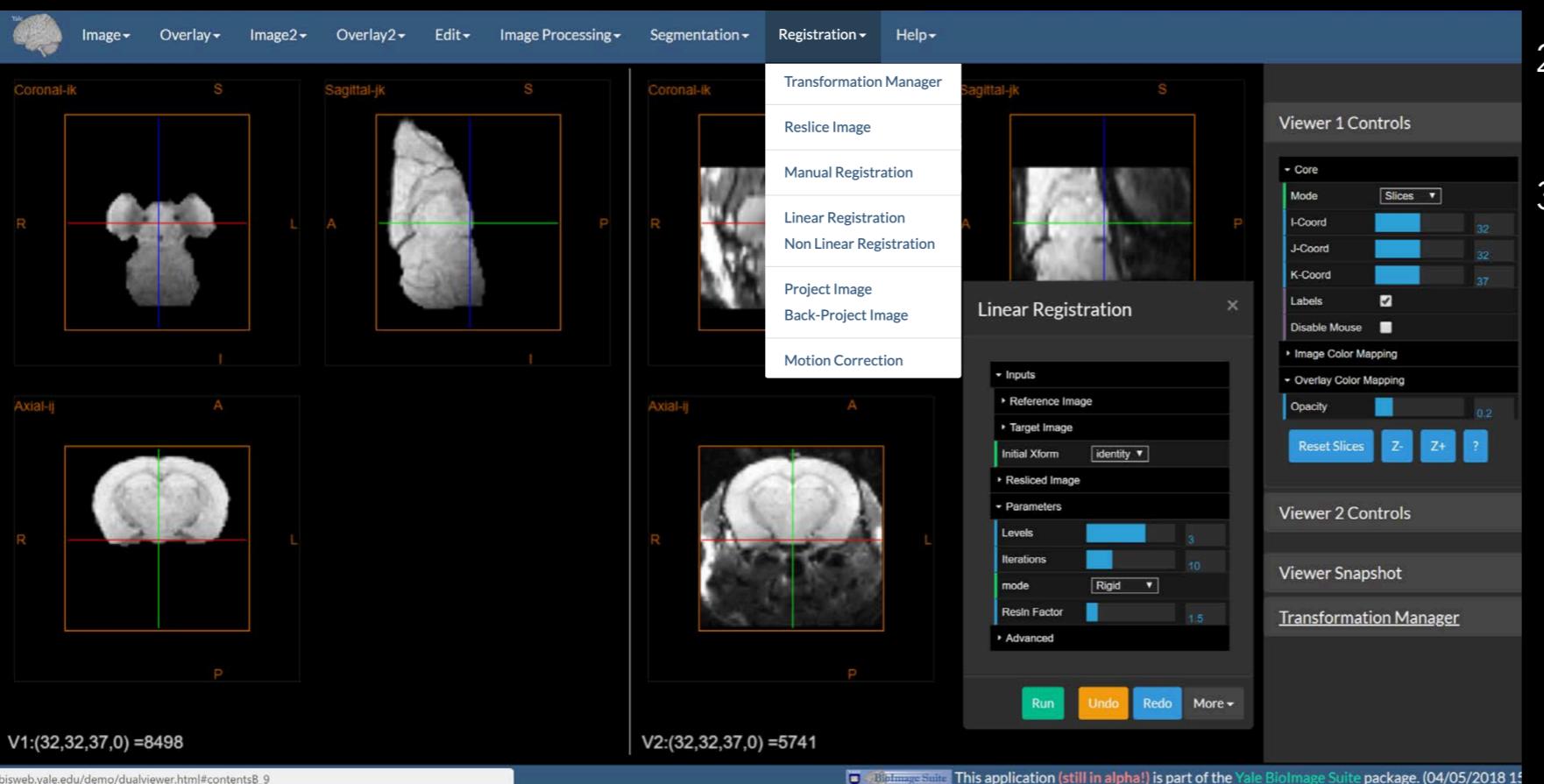
1. Applications > Orthogonal Viewer
2. Load Image and/or Overlay Data
  1. For Demo: File > Load MNI T1 (1mm)
3. Some example operations for demo
  1. **Image Processing > Smooth Image**
    1. Sigma = 5mm
    2. Click "Smooth"
    3. File > Save Image (for next step)
  2. **Image Processing > Combine Images**
    1. File > Load MNI T1 (1mm)
    2. Overlay > Load Overlay (load smoothed image from above)
    3. Input 1: Image, Input 2: Overlay
    4. Operation: Subtract
    5. Click "Execute"




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# IMAGE PROCESSING

## Dual Viewer Tool

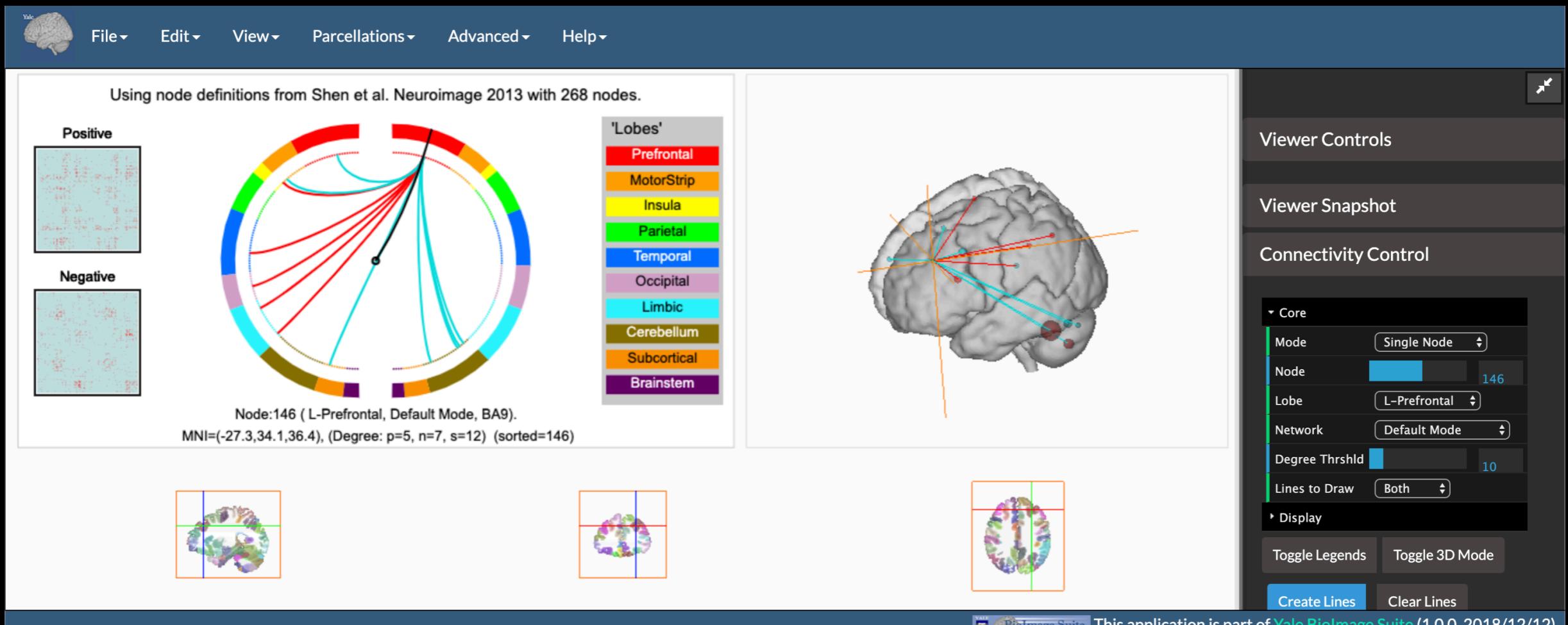


## Directions

1. Applications > Orthogonal Viewer
2. Load Image and/or Overlay Data
  1. For Demo: File > Load MNI T1 (1mm)
3. Some example operations for demo
  1. Image Processing > **Smooth** Image
    1. Sigma = 5mm
    2. Click "Smooth"
    3. File > Save Image (for next step)
  2. Image Processing > **Combine** Images
    1. File > Load MNI T1 (1mm)
    2. Overlay > Load Overlay (load smoothed image from above)
    3. Input 1: Image, Input 2: Overlay
    4. Operation: Subtract
    5. Click "Execute"



# CONNECTIVITY VIEWER



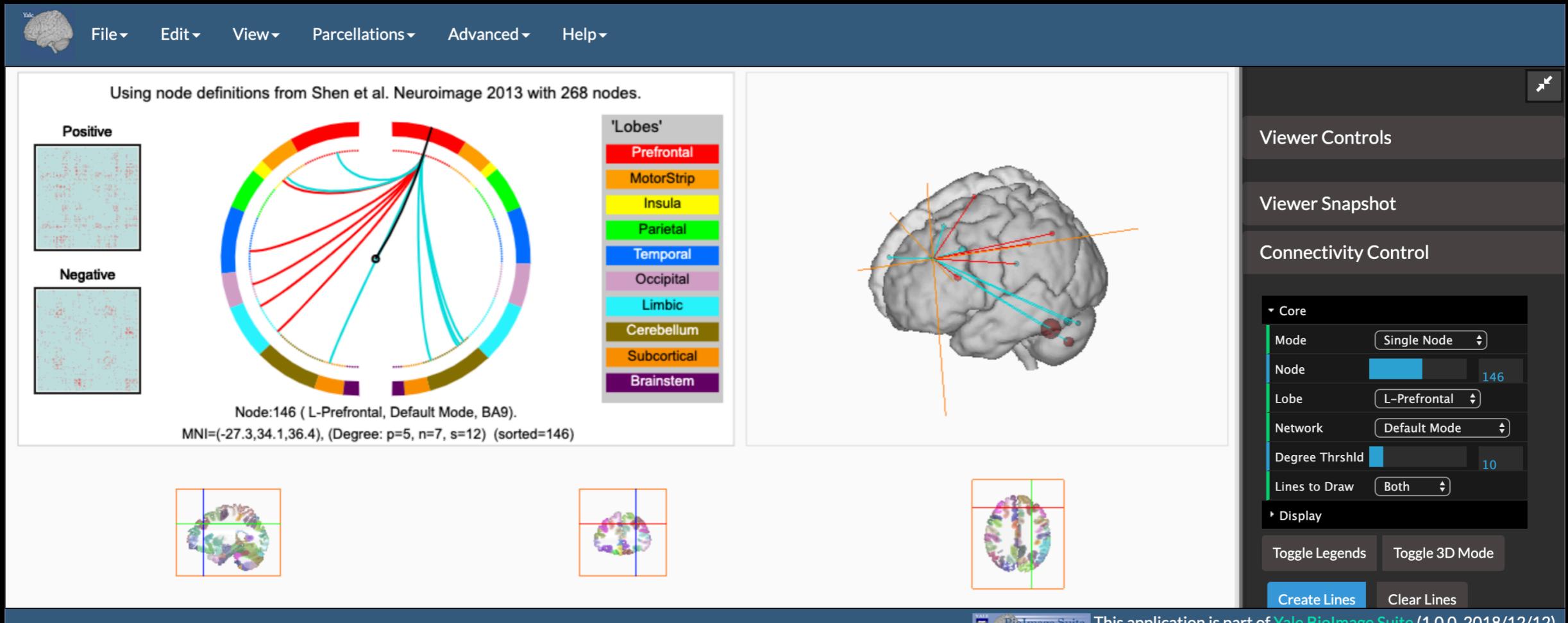
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# CONNECTIVITY VIEWER



Directions

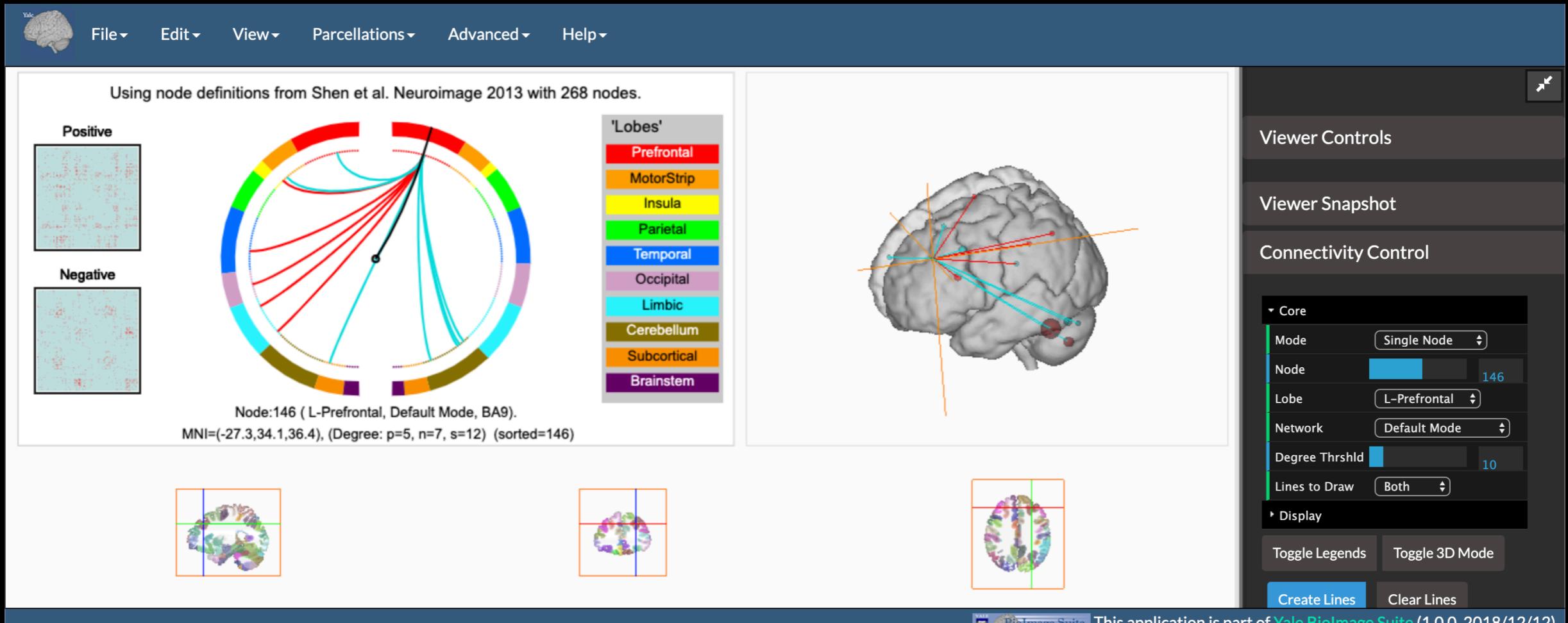
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# CONNECTIVITY VIEWER



## Directions

1. Applications > Connectivity Viewer

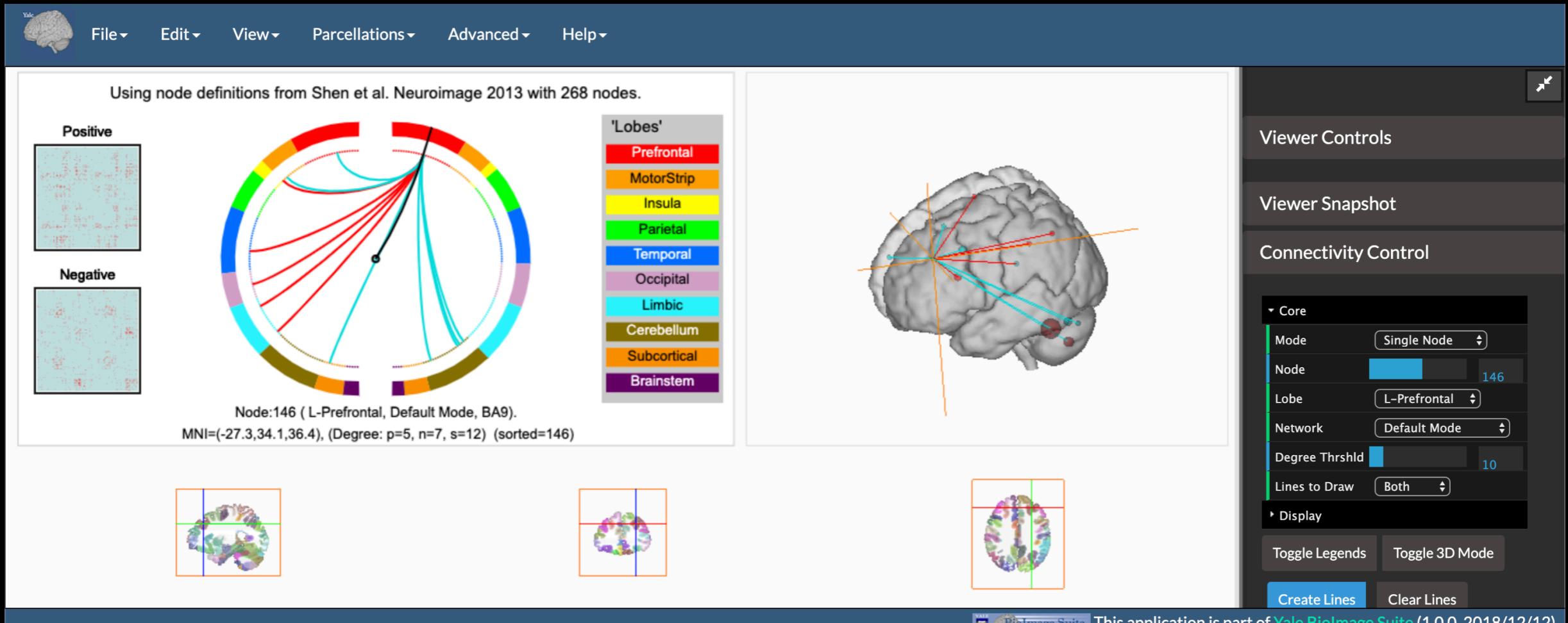
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# CONNECTIVITY VIEWER



## Directions

1. Applications > Connectivity Viewer
2. Load Connectivity Matrices

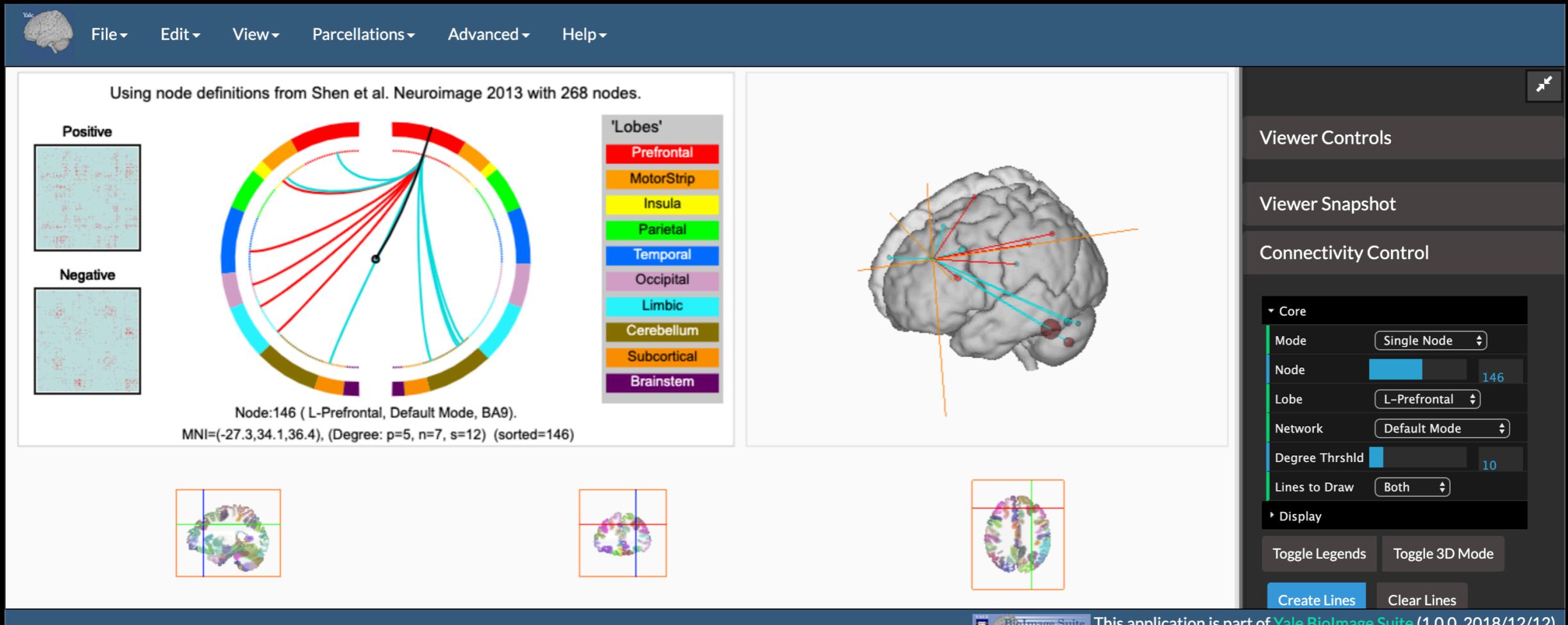
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# CONNECTIVITY VIEWER



## Directions

1. Applications > Connectivity Viewer
2. Load Connectivity Matrices
  1. For Demo: Help > Load Sample Matrices

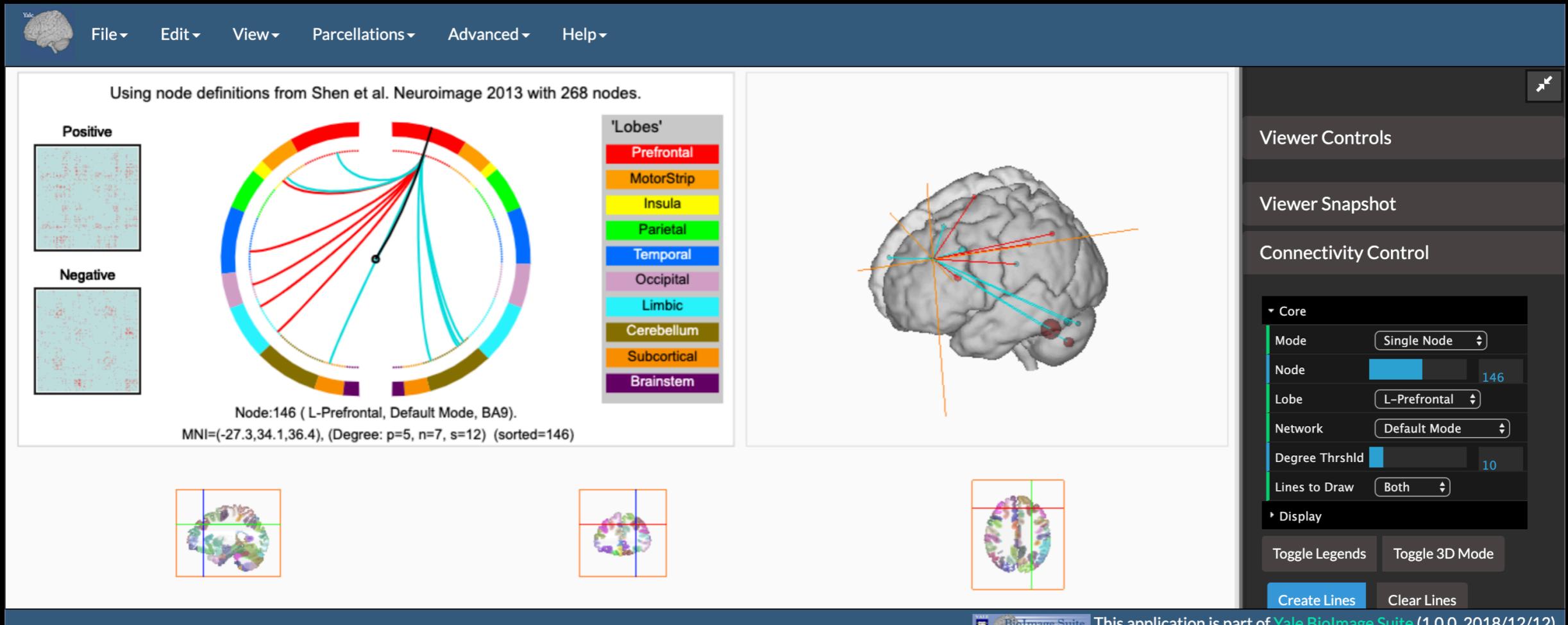
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# CONNECTIVITY VIEWER



## Directions

1. Applications > Connectivity Viewer
2. Load Connectivity Matrices
  1. For Demo: Help > Load Sample Matrices
3. Play with Viewer Controls

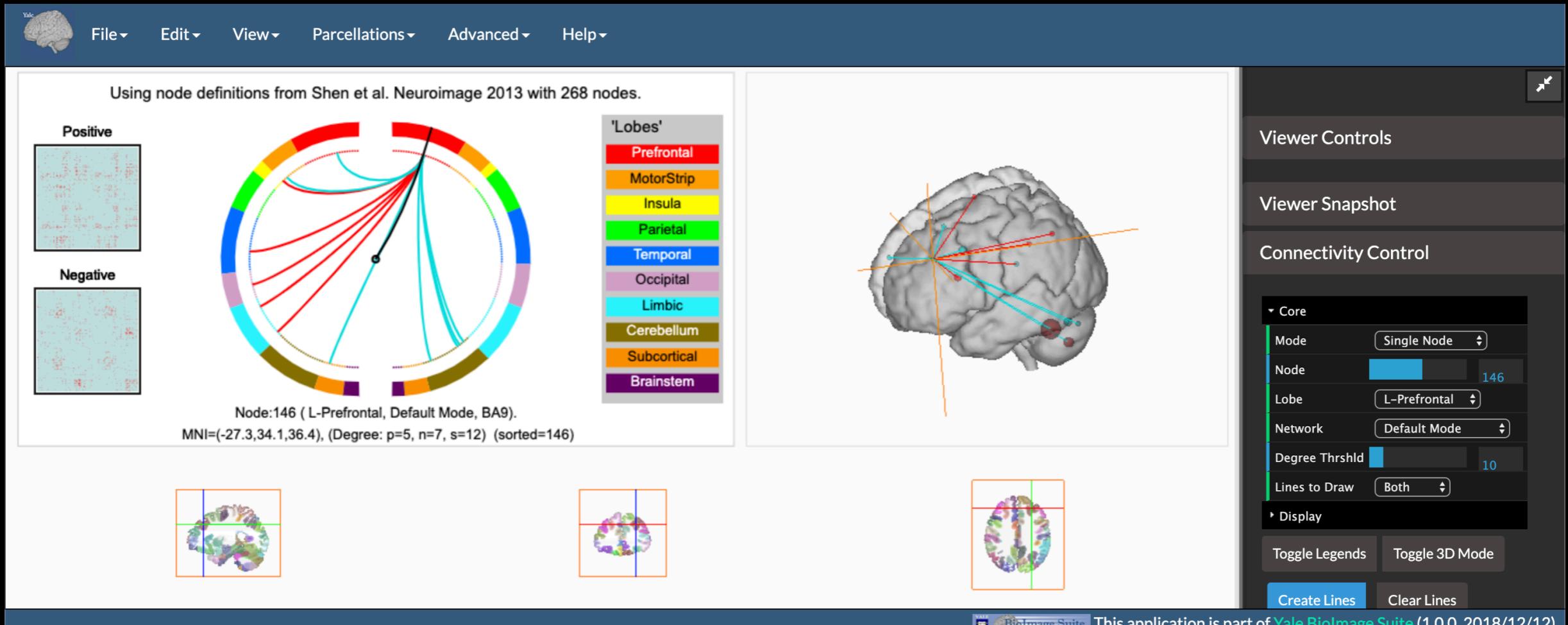
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# CONNECTIVITY VIEWER



## Directions

1. Applications > Connectivity Viewer
2. Load Connectivity Matrices
  1. For Demo: Help > Load Sample Matrices
3. Play with Viewer Controls
  1. Connectivity Control > Mode: All

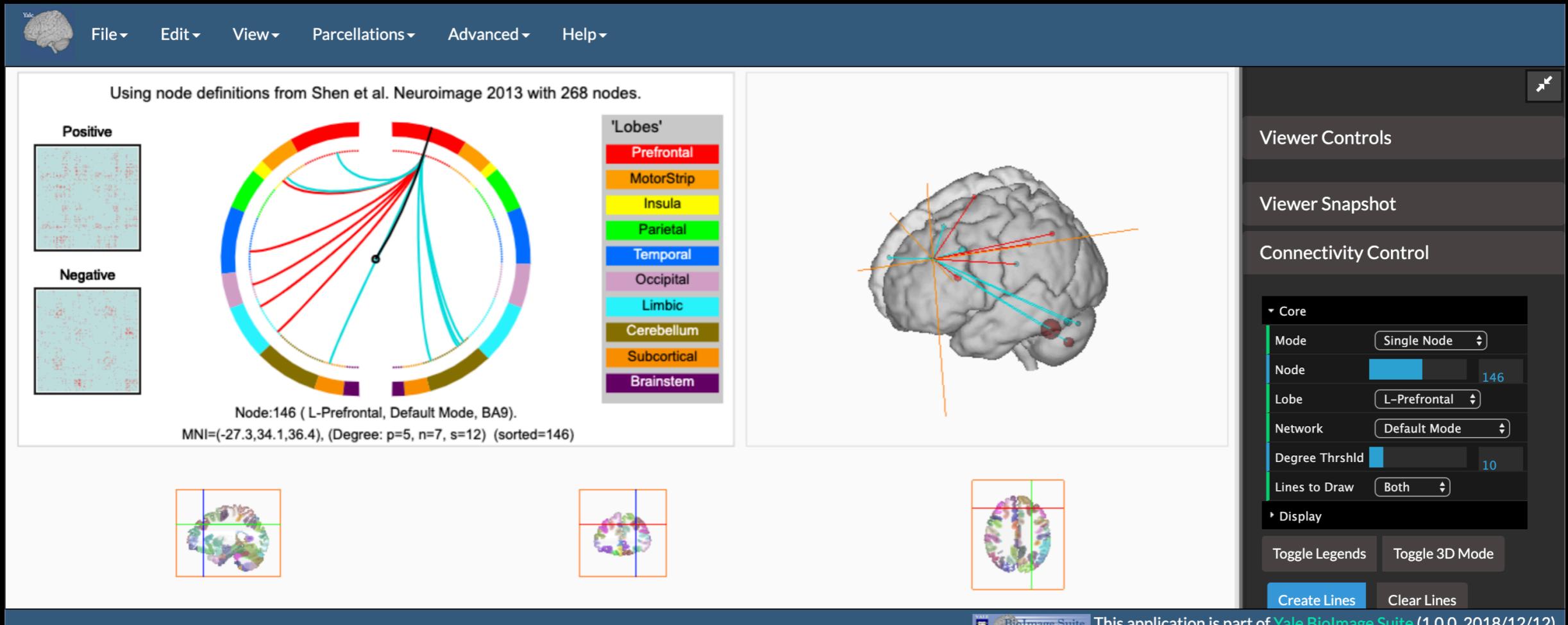
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# CONNECTIVITY VIEWER



## Directions

1. Applications > Connectivity Viewer
2. Load Connectivity Matrices
  1. For Demo: Help > Load Sample Matrices
3. Play with Viewer Controls
  1. Connectivity Control > Mode: All
  2. Click "Create Lines"

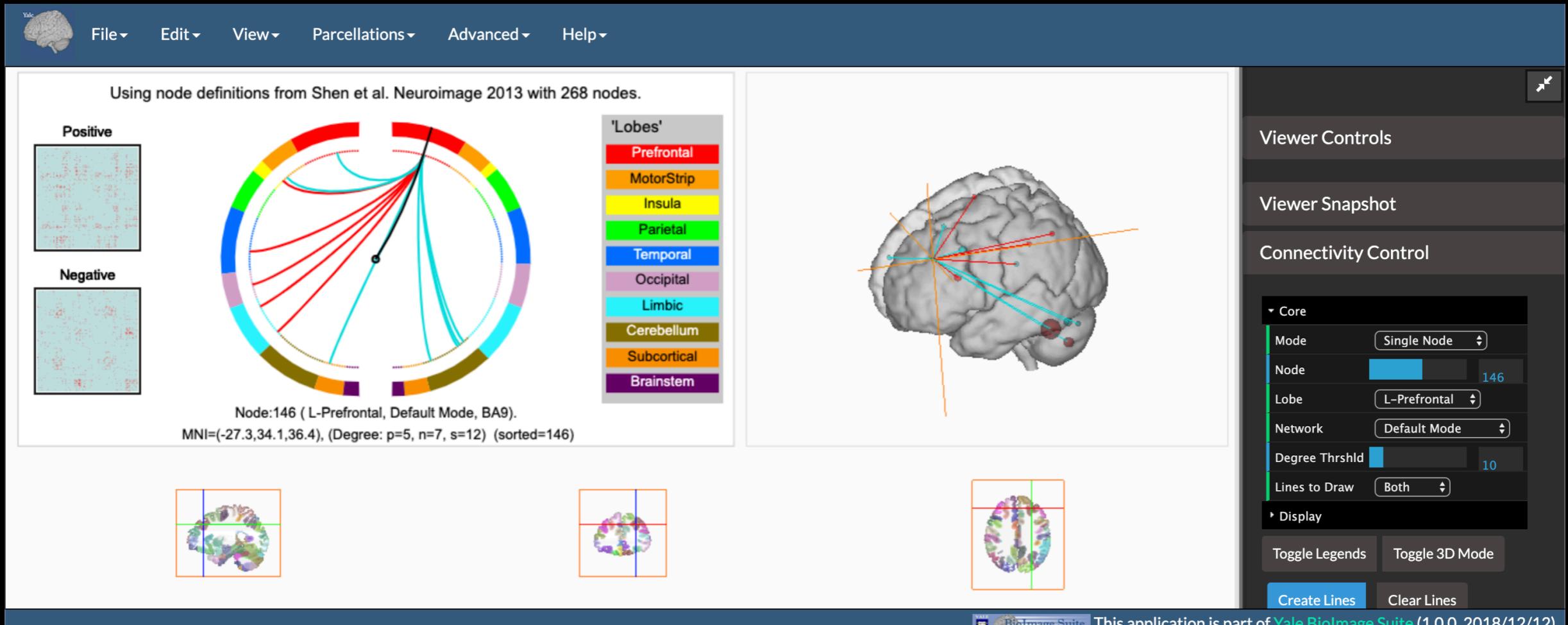
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# CONNECTIVITY VIEWER



## Directions

1. Applications > Connectivity Viewer
2. Load Connectivity Matrices
  1. For Demo: Help > Load Sample Matrices
3. Play with Viewer Controls
  1. Connectivity Control > Mode: All
  2. Click "Create Lines"
  3. Click "Chord Plot", "Summary Matrix"

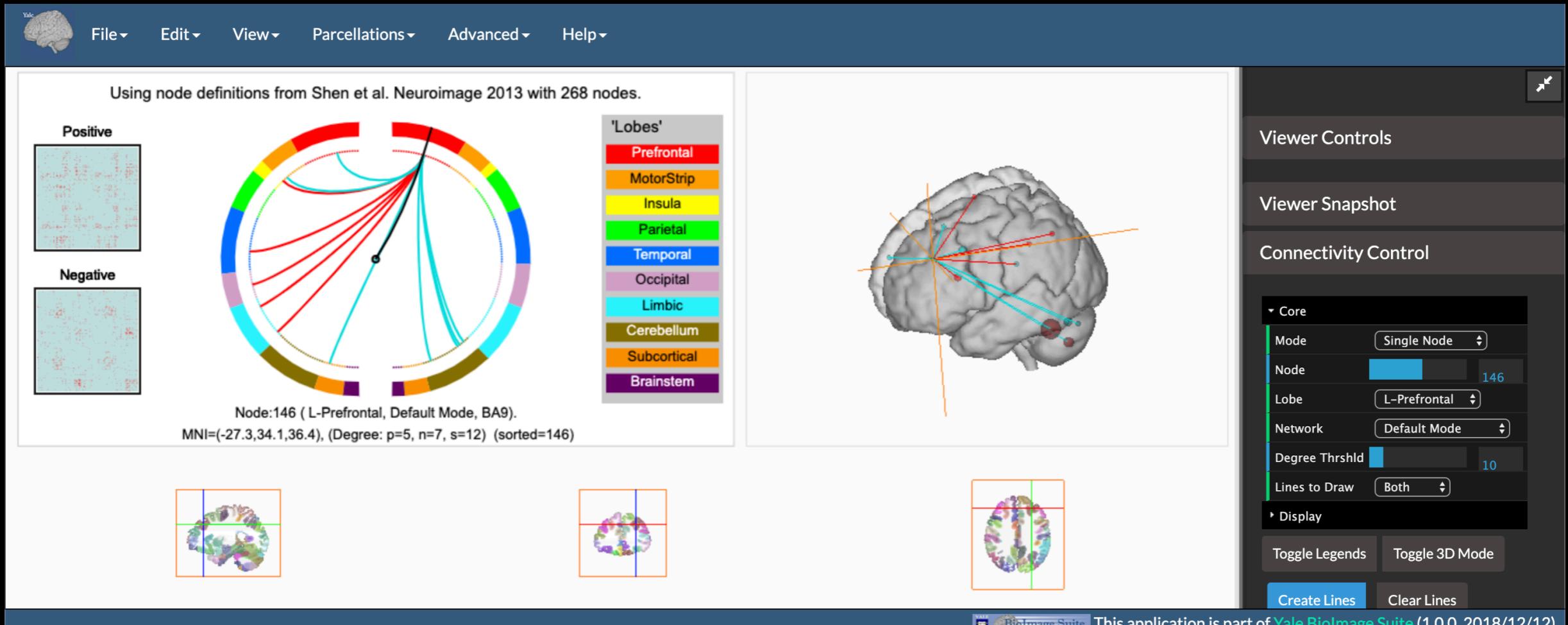
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# CONNECTIVITY VIEWER



## Directions

1. Applications > Connectivity Viewer
2. Load Connectivity Matrices
  1. For Demo: Help > Load Sample Matrices
3. Play with Viewer Controls
  1. Connectivity Control > Mode: All
  2. Click "Create Lines"
  3. Click "Chord Plot", "Summary Matrix"
  4. Click "Export as PNG"

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# REGRESSION TESTS

The screenshot shows the BioImage Suite Web Display Regression Test Runner interface. At the top, there's a menu bar with 'File', 'Overlay', 'Edit', and 'Help'. Below the menu, it says 'BiolImage Suite Web Display Regression Test Runner' with buttons for 'First: 1', 'Last: 10', 'Run Single Test' (highlighted in green), and 'Run Multiple Tests' (highlighted in orange). There are two tabs: 'Orthogonal' (selected) and 'Mosaic'. The main area displays three brain slices: a sagittal slice on the left, a coronal slice in the middle, and a axial slice on the right, each with a red crosshair. To the right of these slices is a 'Viewer Controls' panel with sections for 'Core' (Mode: Slices, I-Coord, J-Coord, K-Coord, Labels checked, Disable Mouse unchecked), 'Image Color Mapping', and 'Overlay Color Mapping'. It also has buttons for 'Reset Slices', 'Z+', and 'Z-'. Below the controls is a 'Viewer Snapshot' section showing a preview of the slices. On the far right, a 'Gold 3' panel displays three brain slices and the text 'Test:2 cc=1.000 P A S S E D'. Underneath this, it says 'Reading app state from images/testdata/viewer.biswebstate', 'Read result from: images/testdata/test2.png? time=1559596918462', 'Result: {"testresult":true,"value":0.999569161867206}', and 'Test:2 cc=1.000 P A S S E D'. At the bottom left, a status message reads 'Tests for version=2018/12/12: completed=2/10, passed=2/10, failed=0/10. Details: Passed=[2], Failed=(none), Intentionally Failed=[1]'. A small brain icon is in the bottom right corner.

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Follow along in the app:



# REGRESSION TESTS

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The screenshot shows the BioImage Suite Web Display Regression Test Runner interface. At the top, there's a menu bar with 'File', 'Overlay', 'Edit', and 'Help'. Below it, a toolbar has buttons for 'First: 1', 'Last: 10', 'Run Single Test' (highlighted in green), and 'Run Multiple Tests' (highlighted in orange). The main area displays three brain slices in orthogonal view (left, right, and bottom). To the right is a 'Viewer Controls' panel with sections for 'Core' (Mode: Slices, I-Coord, J-Coord, K-Coord, Labels checked, Disable Mouse unchecked), 'Image Color Mapping', and 'Overlay Color Mapping'. It includes buttons for 'Reset Slices', 'Z+', and 'Z-'. At the bottom of the panel is a 'Viewer Snapshot' section. On the far right, a 'Gold 3' panel shows three brain slices and displays the text: 'Test: 2 cc=1.000 P A S S E D', 'Reading app state from images/testdata/viewer.biswebstate', 'Read result from: images/testdata/test2.png? time=1559596918462', 'Result: {"testresult":true,"value":0.999569161867206}', and 'Test: 2 cc=1.000 P A S S E D'. At the very bottom left, a status message reads: 'Tests for version=2018/12/12: completed=2/10, passed=2/10, failed=0/10. Details: Passed=[2], Failed=(none), Intentionally Failed=[1]'.



Follow along in the app:



# REGRESSION TESTS

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The screenshot shows the BioImage Suite Web Display Regression Test Runner interface. At the top, there's a menu bar with 'File', 'Overlay', 'Edit', and 'Help'. Below it, a toolbar has buttons for 'First: 1', 'Last: 10', 'Run Single Test' (green), and 'Run Multiple Tests' (orange). The main area displays four brain slices in a 2x2 grid. On the left, there are buttons for 'Orthogonal' and 'Mosaic' view modes. A central panel titled 'Viewer Controls' contains settings for 'Mode' (set to 'Slices'), coordinate sliders for I-Coord, J-Coord, and K-Coord, a 'Labels' checkbox (checked), and a 'Disable Mouse' checkbox. It also includes sections for 'Image Color Mapping' and 'Overlay Color Mapping'. Buttons for 'Reset Slices', 'Z+', and 'Z-' are at the bottom. To the right of the slices is a 'Gold 3' panel showing three brain slices and a status message: 'Test:2 cc=1.000 P A S S E D'. Below this, log messages show the reading of app state from 'images/testdata/viewer.biswebstate' and the result from 'images/testdata/test2.png?time=1559596918462'. The log also includes a 'Result' section with JSON data and another test message: 'Test:2 cc=1.000 P A S S E D'. At the bottom of the interface, a status bar displays: 'Tests for version=2018/12/12: completed=2/10, passed=2/10, failed=0/10. Details: Passed=[2], Failed=(none), Intentionally Failed=[1]'.

Directions





# REGRESSION TESTS

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BioImage Suite Web Display Regression Test Runner

First: 1 Last: 10 Run Single Test Run Multiple Tests

Orthogonal Mosaic

Tests for version=2018/12/12: completed=2/10, passed=2/10, failed=0/10. Details: Passed=[2], Failed=(none), Intentionally Failed=[1]

## Directions

1. Developer Info > Run Display Regression Tests





# REGRESSION TESTS

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BioImage Suite Web Display Regression Test Runner

First: 1 Last: 10 Run Single Test Run Multiple Tests

Orthogonal Mosaic

Viewer Controls

Core Mode Slices  
I-Coord J-Coord K-Coord Labels Disable Mouse  
Image Color Mapping Overlay Color Mapping  
Reset Slices Z- Z+ ?  
Viewer Snapshot

Gold 3

Test:2 cc=1.000 PASSED

Reading app state from images/testdata/viewer.biswebstate  
Read result from: images/testdata/test2.png?time=1559596918462  
Result:  
{"testresult":true,"value":0.999569161867206}

Test:2 cc=1.000 PASSED

Tests for version=2018/12/12: completed=2/10, passed=2/10, failed=0/10. Details: Passed=[2], Failed=(none), Intentionally Failed=[1]

## Directions

1. Developer Info > Run Display Regression Tests
1. Click "Run Multiple Tests"





# REGRESSION TESTS

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BioImage Suite Web Display Regression Test Runner

First: 1 Last: 10 Run Single Test Run Multiple Tests

Orthogonal Mosaic

Viewer Controls

Core

- Mode: Slices
- I-Coord: [progress bar]
- J-Coord: [progress bar]
- K-Coord: [progress bar]
- Labels:
- Disable Mouse:

Image Color Mapping

Overlay Color Mapping

Reset Slices Z-

Z+ ?

Viewer Snapshot

Gold 3

Test:2 cc=1.000 PASSED

Reading app state from images/testdata/viewer.biswebstate

Read result from: images/testdata/test2.png? time=1559596918462

Result: {"testresult":true,"value":0.999569161867206}

Test:2 cc=1.000 PASSED

Tests for version=2018/12/12: completed=2/10, passed=2/10, failed=0/10. Details: Passed=[2], Failed=(none), Intentionally Failed=[1]

## Directions

1. Developer Info > Run Display Regression Tests
  1. Click "Run Multiple Tests"
  2. Can also run Module Regression Tests





# REGRESSION TESTS

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BioImage Suite Web Display Regression Test Runner

First: 1 Last: 10 Run Single Test Run Multiple Tests

Orthogonal Mosaic

Viewer Controls

Core Mode Slices  
I-Coord J-Coord K-Coord Labels Disable Mouse  
Image Color Mapping Overlay Color Mapping  
Reset Slices Z- Z+ ?  
Viewer Snapshot

Gold 3

Test:2 cc=1.000 PASSED

Reading app state from images/testdata/viewer.biswebstate  
Read result from: images/testdata/test2.png?time=1559596918462  
Result:  
{"testresult":true,"value":0.999569161867206}

Test:2 cc=1.000 PASSED

Tests for version=2018/12/12: completed=2/10, passed=2/10, failed=0/10. Details: Passed=[2], Failed=(none), Intentionally Failed=[1]

## Directions

1. Developer Info > Run Display Regression Tests
  1. Click "Run Multiple Tests"
  2. Can also run Module Regression Tests
    1. Specify module to test under "Testname"





# REGRESSION TESTS

Biopsy your software!

BioImage Suite Web Display Regression Test Runner  
First: 1 Last: 10 Run Single Test Run Multiple Tests

Orthogonal Mosaic

Viewer Controls  
Core Mode Slices  
I-Coord J-Coord K-Coord Labels  
Test: 2 cc=1.000 PASSED

Biome Suite Web Regression Test Runner  
First: 0 Last: 87 Testname: computeCorrelation WebWorker Run Tests

Running Tests  
Executing tests 0:87 (Max index=87). Only running tests with name=computeCorrelation  
Tests for version=2018/12/12: complete

**Test 3: computeCorrelation**

- Command: computeCorrelation -i testdata/ButterWorthOutput.csv --zscore false
- Test details: --test\_target testdata/newtests/goldcorrelation.matr --test\_type matrix --test\_comparision ssd --test\_threshold 0.01
- Should pass: true

.... test execution time=0.21s  
.... WASM memory size=16 MB.

Test completed, now checking results.

Comparing matrix using ssd and threshold=0.01 Module computeCorrelation test passed.  
deviation (ssd) from expected: 2.537576312709809e-7 < 0.01

► Details

Tests for version=2018/09/03: completed=1/88, passed=1/88, failed=0/88, skipped=87/88

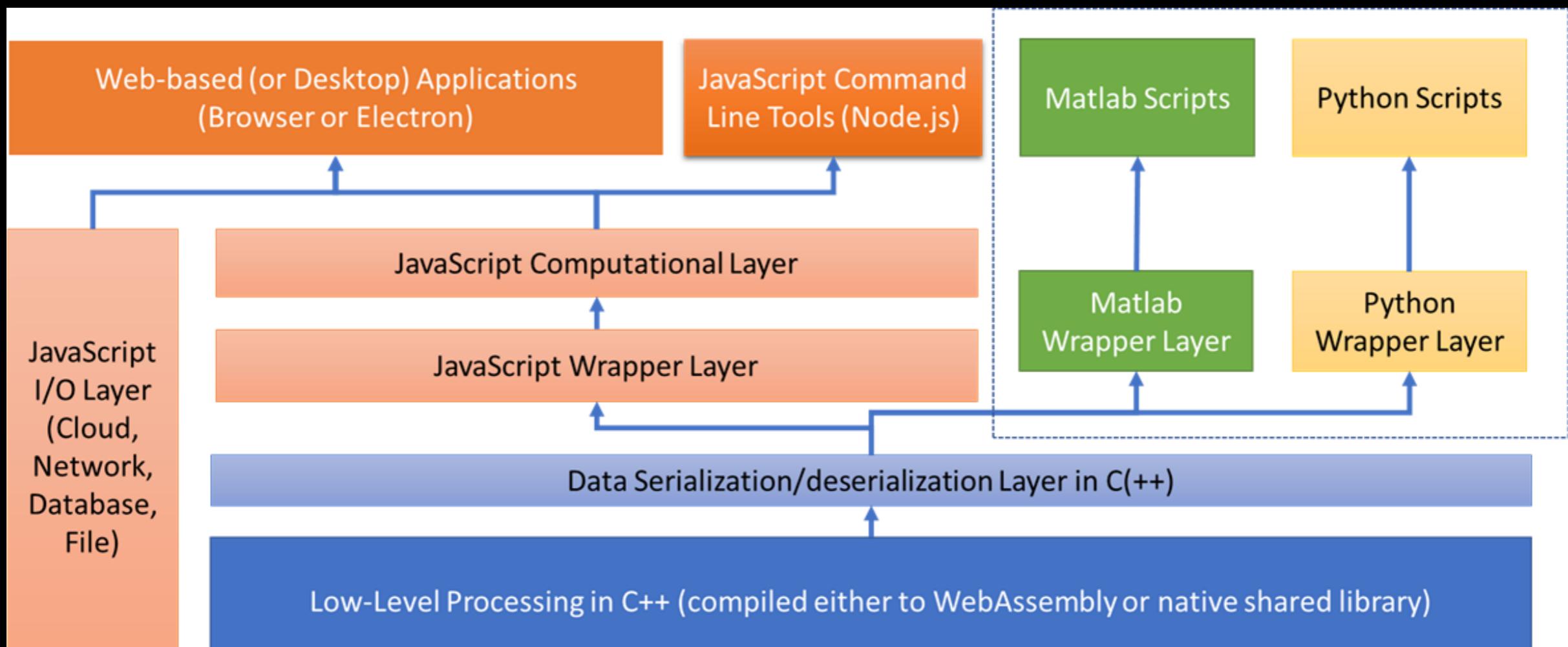
```
{
  "command": "computeCorrelation -i testdata/ButterWorthOutput.csv --zscore false",
  "test": "--test_target testdata/newtests/goldcorrelation.matr --test_type matrix"
}
```

## Directions

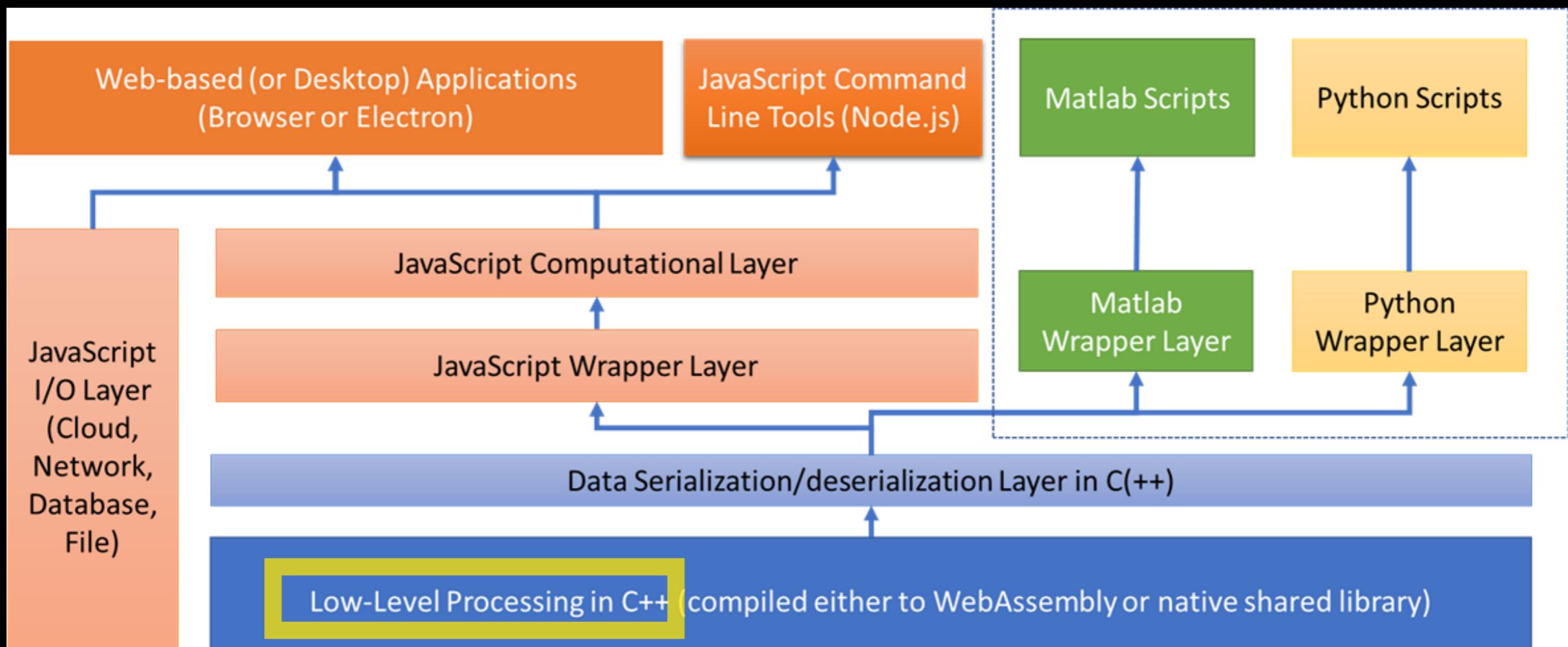
1. Developer Info > Run Display Regression Tests
  1. Click "Run Multiple Tests"
  2. Can also run Module Regression Tests
  1. Specify module to test under "Testname"



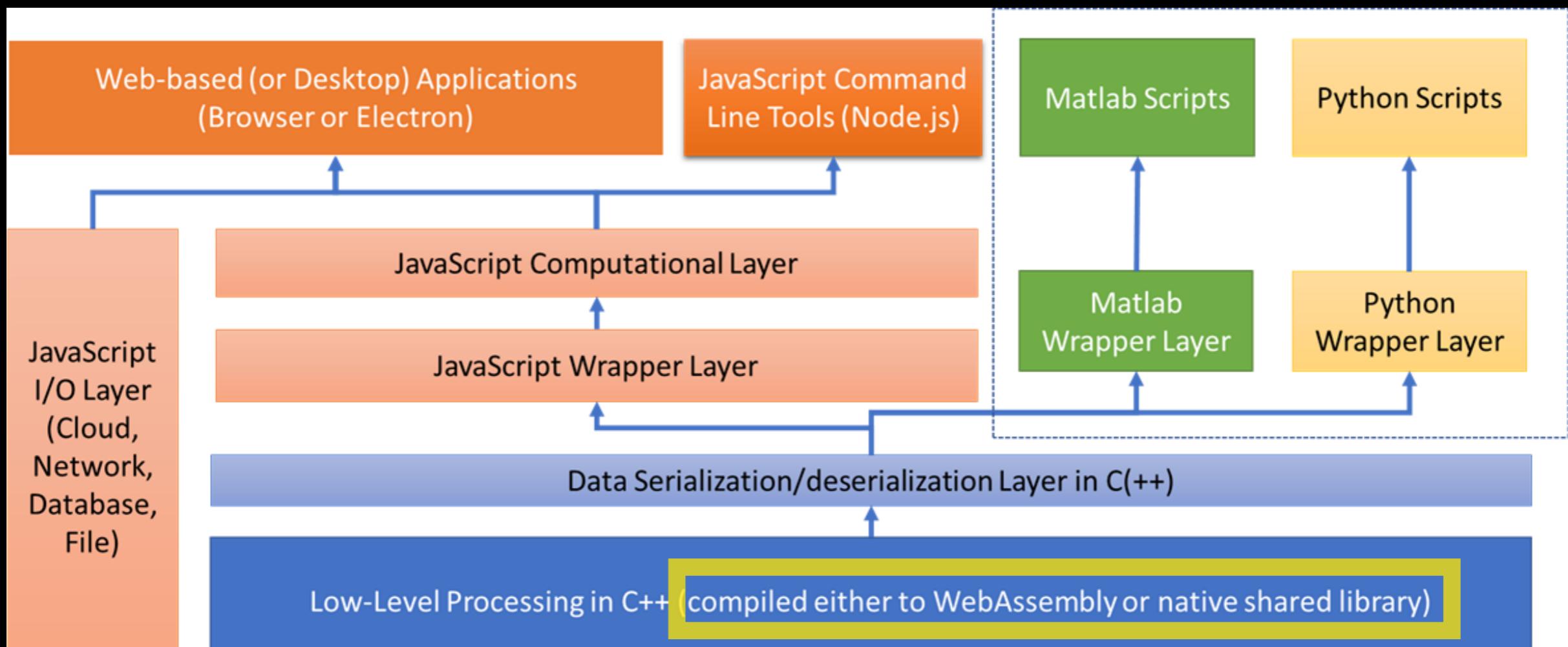
# ARCHITECTURE



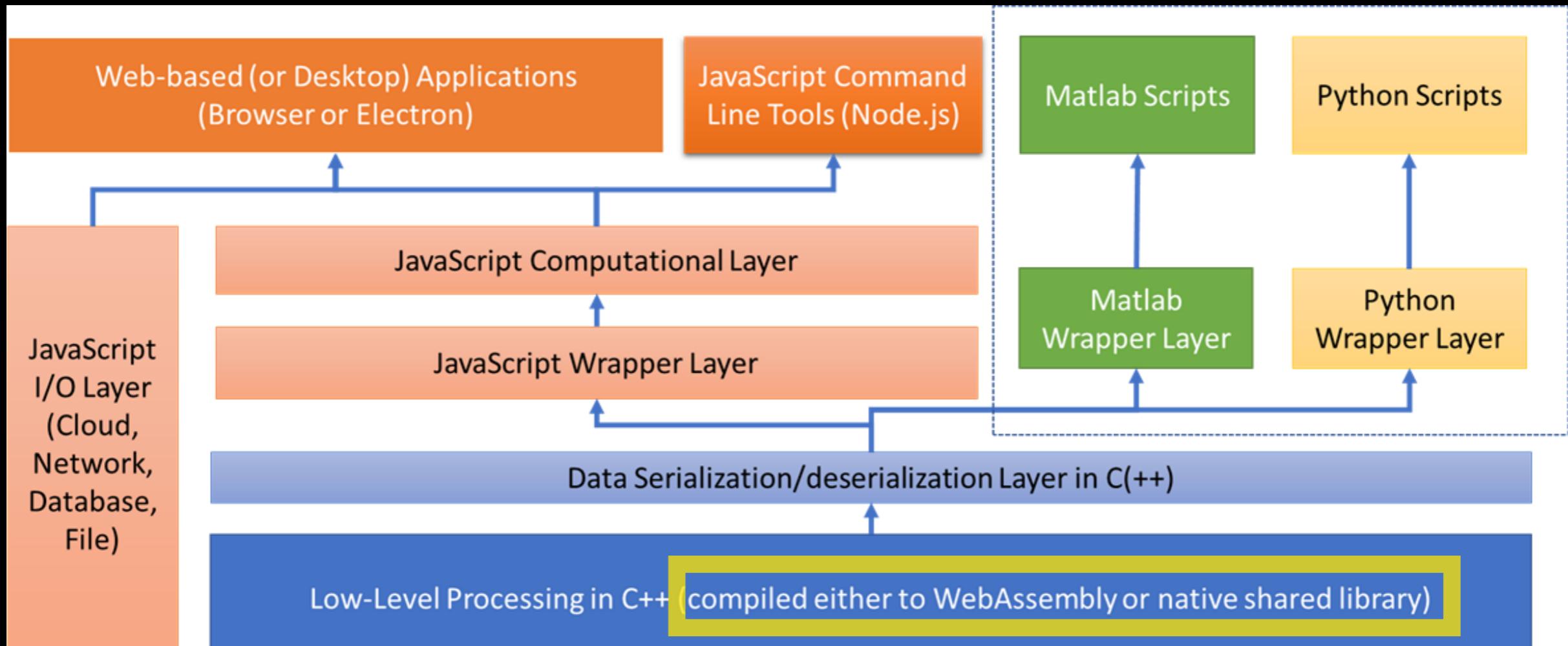
# ARCHITECTURE



# ARCHITECTURE



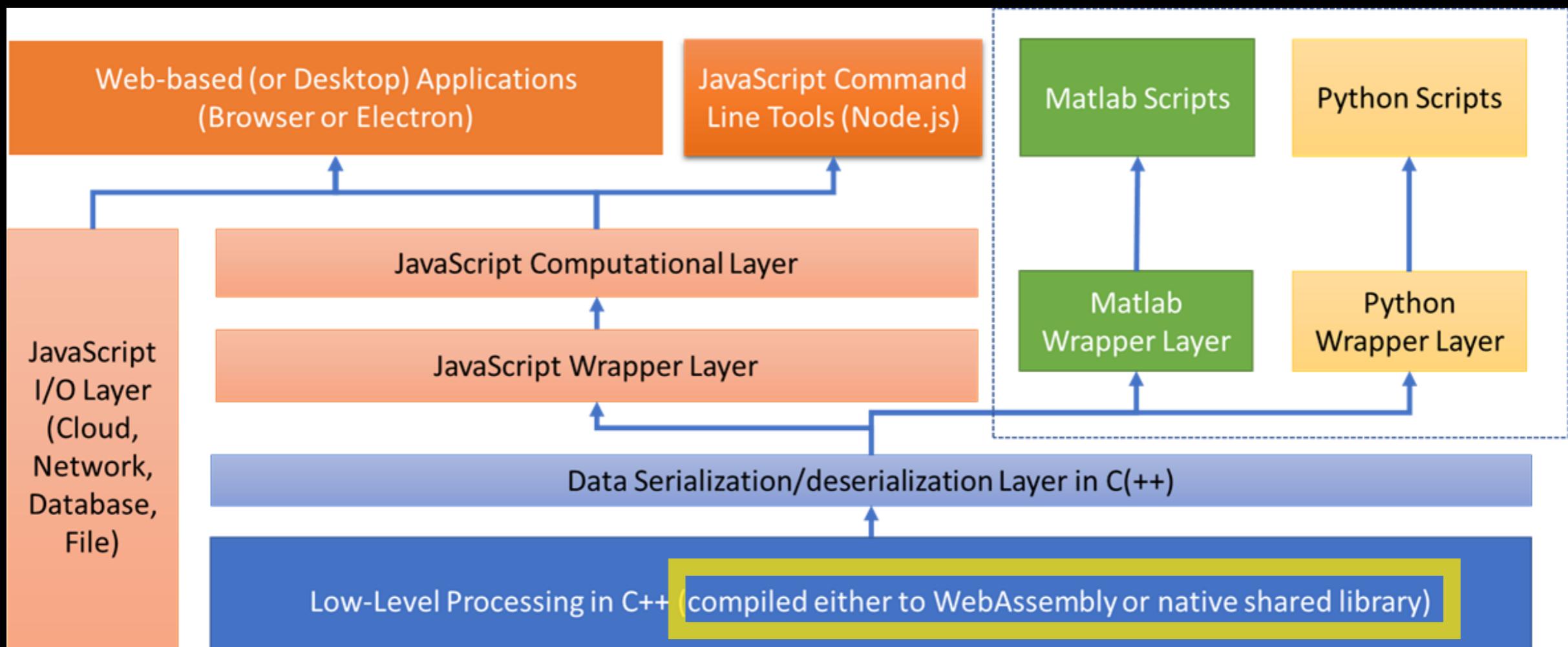
# ARCHITECTURE



Makes C++ easy to use in browser



# ARCHITECTURE

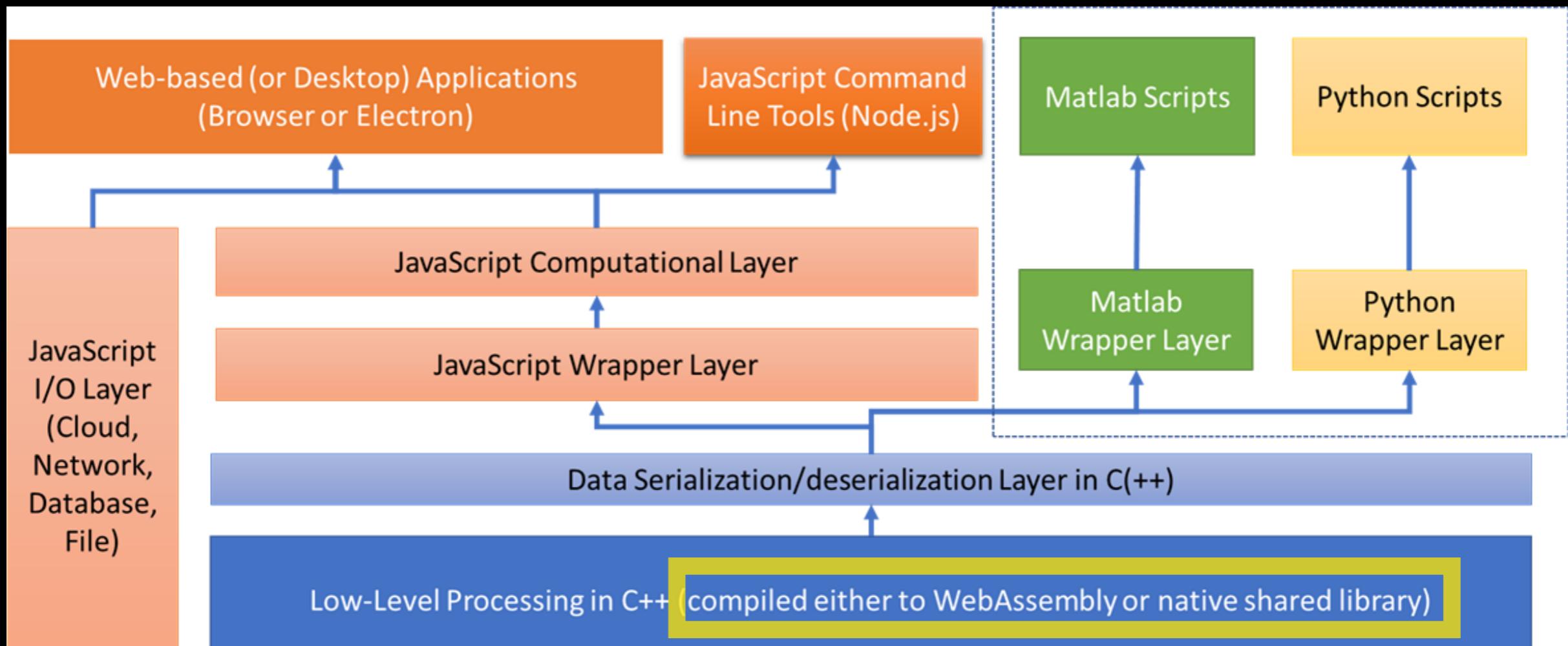


Makes C++ easy to use in browser

Compared with C++:



# ARCHITECTURE



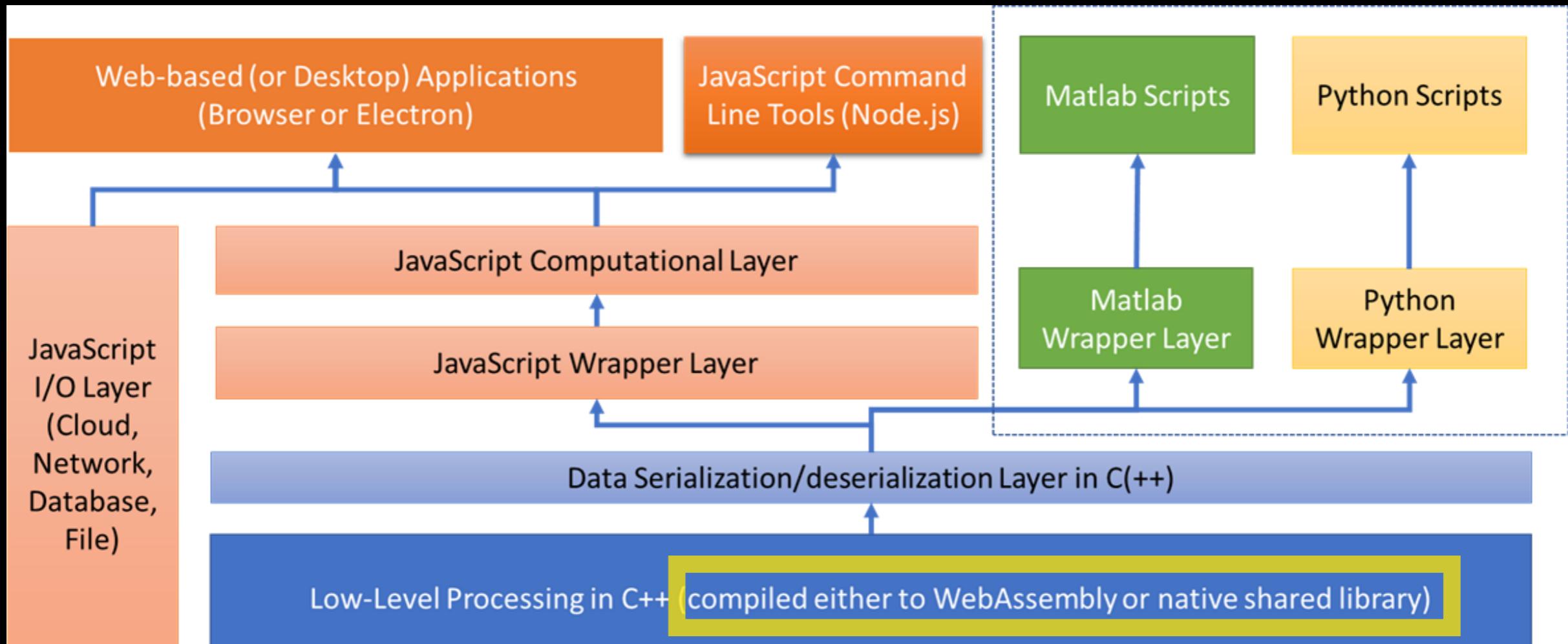
Makes C++ easy to use in browser



Compared with C++:  
JavaScript 50% speed



# ARCHITECTURE



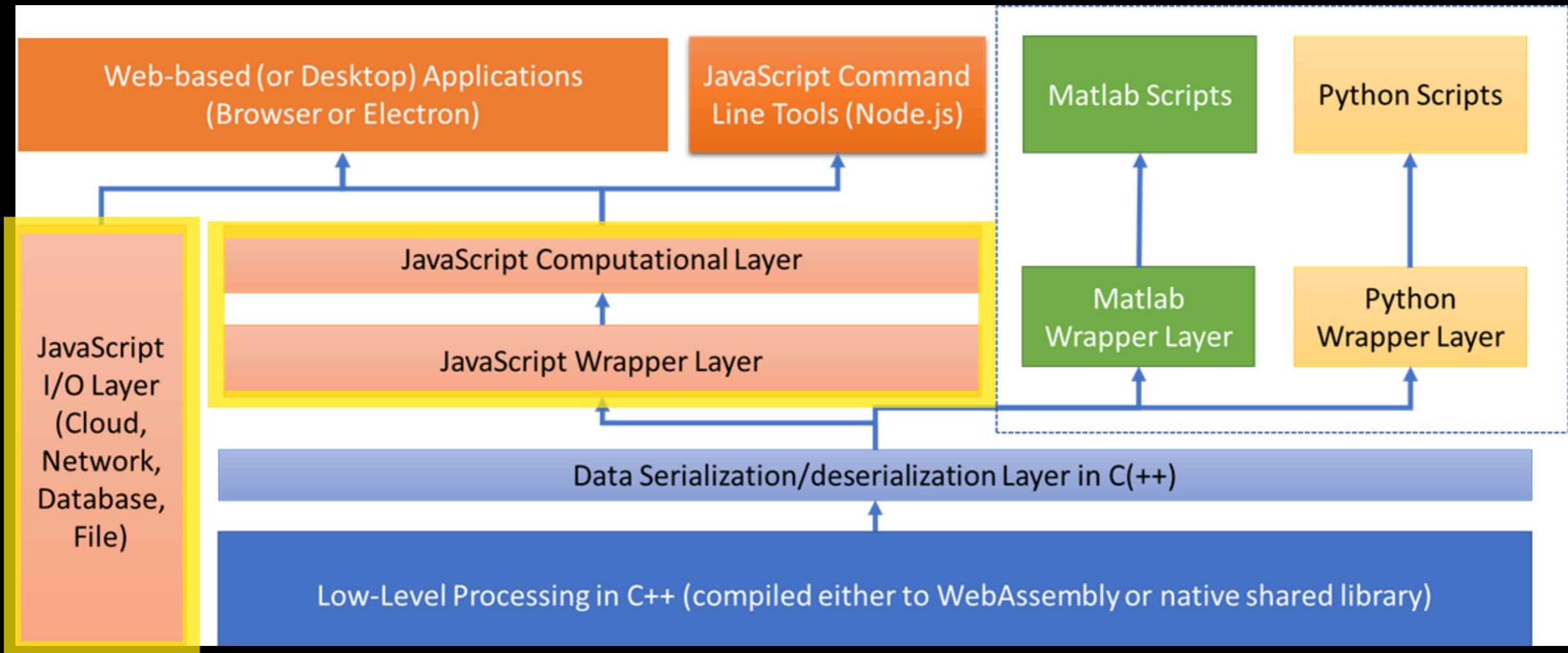
Makes C++ easy to use in browser



Compared with C++:  
JavaScript 50% speed  
WebAssembly 90% speed



# ARCHITECTURE



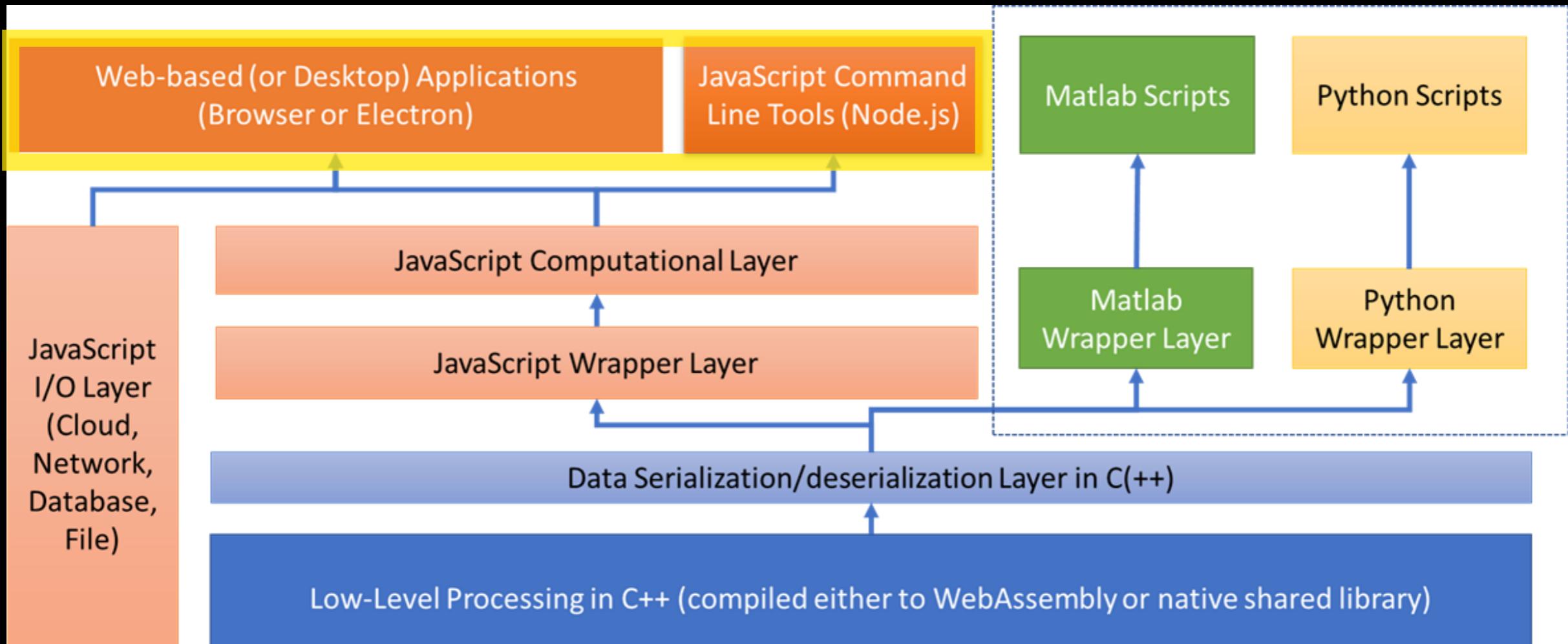
Makes C++ easy to use in browser



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# ARCHITECTURE



Makes C++ easy to use in browser

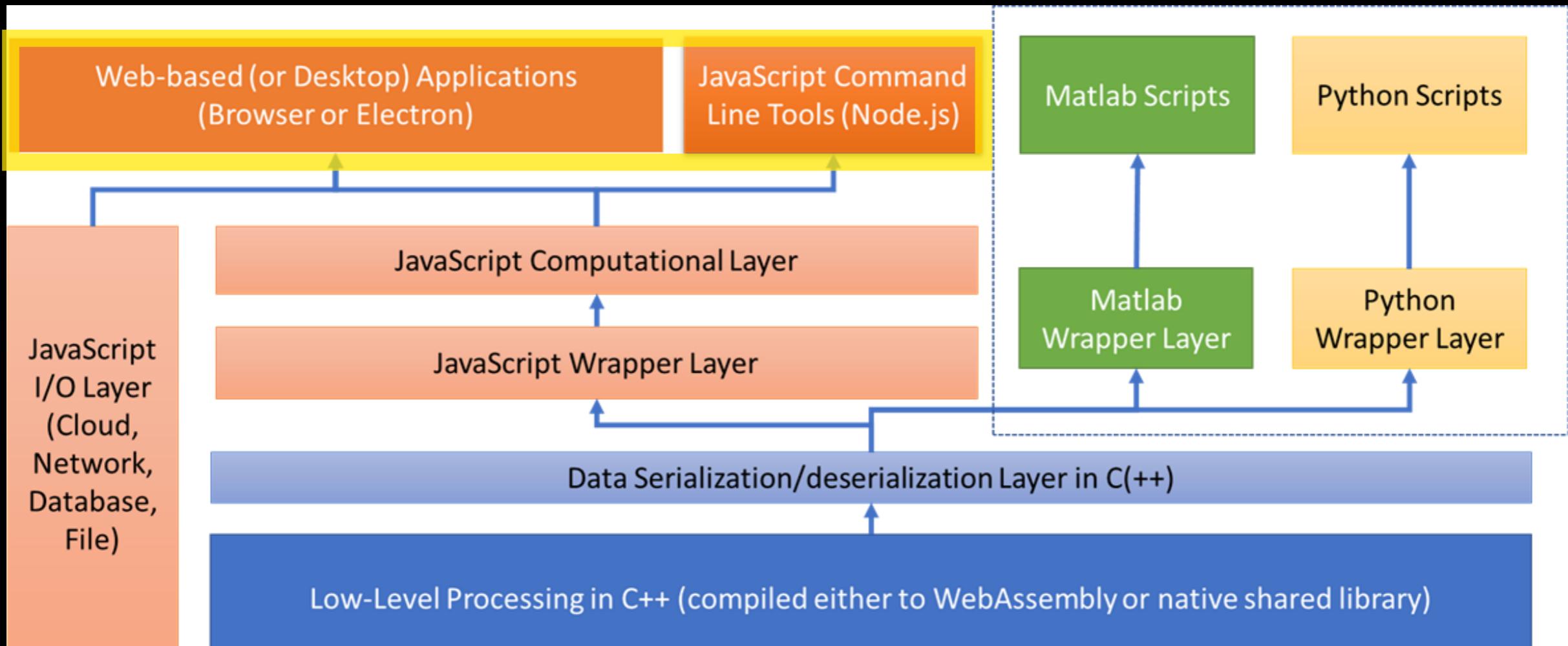


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# ARCHITECTURE

No installation!



Makes C++ easy to use in browser

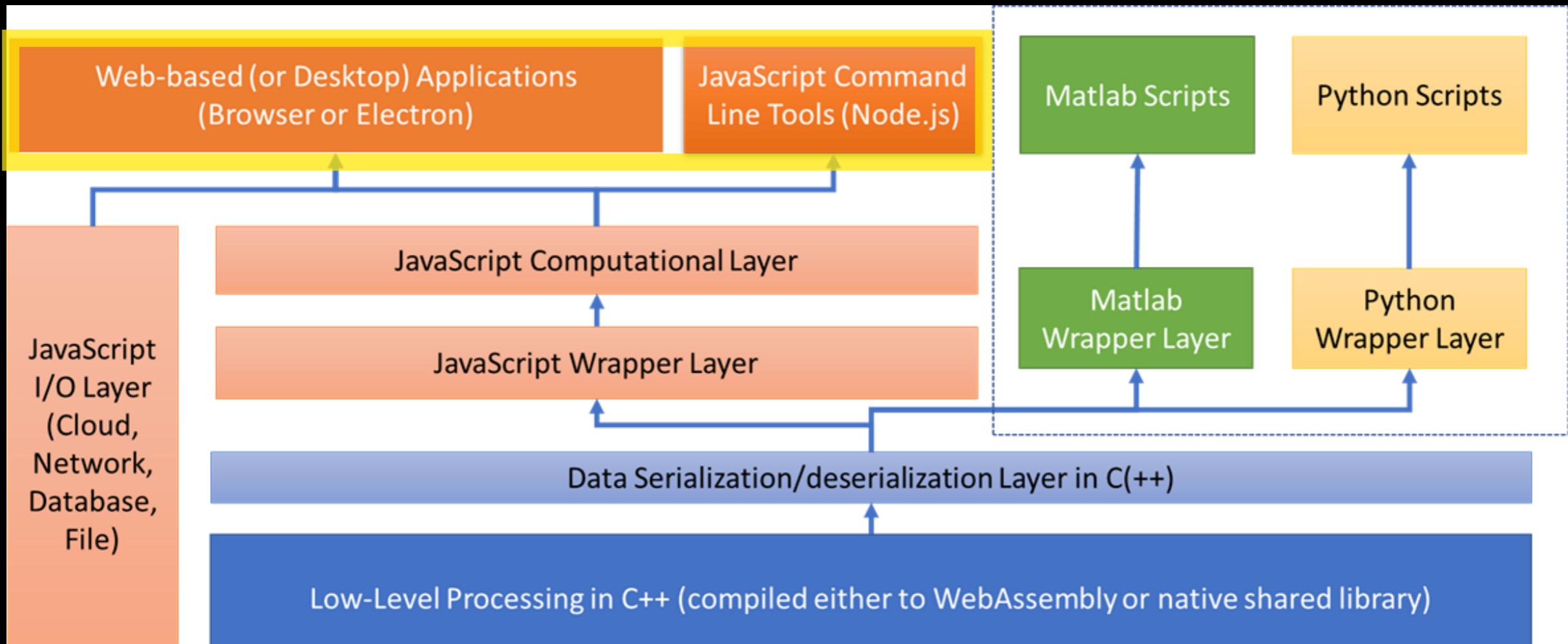


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# ARCHITECTURE

No installation!  
No servers!



Makes C++ easy to use in browser

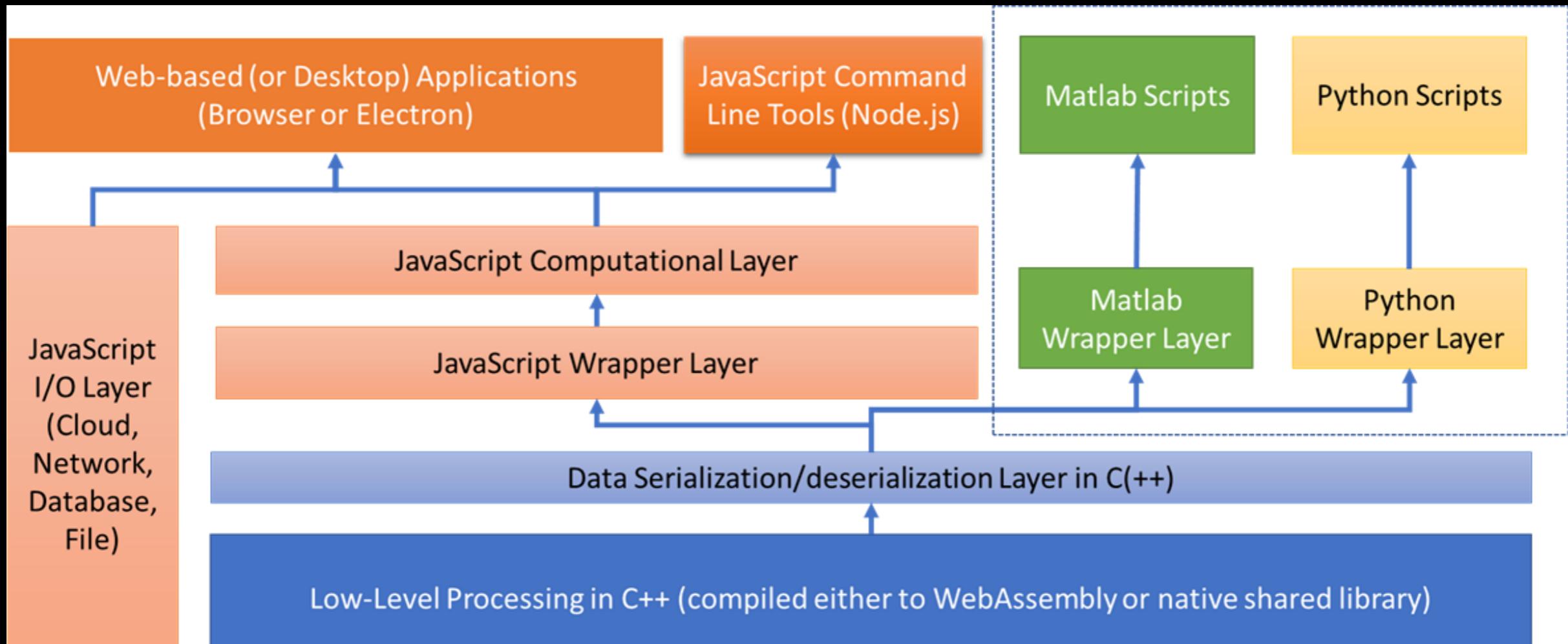


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Makes C++ easy to use in browser

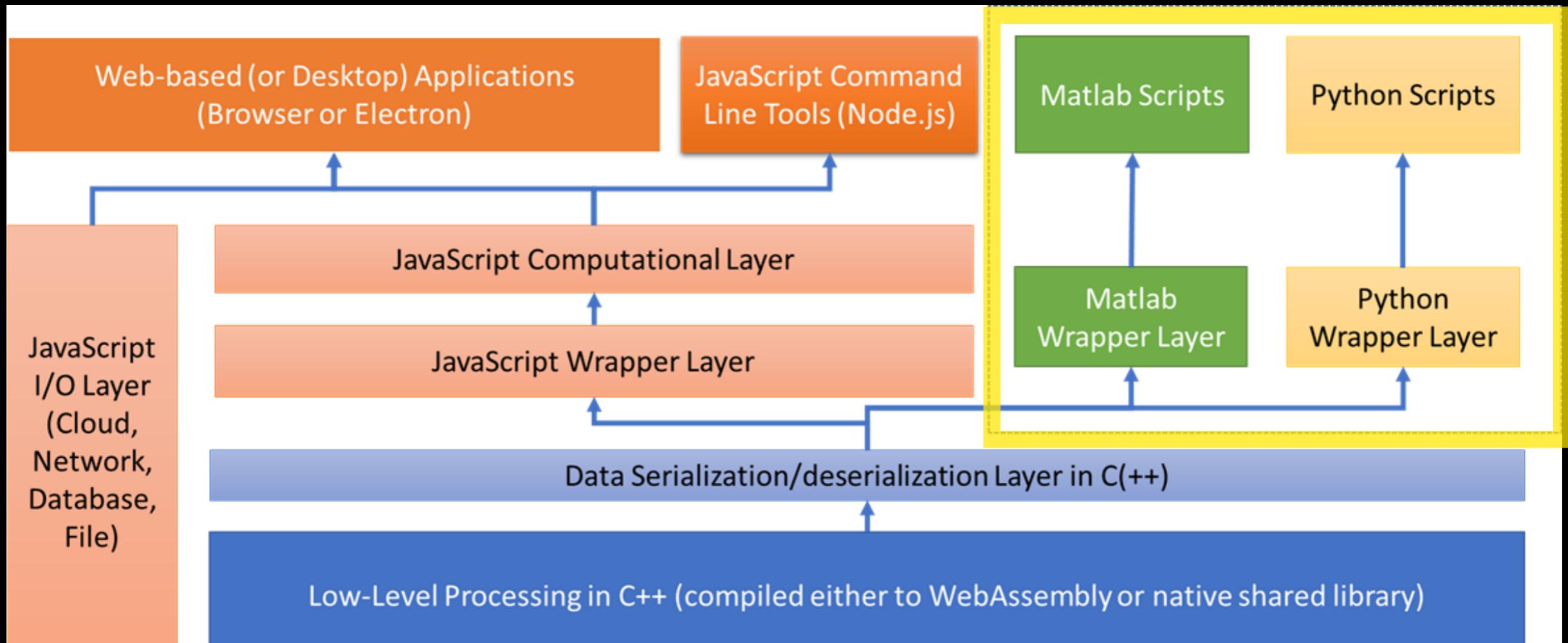


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# ARCHITECTURE

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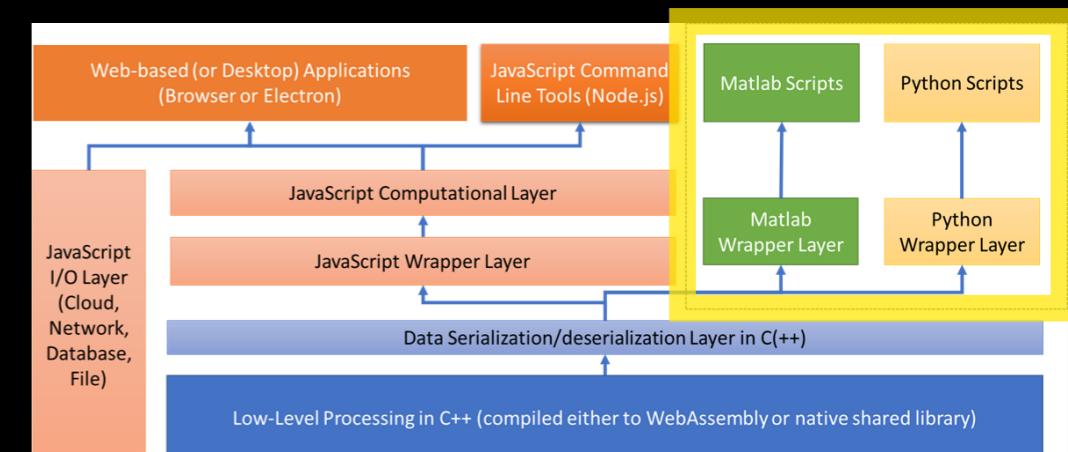
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Compared with C++:  
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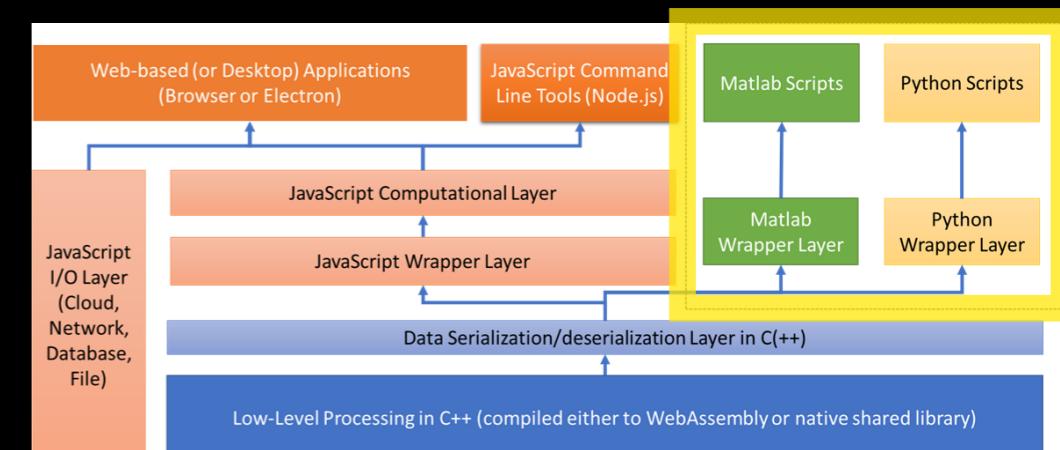


# ARCHITECTURE



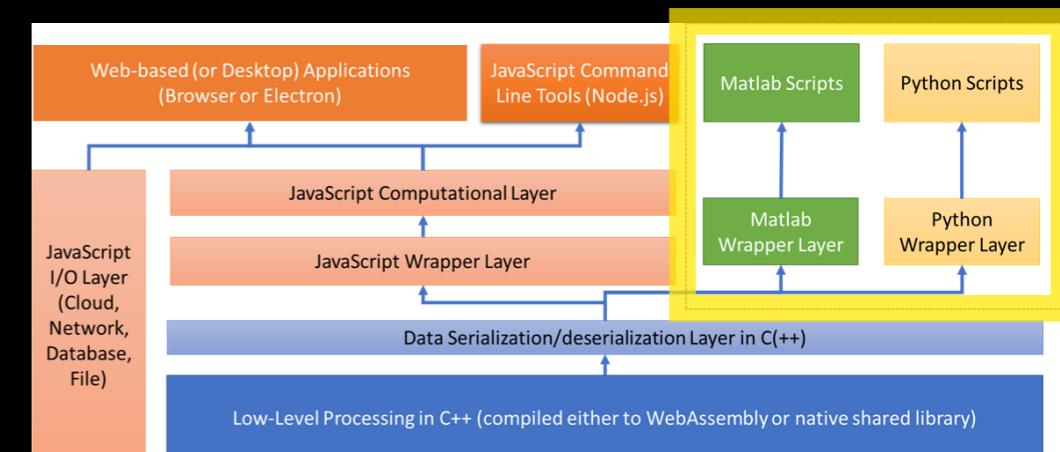
# ARCHITECTURE

Example of **Individualized Parcellation** module called by Matlab, Python, and JavaScript (Salehi et al., 2018)



# ARCHITECTURE

Example of **Individualized Parcellation** module called by Matlab, Python, and JavaScript (Salehi et al., 2018)



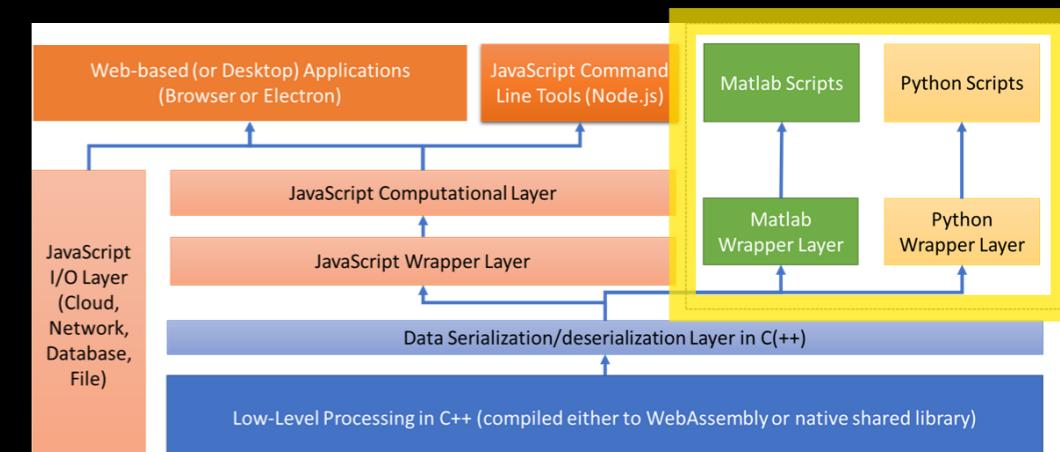
**JS** (js/modules/individualizedParcellation.js)

```
let paramobj= { 'numberofexemplars' : vals.numregions, "usefloat" : true , "saveexemplars": saveexemplars };  
this.outputs['output']= await biswrap.individualizedParcellationWASM(fmri, group, paramobj, vals.debug);
```



# ARCHITECTURE

Example of **Individualized Parcellation** module called by Matlab, Python, and JavaScript (Salehi et al., 2018)



**JS** (js/modules/individualizedParcellation.js)

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let paramobj= { 'numberofexemplars' : vals.numregions, "usefloat" : true , "saveexemplars": saveexemplars };
this.outputs['output']= await biswrap.individualizedParcellationWASM(fmri, group, paramobj, vals.debug);
```

**Python** (python/modules/individualizedParcellation.py)

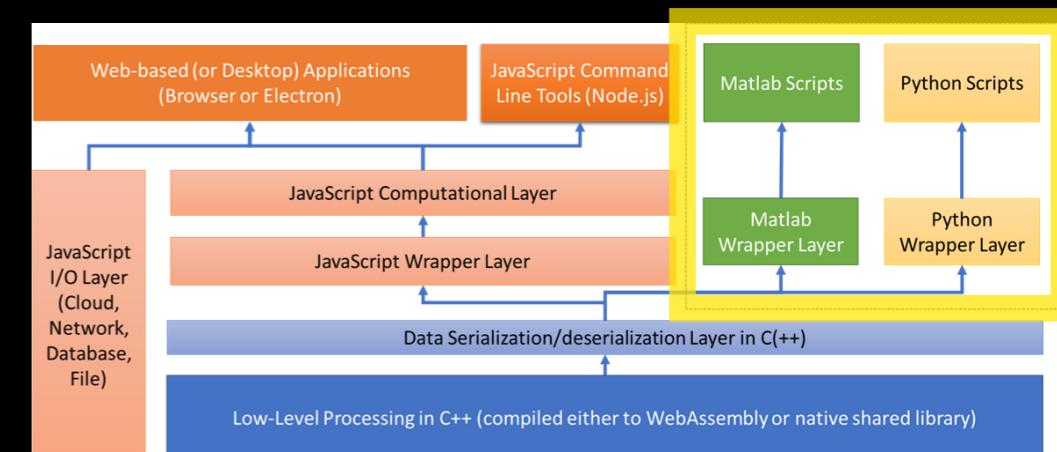
```
paramobj= {
    'numberofexemplars' : vals['numregions'],
    'usefloat' : self.parseBoolean(vals['usefloat']),
    'saveexemplars' : self.parseBoolean(vals['saveexemplars']),
};
```

```
self.outputs['output']=libbis.individualizedParcellationWASM(fmri,group,paramobj,debug);
```



# ARCHITECTURE

Example of **Individualized Parcellation** module called by Matlab, Python, and JavaScript (Salehi et al., 2018)



**JS** (js/modules/individualizedParcellation.js)

```
let paramobj= { 'numberofexemplars' : vals.numregions, "usefloat" : true , "saveexemplars": saveexemplars };
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**Python** (python/modules/individualizedParcellation.py)

```
paramobj= {
    'numberofexemplars' : vals['numregions'],
    'usefloat' : self.parseBoolean(vals['usefloat']),
    'saveexemplars' : self.parseBoolean(vals['saveexemplars']),
};

self.outputs['output']=libbis.individualizedParcellationWASM(fmri,group,paramobj,debug);
```

**Matlab** (matlab/test\_indiv.m)

```
paramobj.numexemplars=numexemplars;
paramobj.usefloat='true';
paramobj.saveexemplars='false';
indiv_ptr=lib.individualizedParcellationWASM(fmri_smoothed,resliced_group, paramobj,debug);
```



# COMMAND LINE TOOLS



[https://www.npmjs.com/  
package/biswebnode](https://www.npmjs.com/package/biswebnode)

```
[steph@Stephanies-MacBook-Pro data]$ biswebnode linearRegistration
+++++
.... Using node.js version 10.16.0 (OK=true)
.... This program is part of the commandline suite of tools from BioImage Suite Web.
.... See https://github.com/bioimagesuiteweb/bisweb for more information.
....
.... BioImage Suite Web user preferences loaded from /Users/steph/.bisweb
..., {"orientationOnLoad": "None", "snapshotScale": 2, "snapshotDownWhite": true, "fileSource": "local", "showWelcome": true, "favoriteFolders": ["~/Desktop"], "recentProjects": [{"name": "Project 1", "path": "/Users/steph/Desktop/Project 1"}, {"name": "Project 2", "path": "/Users/steph/Desktop/Project 2"}], "recentImages": [{"name": "Image 1", "path": "/Users/steph/Desktop/Project 1/1.png"}, {"name": "Image 2", "path": "/Users/steph/Desktop/Project 1/2.png"}]}
+++++
+++++ Executing module linearRegistration
+++++
---- Not enough arguments passed to run this tool

Usage: biswebnode linearRegistration [options]

Options:

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  --intscale [n]          Determines the intensity scaling post image normalization
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  --resolution [n]         Factor to reduce the resolution prior to registration
  --debug [s]              Toggles debug logging
  --steps [n]              Number of steps in multiresolution optimization
  --mode [s]               registration mode, one of [ Rigid Similarity Affine9 Affine ]
  --useheader [s]          use header orientation for initial matrix
  -r --reference <s>     The reference image
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  --initial [s]            (optional) The initial transformation (optional)
  -o --output <s>          The output transformation
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# COMMAND LINE TOOLS



[https://www.npmjs.com/  
package/biswebnode](https://www.npmjs.com/package/biswebnode)

## Directions

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[steph@Stephanies-MacBook-Pro data]$ biswebnode linearRegistration
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.... Executing module linearRegistration
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# COMMAND LINE TOOLS



[https://www.npmjs.com/  
package/biswebnode](https://www.npmjs.com/package/biswebnode)

## Directions

1. Install node (<https://nodejs.org/en/download/>)

```
[steph@Stephanies-MacBook-Pro data]$ biswebnode linearRegistration
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# COMMAND LINE TOOLS



[https://www.npmjs.com/  
package/biswebnode](https://www.npmjs.com/package/biswebnode)

## Directions

1. Install node (<https://nodejs.org/en/download/>)
2. Install BISWeb tools: sudo npm install -g biswebnode

```
[steph@Stephanies-MacBook-Pro data]$ biswebnode linearRegistration
+++++
.... Using node.js version 10.16.0 (OK=true)
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# COMMAND LINE TOOLS



[https://www.npmjs.com/  
package/biswebnode](https://www.npmjs.com/package/biswebnode)

## Directions

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Done!

```
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# COMMAND LINE TOOLS



[https://www.npmjs.com/  
package/biswebnode](https://www.npmjs.com/package/biswebnode)

## Directions

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Example usage:

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Usage: biswebnode linearRegistration [options]

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# COMMAND LINE TOOLS



[https://www.npmjs.com/  
package/biswebnode](https://www.npmjs.com/package/biswebnode)

## Directions

1. Install node (<https://nodejs.org/en/download/>)
2. Install BISWeb tools: `sudo npm install -g biswebnode`

Done!

Example usage:

- Image processing:  
`biswebnode smoothImage -h`

```
[steph@Stephanies-MacBook-Pro data]$ biswebnode linearRegistration
+++++
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Usage: biswebnode linearRegistration [options]

Options:

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  --initial [s]            (optional) The initial transformation (optional)
  -o --output <s>          The output transformation
  --resliced [s]           (optional) The resliced image
  --paramfile [s]          Specifies that parameters should be read from a file as opposed to parsed from the command line.
  --silent                Run in silent mode (no output on the console)
  -h, --help                output usage information
```



# COMMAND LINE TOOLS



[https://www.npmjs.com/  
package/biswebnode](https://www.npmjs.com/package/biswebnode)

## Directions

1. Install node (<https://nodejs.org/en/download/>)
2. Install BISWeb tools: sudo npm install -g biswebnode

Done!

Example usage:

- Image processing: **biswebnode smoothImage -h**
- Regression tests: **biswebnode regressiontests --last 20 --run 1**



```
[steph@Stephanies-MacBook-Pro data]$ biswebnode linearRegistration
+++++
.... Using node.js version 10.16.0 (OK=true)
.... This program is part of the commandline suite of tools from BioImage Suite Web.
.... See https://github.com/bioimagesuiteweb/bisweb for more information.
....
.... BioImage Suite Web user preferences loaded from /Users/steph/.bisweb
..., {"orientationOnLoad": "None", "snapshotScale": 2, "snapshotDownwhite": true, "filesource": "local", "showwelcome": true, "favoriteFolders": [], "internal": false, "darkmode": false}
....
+++++ Executing module linearRegistration
+++++
---- Not enough arguments passed to run this tool

Usage: biswebnode linearRegistration [options]

Options:
  -V, --version           output the version number
  --doreslice [s]         If true also output a resliced targed image using the current transform
  --norm [s]              If true normalize input intensities by saturating using cumulative histogram
  --intscale [n]           Determines the intensity scaling post image normalization
  --numbins [n]            Number of bins in joint histogram
  --imagesmoothing [n]   Amount of image smoothing to perform
  --metric [s]             Metric to compare registration
  --optimization [s]       Optimization Method
  --steps [s]              Number of steps to run
  --levels [s]             Number of levels to run
  --iterat [s]              Number of iterations to run
  --resolution [s]          Resolution to run at
  --debug [s]               Debug level
  --steps [s]              Number of steps to run
  --mode [s]               Mode to run in
  --useheader [s]           Use header information
  -r --ref [s]              Reference image
  -t --tar [s]              Target image
  --initial [s]             Initial transform
  -o --out [s]              Output directory
  --reslice [s]             Reslice target
  --paramf [s]              Parameter file
  --silent [s]              Silent mode
  -h, --help [s]            Help mode

[steph@Stephanies-MacBook-Pro data]$ biswebnode regressiontests --last 20 --run 1
+++++
.... Using node.js version 10.16.0 (OK=true)
.... This program is part of the commandline suite of tools from BioImage Suite Web.
.... See https://github.com/bioimagesuiteweb/bisweb for more information.
....
.... BioImage Suite Web user preferences loaded from /Users/steph/.bisweb
..., {"orientationOnLoad": "None", "snapshotScale": 2, "snapshotDownwhite": true, "filesource": "local", "showwelcome": true, "favoriteFolders": [], "internal": false, "darkmode": false}
....
+++++ Executing module regressiontests
+++++
---- Invoking module RegressionTest ...
oooo Loaded all inputs.
oooo Parsed : {"first": 0, "last": 20, "testname": "", "run": "1", "testlist": "", "testdir": "", "debug": false}
[19:13:25] /usr/local/lib/node_modules/biswebnode/lib/mocha /usr/local/lib/node_modules/biswebnode/test/test_module.js --first 0 --last 20
....
.... Using node.js version 10.16.0 (OK=true)
.... This program is part of the commandline suite of tools from BioImage Suite Web.
.... See https://github.com/bioimagesuiteweb/bisweb for more information.
....

[19:13:26] Beginning module tests
[19:13:26]   Testscript= node /usr/local/lib/node_modules/biswebnode/lib/bisweb-test.js  /usr/local/lib/node_modules/biswebnode/test
[19:13:26]   Reading https://bioimagesuiteweb.github.io/test/module_tests.json
[19:13:26]   Running tests: 0 : 20 out a total of= 90 tests. Filter name=all
    ✓ [19:13:26]   This is a required placeholder to allow before() to work
[19:13:26] -----
[19:13:26] /usr/local/lib/node_modules/biswebnode/test>node /usr/local/lib/node_modules/biswebnode/lib/bisweb-test.js smoothImage --sigma 2.0 --radiusfactor 2.0
NI_2mm_resliced.nii.gz --test_target testdata/newtests/goldsmooth2sigma.nii.gz --test_base_directory https://bioimagesuiteweb.github.io/test/
....
.... Using node.js version 10.16.0 (OK=true)
.... This program is part of the commandline suite of tools from BioImage Suite Web.
.... See https://github.com/bioimagesuiteweb/bisweb for more information.
```



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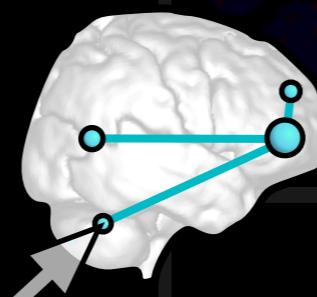
Haley Garbus

John Onofrey

Dana Casetti

NIH R24 MH114805. (PIs: X.P. & D.S.)

NIH DSPAN F99/K00 F99NS108557 (PI: S.N.)



# THANK YOU! QUESTIONS?



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