

m/z Imaging Data

Spots per Line: 10 Spot Spacing: 200 um

Number of Lines: 10 Line Spacing: 200

Load Data Data loaded :

m/zXML File

- m/zXML File
- imzML File**
- IMG File
- m/zXML Folder
- ASCII Folder
- MAT File

Normalization: none

Reference peak: 519.14

Norm Cutoff: 1e+003

Appearance

Interpolation Type: linear

Order: 2

Edit Colormap

- Instructions**
- 1- Load m/zXML file, imzML file, ..., MAT session file.
 - 2- Select m/z of interest, change interpolation and perform post processing if needed.
 - 3- Change colormap and view MS using toolbar menu functions.

MSiReader



This tutorial contains navigation buttons that enable you to move throughout the tutorial.

Please use the navigation buttons and not the page up/page down or arrow keys to navigate through the tutorials.

This is the 'Next' button. It takes you to the next frame or stop point.



This is the 'Previous' button. It takes you to the previous frame or stop point.



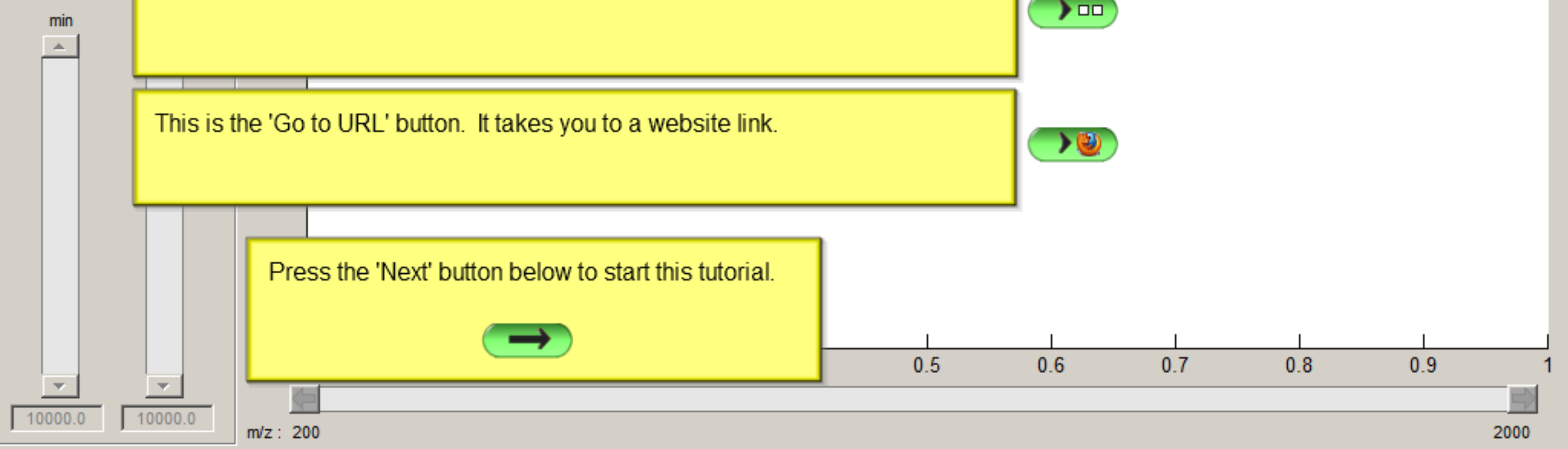
This is the 'Go to frame' button. It takes you to a specified frame.



This is the 'Go to URL' button. It takes you to a website link.



Press the 'Next' button below to start this tutorial.



m/z Imaging Data

Spots per Line: 10 Spot Spacing: 200 um
Number of Lines: 10 Line Spacing: 200 um

Load Data Data loaded :

m/zXML File

- m/zXML File
- imzML File**
- IMG File
- m/zXML Folder
- ASCII Folder
- MAT File

Normalization: none

Reference peak: 519.14

Norm Cutoff: 1e+003

Appearance

Interpolation Type: linear

Order: 2

Instructions

- 1- Load m/zXML file, imzML file, ..., MAT session file.
- 2- Select m/z of interest, change interpolation and perform post processing if needed.
- 3- Change colormap and view MS using toolbar menu functions.

MSiReader 0.06



Heatmap Mode

MSi File Data
 Custom Data **Load**

MS Navigation

m/z: 369.35

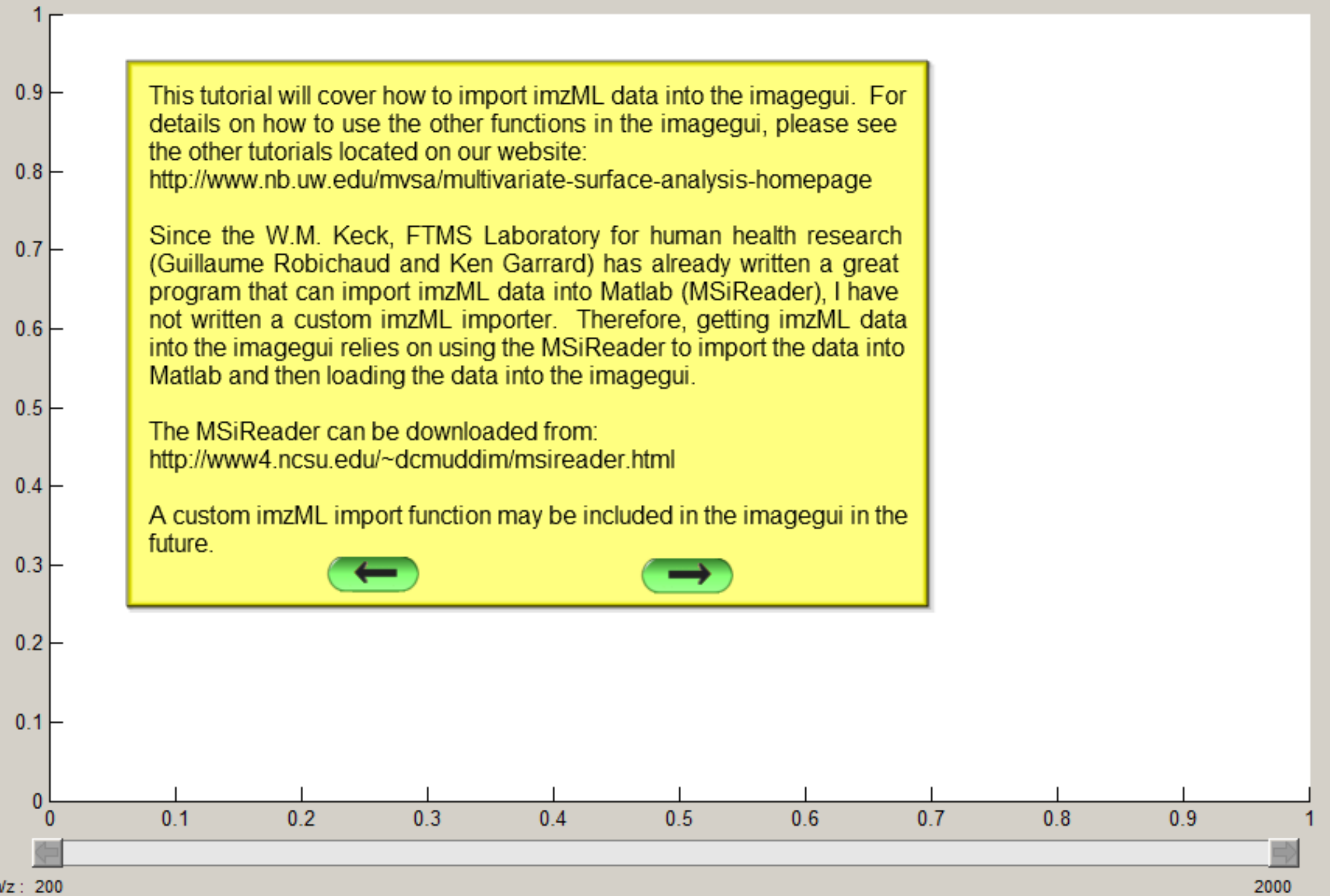
m/z Window: 0.1 Da

Intensity: max of window

m/z Step: 0.01

Scale Override: 10000

min: 10000.0 max: 10000.0





m/z Imaging Data

Spots per Line Spot Spacing um

Number of Lines Line Spacing um

MSiReader 0.06



Load Data Data loaded :

- mzXML File
- mzXML File
- imzML File**
- IMG File
- mzXML Folder
- ASCII Folder
- MAT File

Open the MSiReader and change the data type to "imzML File".

Normalization

Reference peak

Norm Cutoff

Appearance

Interpolation Type

Order

[Edit Colormap](#)

- Instructions**
- 1- Load mzXML file, imzML file, ..., MAT session file.
 - 2- Select m/z of interest, change interpolation and perform post processing if needed.
 - 3- Change colormap and view MS using toolbar menu functions.

MS navigation

m/z

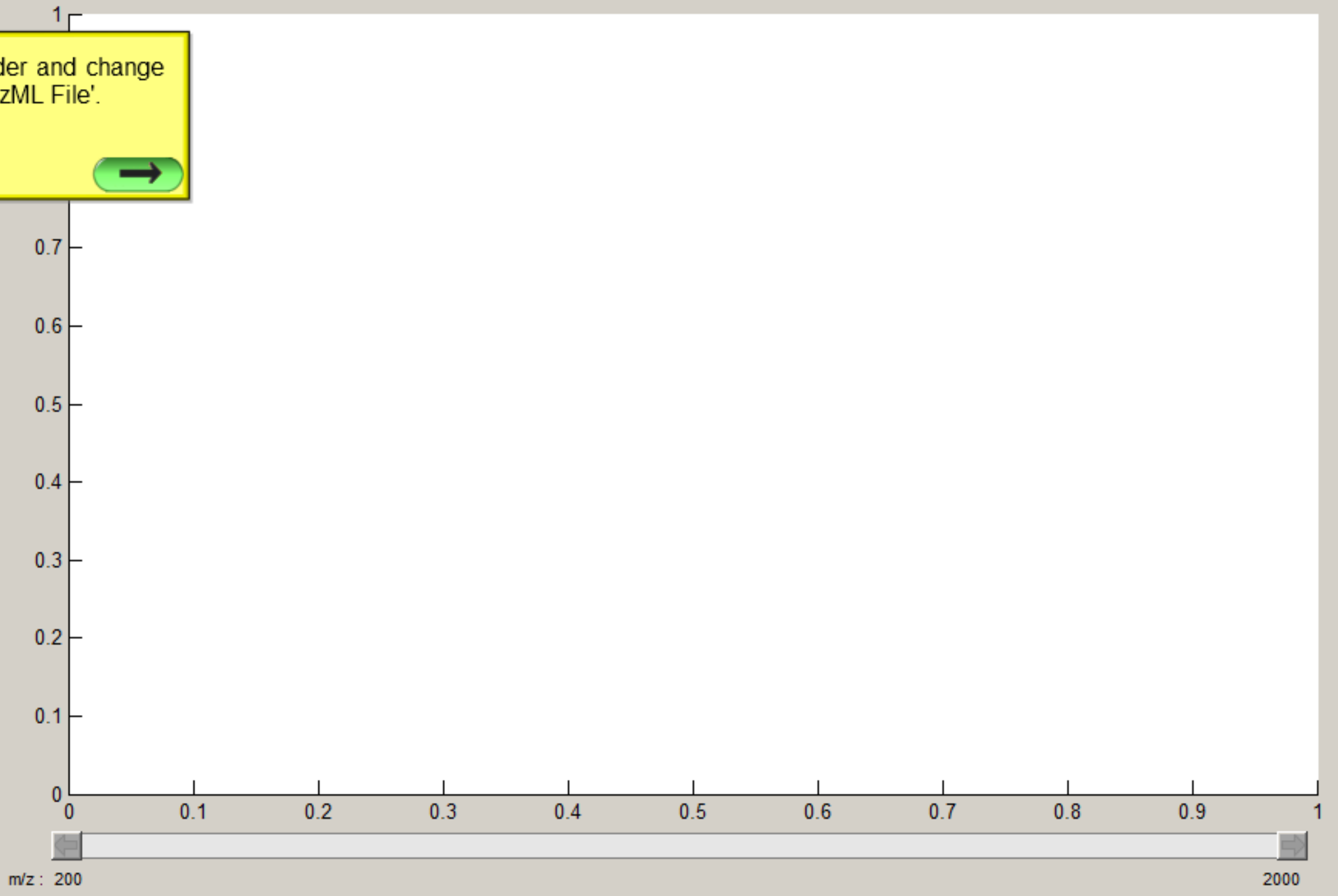
m/z Window Da

Intensity

m/z Step

Scale Override

min max





m/z Imaging Data

Spots per Line Spot Spacing um

Number of Lines Line Spacing um

MSiReader 0.06



Data loaded:

imzML

Press the 'Load Data' button.

Post Processing

Noise Correction

BG File : none

Normalization

Reference peak

Norm Cutoff

MSi File Data

Custom Data

MS Navigation

m/z

m/z Window

Intensity

m/z Step

Scale Override

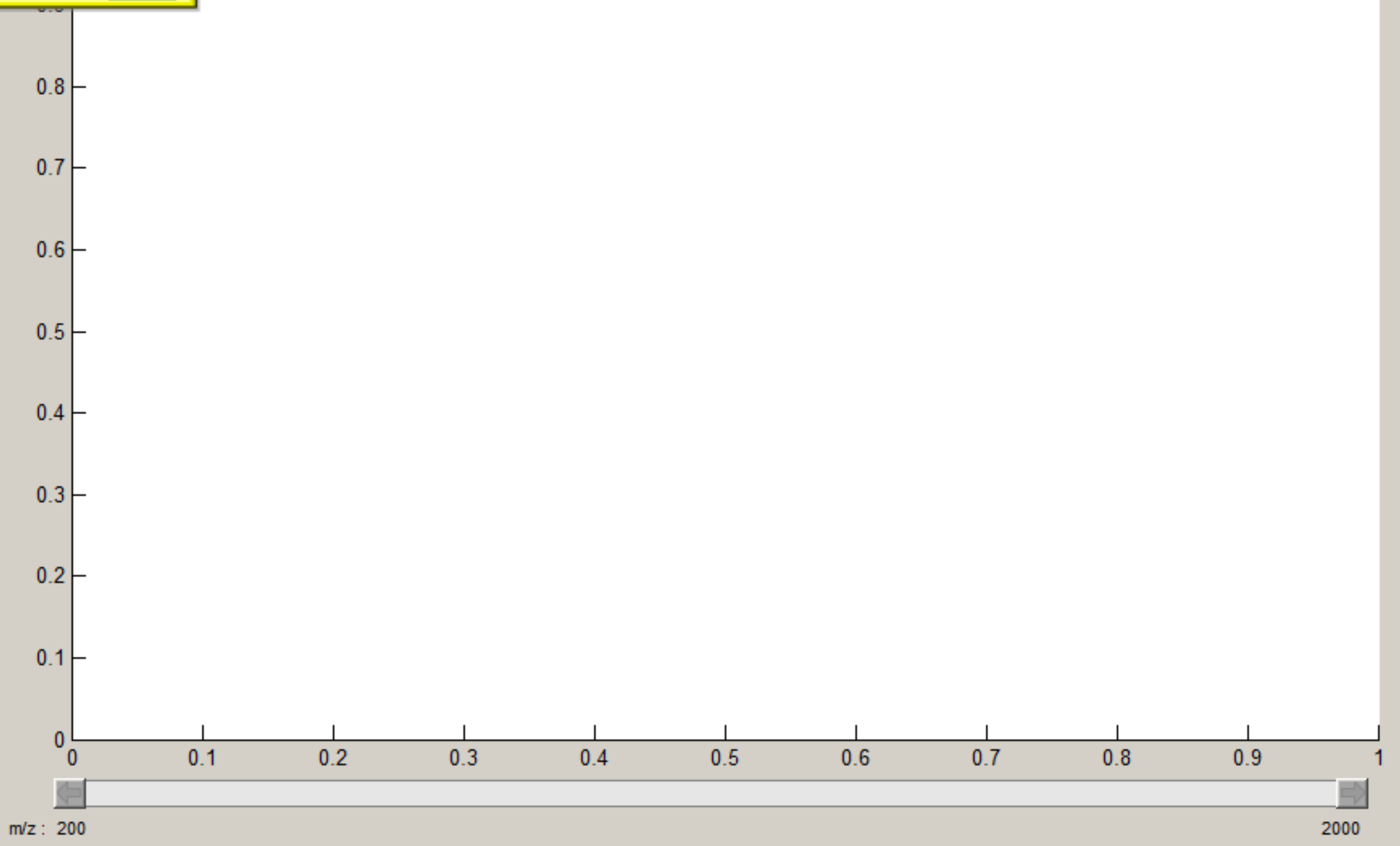
min max

Appearance

Interpolation Type

Order

- Instructions**
- 1- Load mzXML file, imzML file, ..., MAT session file.
 - 2- Select m/z of interest, change interpolation and perform post processing if needed.
 - 3- Change colormap and view MS using toolbar menu functions.



Select .imzML file to load

Look in:

Name	Date modified	Type	Size
S043_Processed.imzML	2/16/2011 5:24 PM	IMZML File	42,129 KB
S042_Continuous.imzML	2/16/2011 5:09 PM	IMZML File	25,169 KB
MALDI_TOF_example.imzML	1/21/2015 1:09 PM	IMZML File	6,354 KB
HR2MSI mouse urinary bladder S096.imzML	1/28/2015 3:37 PM	IMZML File	54,880 KB
Example_Processed.imzML	2/16/2011 4:28 PM	IMZML File	23 KB
Example_Continuous.imzML	2/16/2011 4:27 PM	IMZML File	23 KB
zcorrectorgui	9/6/2013 4:29 PM	File folder	
TestingFiles	2/7/2014 11:46 AM	File folder	
spectragui	3/31/2014 8:30 AM	File folder	
slices	4/30/2013 1:54 PM	File folder	
Nick	2/6/2013 9:57 AM	File folder	
New folder	9/4/2013 8:37 AM	File folder	
imagegui	8/23/2013 3:32 PM	File folder	
dpagtest	11/19/2014 10:0...	File folder	
beamwidthtest	7/15/2014 10:07...	File folder	
07_15_13 tripalmitin 18_IonoptikaIA2DspectrV2	7/31/2013 9:41 AM	File folder	

File name:

Files of type:

FOR HUMAN HEALTH RESEARCH

Choose the imzML file you want to load and press the 'Open' button.

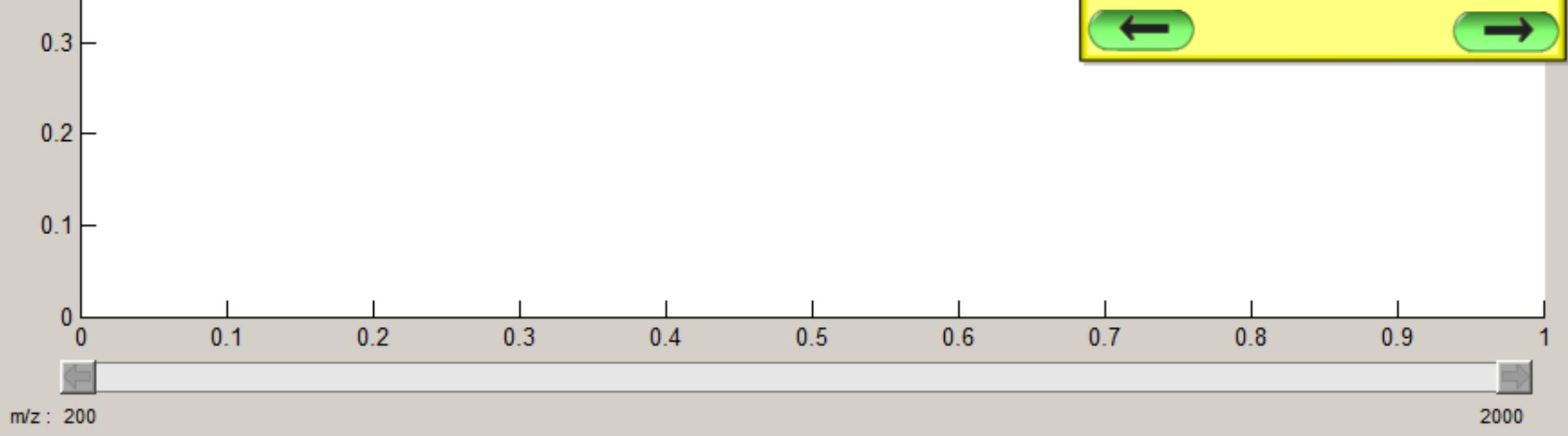
← →

Edit Colormap

Instructions

- 1- Load mzXML file, imzML file, ..., MAT session file.
- 2- Select m/z of interest, change interpolation and perform post processing if needed.
- 3- Change colormap and view MS using toolbar menu functions.

10000.0 10000.0



m/z Imaging Data

Spots per Line: 10 Spot Spacing: 200 um

Number of Lines: 10 Line Spacing: 200 um

Load Data Data loaded: Loading ...

imzML File

Post Processing

Noise Correction

BG File: none

Normalization: none

Reference peak: 519.14

Norm Cutoff: 1e+003

Appearance

Interpolation Type: linear

Order: 2

Edit Colormap

- Instructions**
- 1- Load mzXML file, imzML file, ..., MAT session file.
 - 2- Select m/z of interest, change interpolation and perform post processing if needed.
 - 3- Change colormap and view MS using toolbar menu functions.

Heatmap Mode

MSi File Data

Custom Data Load

MS Navigation

m/z: 369.35

m/z Window: 0.1 Da

Intensity: max of window

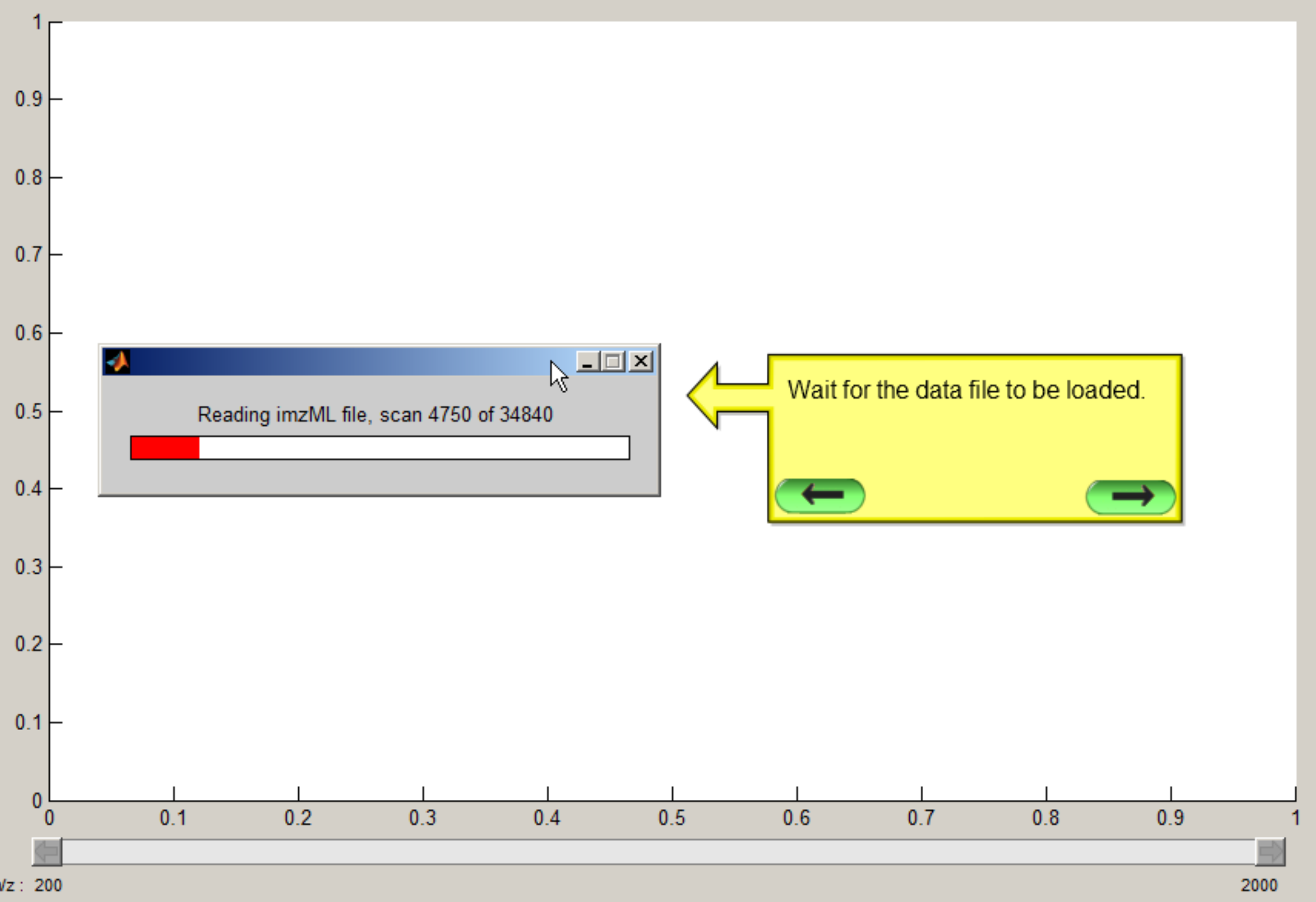
m/z Step: 0.01

Scale Override: 10000

min: 10000.0 max: 10000.0

MSiReader 0.06

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Reading imzML file, scan 4750 of 34840

Progress bar: [Red segment] [White segment]

Wait for the data file to be loaded.

← →

m/z Imaging Data

Spots per Line: 260 Spot Spacing: 200 um

Number of Lines: 134 Line Spacing: 200 um

Clear Data Data loaded: HR2MSI mouse urinary bladder S096.imzML

imzML File: [dropdown]

Post Processing

Noise Correction

BG File: none

Normalization: none [dropdown]

Reference peak: 519.14

Norm Cutoff: 1000

Appearance

Interpolation Type: linear [dropdown]

Order: 2 [dropdown]

Edit Colormap

- Instructions**
- 1- Load mzXML file, imzML file, ..., MAT session file.
 - 2- Select m/z of interest, change interpolation and perform post processing if needed.
 - 3- Change colormap and view MS using toolbar menu functions.

Heatmap Mode

MSi File Data

Custom Data [Load]

MS Navigation

m/z: 700

m/z Window: 0.1 Da [dropdown]

Intensity: max of window [dropdown]

m/z Step: 0.01

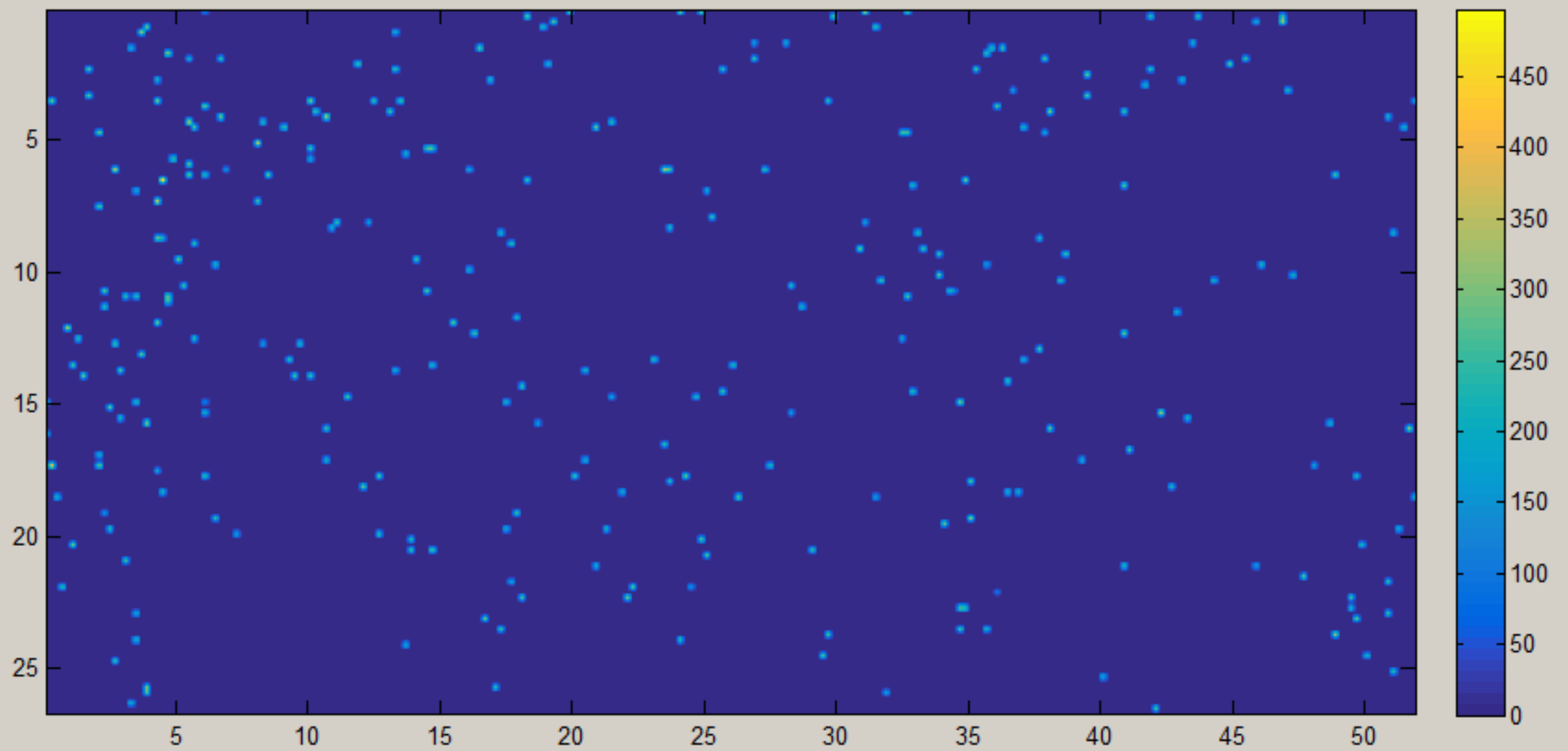
Scale Override: 497.438

min [slider] max [slider]

0 497.438

Press the 'Select all pixels' button.

Select all pixels



m/z Imaging Data

Spots per Line: 260 Spot Spacing: 200 um
Number of Lines: 134 Line Spacing: 200 um

Clear Data Data loaded: HR2MSI mouse urinary bladder S096.imzML

imzML File

MSiReader 0.06



Image Area = 1393.6 Intensity: Mean = 2.32885 StdDev = 25.9607 Range = 0 to 497.438

Post Processing

Noise Correction

BG File: none

Normalization: none

Reference peak: 519.14

Norm Cutoff: 1000

Heatmap Mode

MSi File Data
 Custom Data Load

MS Navigation

m/z: 700

m/z Window: 0.1 Da

Intensity: max of window

m/z Step: 0.01

Scale Override: 497.438

Appearance

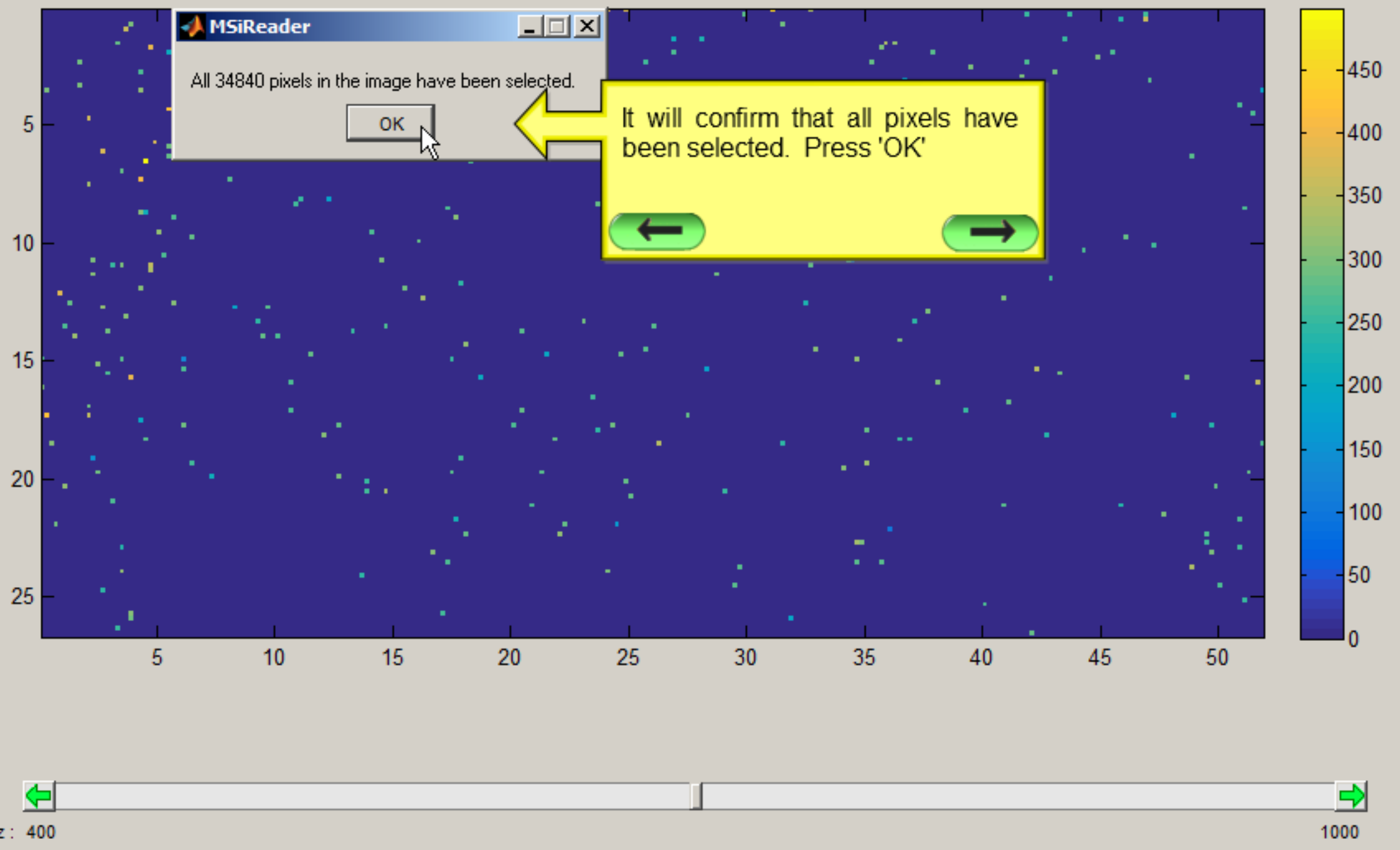
Interpolation Type: linear

Order: 0

Edit Colormap

- Instructions**
- 2- Use the spectrum generator tool to plot peaks in the selected ROI.
 - 3- The ROI can be moved in the image to generate another peaks plot.
 - 4- Click the ROI tool again to exit and resume processing.

min: 0 max: 497.438



m/z Imaging Data

Spots per Line	260	Spot Spacing	200
Number of Lines	134	Line Spacing	200

Export and/or view mass spectrum data from selected pixels

MSiReader 0.06

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Image Area = 1393.6 Intensity: Mean = 2.32885 StdDev = 25.9607 Range = 0 to 497.438

Press this button to 'Export and/or view mass spectrum data from selected pixels'

← →

Noise Correction

BG File : none

Normalization: none

Reference peak: 519.14

Norm Cutoff: 1000

MSi File Data

Custom Data

MS Navigation

m/z: 700

m/z Window: 0.1 Da

Intensity: max of window

m/z Step: 0.01

Scale Override: 497.438

min max

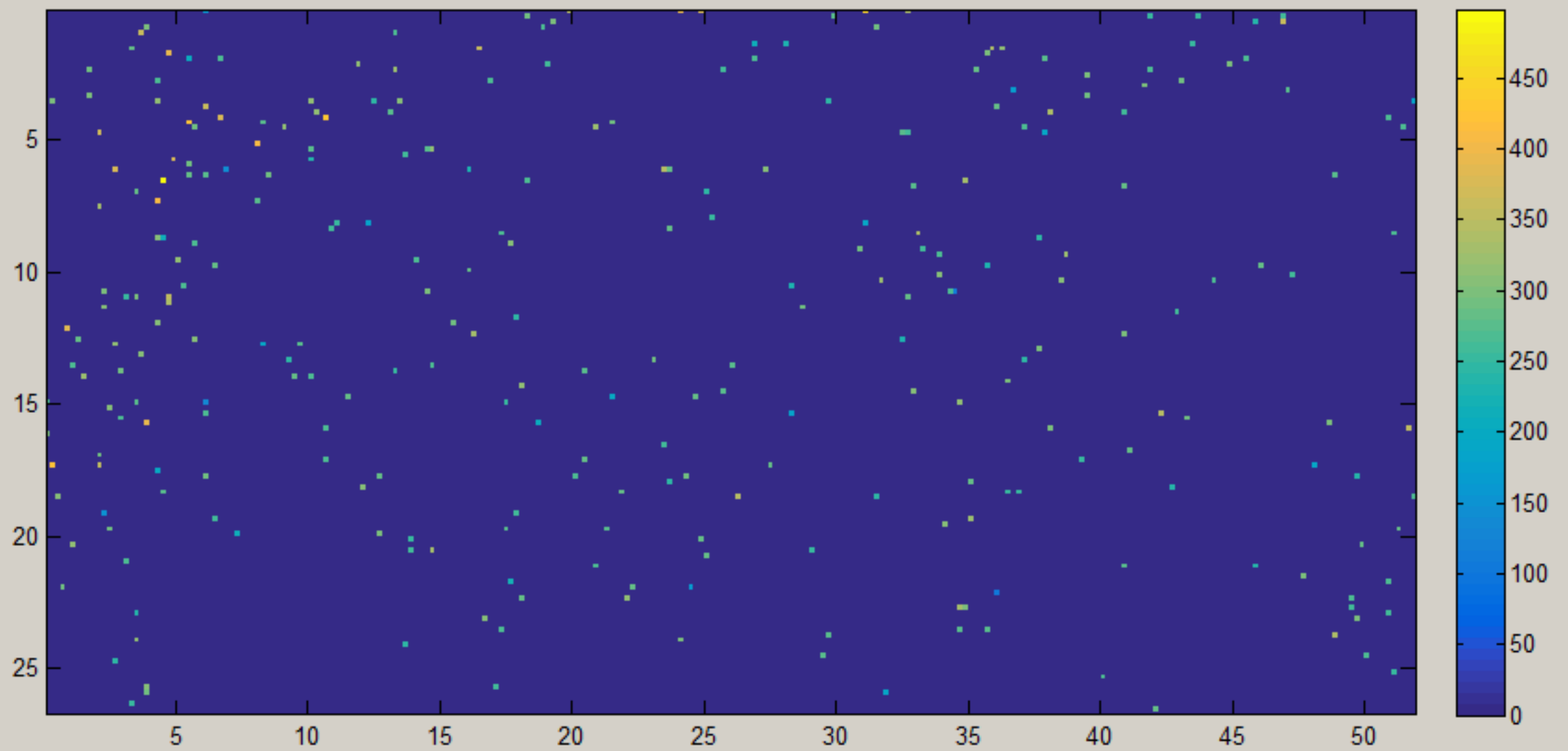
0 497.438

Appearance

Interpolation Type: linear

Order: 0

- Instructions
- 2- Use the spectrum generator tool to plot peaks in the selected ROI.
 - 3- The ROI can be moved in the image to generate another peaks plot.
 - 4- Click the ROI tool again to exit and resume processing.



m/z Imaging Data

Spots per Line: Spot Spacing: um

Number of Lines: Line Spacing: um

Data loaded: HR2MSI mouse urinary bladder S096.imzML

MSiReader 0.06



Image Area = 1393.6 Intensity: Mean = 2.32885 StdDev = 25.9607 Range = 0 to 497.438

Post Processing

Noise Correction

BG File: none

Normalization:

Reference peak:

Norm Cutoff:

Appearance

Interpolation Type:

Order:

MSi Spectrum W.M. KECK FTMS LABORATORY FOR HUMAN HEALTH RESEARCH

Choose options ...

Algorithm for Peak Centroid Calculation

Parabolic Centroid MS Peaks Peak Threshold:

Mass Spectrum Display

Plot Mass Spectrum Include Peak Markers

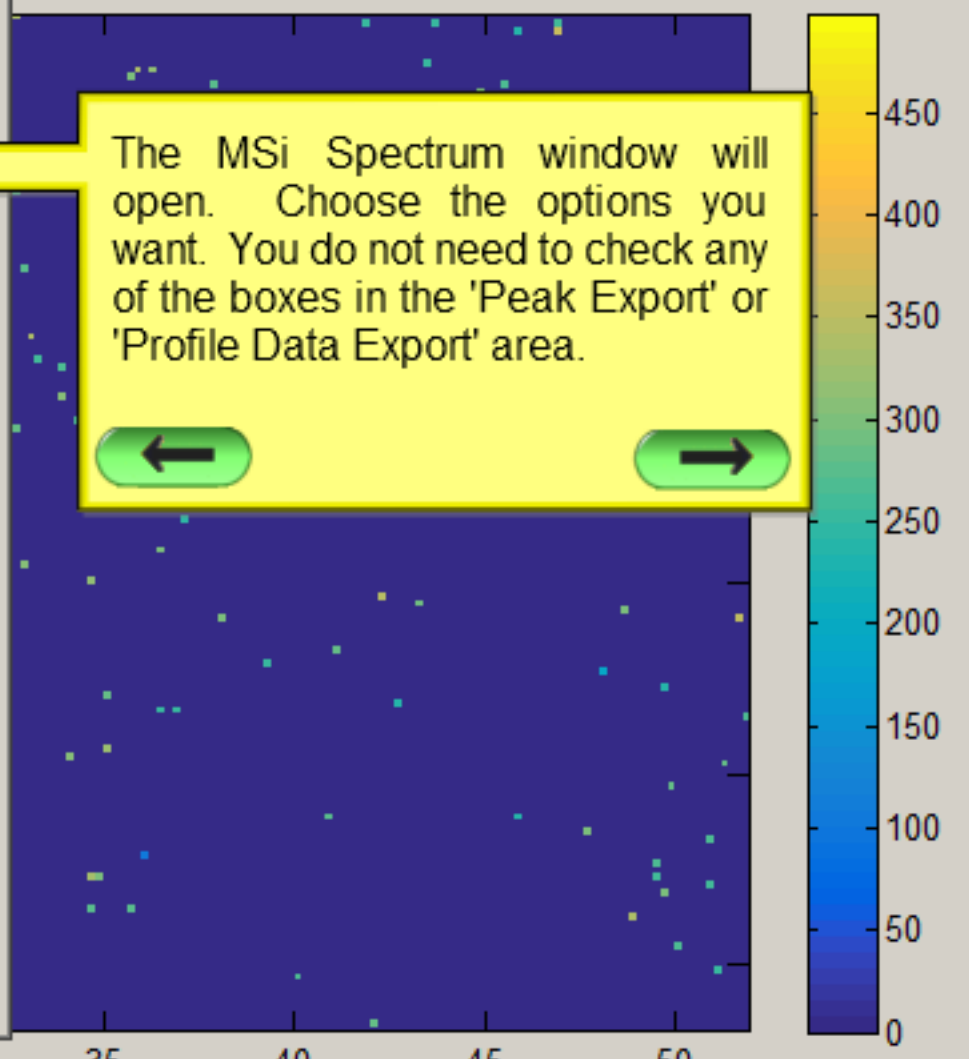
Peak Export (centroided data)

Export Peaks to .XLS File Send Peaks List to Clipboard

Use Data Processing Template Include Intensity Values

Profile Data Export

Export Averaged m/z and Intensity Export Raw Data for each Pixel



The MSi Spectrum window will open. Choose the options you want. You do not need to check any of the boxes in the 'Peak Export' or 'Profile Data Export' area.

- Instructions**
- 2- Use the spectrum generator tool to plot peaks in the selected ROI.
 - 3- The ROI can be moved in the image to generate another peaks plot.
 - 4- Click the ROI tool again to exit and resume processing.

m/z : 400

1000

m/z Imaging Data

Spots per Line: 260 Spot Spacing: 200 um
Number of Lines: 134 Line Spacing: 200 um

Clear Data Data loaded: HR2MSI mouse urinary bladder S096.imzML

imzML File

MSiReader 0.06



Image Area = 1393.6 Intensity: Mean = 2.32885 StdDev = 25.9607 Range = 0 to 497.438

Post Processing

Noise Correction
BG File: none

Normalization: none
Reference peak: 519.14
Norm Cutoff: 1000

Appearance

Interpolation Type: linear
Order: 0

Edit Colormap

MSi Spectrum W.M. KECK FTMS LABORATORY FOR HUMAN HEALTH RESEARCH

Choose options ...

Algorithm for Peak Centroid Calculation:
 Parabolic Centroid MS Peaks Peak Threshold: 100

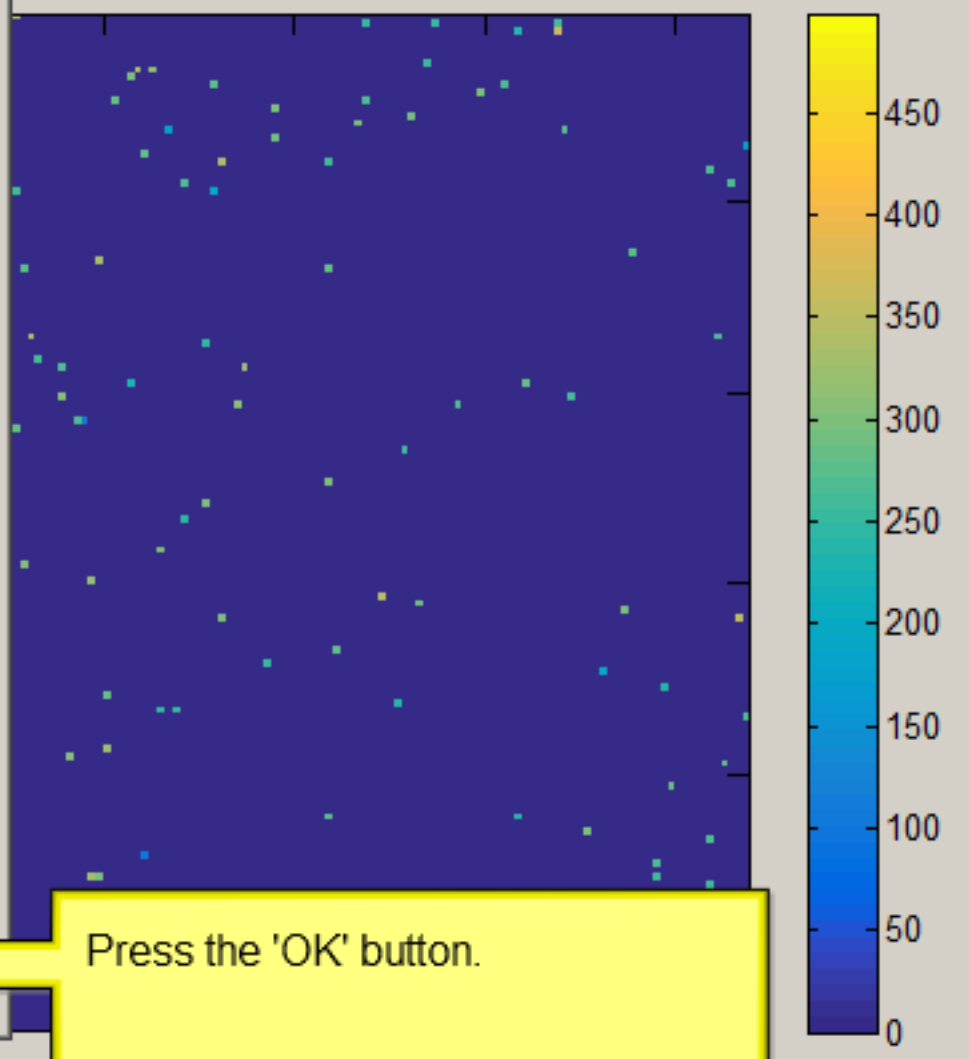
Mass Spectrum Display:
 Plot Mass Spectrum Include Peak Markers

Peak Export (centroided data):
 Export Peaks to .XLS File Send Peaks List to Clipboard
 Use Data Processing Template Include Intensity Values

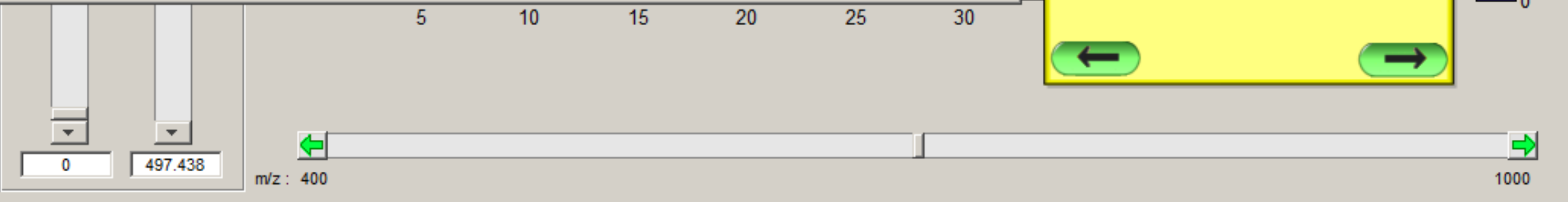
Profile Data Export:
 Export Averaged m/z and Intensity Export Raw Data for each Pixel

Browse

Cancel OK



- Instructions**
- 2- Use the spectrum generator tool to plot peaks in the selected ROI.
 - 3- The ROI can be moved in the image to generate another peaks plot.
 - 4- Click the ROI tool again to exit and resume processing.



Press the 'OK' button.

m/z Imaging Data

Spots per Line: 260 Spot Spacing: 200 um

Number of Lines: 134 Line Spacing: 200 um

Clear Data Data loaded: HR2MSI mouse urinary bladder S096.imzML

imzML File

Post Processing

Noise Correction

BG File: none

Normalization: none

Reference peak: 519.14

Norm Cutoff: 1000

Appearance

Interpolation Type: linear

Order: 0

Edit Colormap

- Instructions**
- 2- Use the spectrum generator tool to plot peaks in the selected ROI.
 - 3- The ROI can be moved in the image to generate another peaks plot.
 - 4- Click the ROI tool again to exit and resume processing.

Heatmap Mode

MSi File Data

Custom Data Load

MS Navigation

m/z: 700

m/z Window: 0.1 Da

Intensity: max of window

m/z Step: 0.01

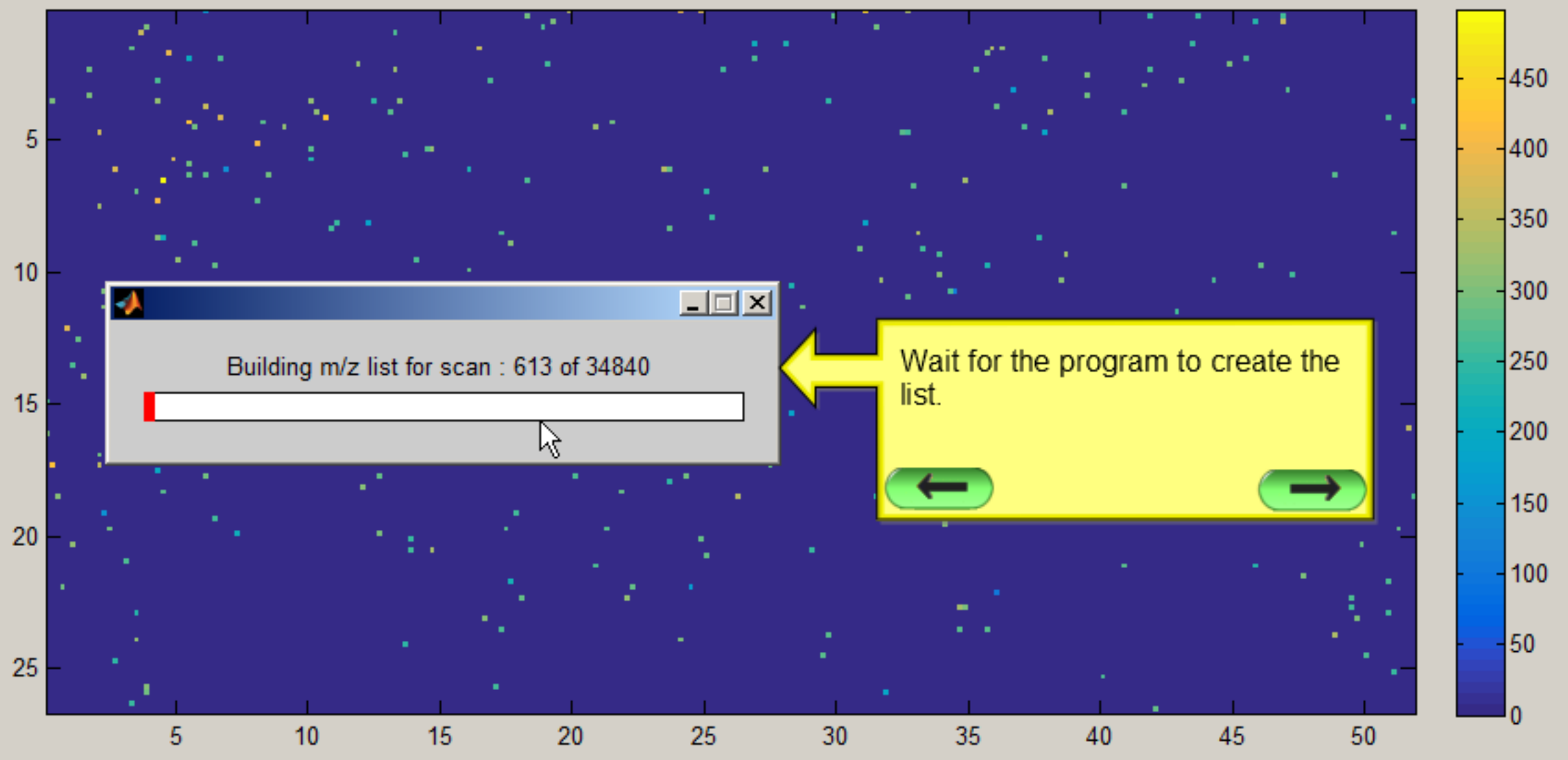
Scale Override: 497.438

min: 0 max: 497.438

MSiReader 0.06

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Image Area = 1393.6 Intensity: Mean = 2.32885 StdDev = 25.9607 Range = 0 to 497.438



m/z Imaging Data

Spots per Line: 260 Spot Spacing: 200 um

Number of Lines: 134 Line Spacing: 200 um

Clear Data Data loaded: HR2MSI S096.im

imzML File

MSiReader

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Post Processing

Noise Correction

BG File: none

Normalization: none

Reference peak: 519.14

Norm Cutoff: 1000

Appearance

Interpolation Type: linear

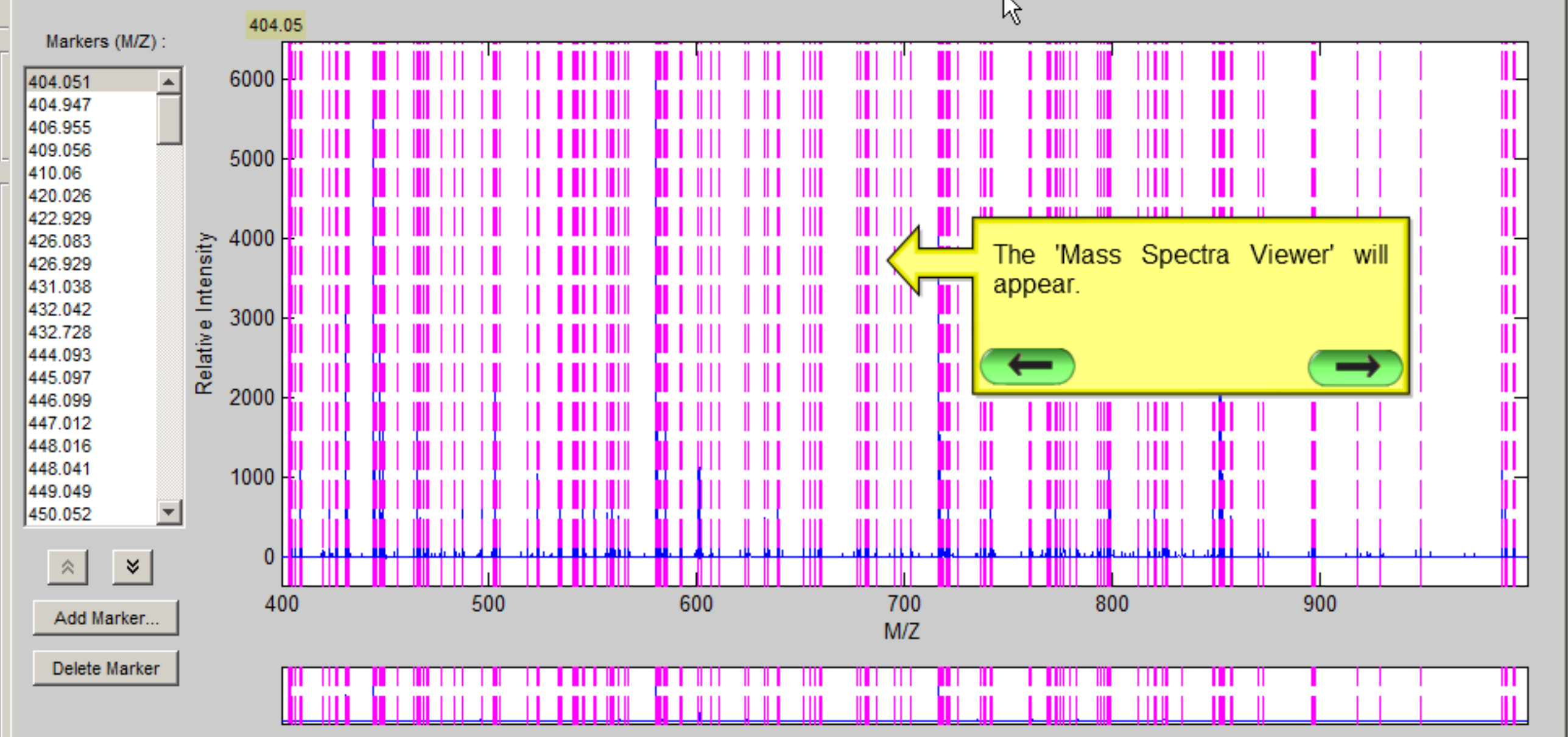
Order: 0

Edit Colormap

- Instructions**
- 2- Use the spectrum generator tool to plot peaks in the selected ROI.
 - 3- The ROI can be moved in the image to generate another peaks plot.
 - 4- Click the ROI tool again to exit and resume processing.

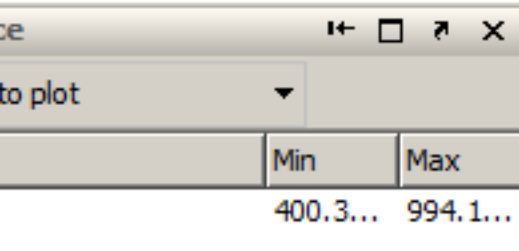
Mass Spectra Viewer

File Tools Window Help



0 497.438

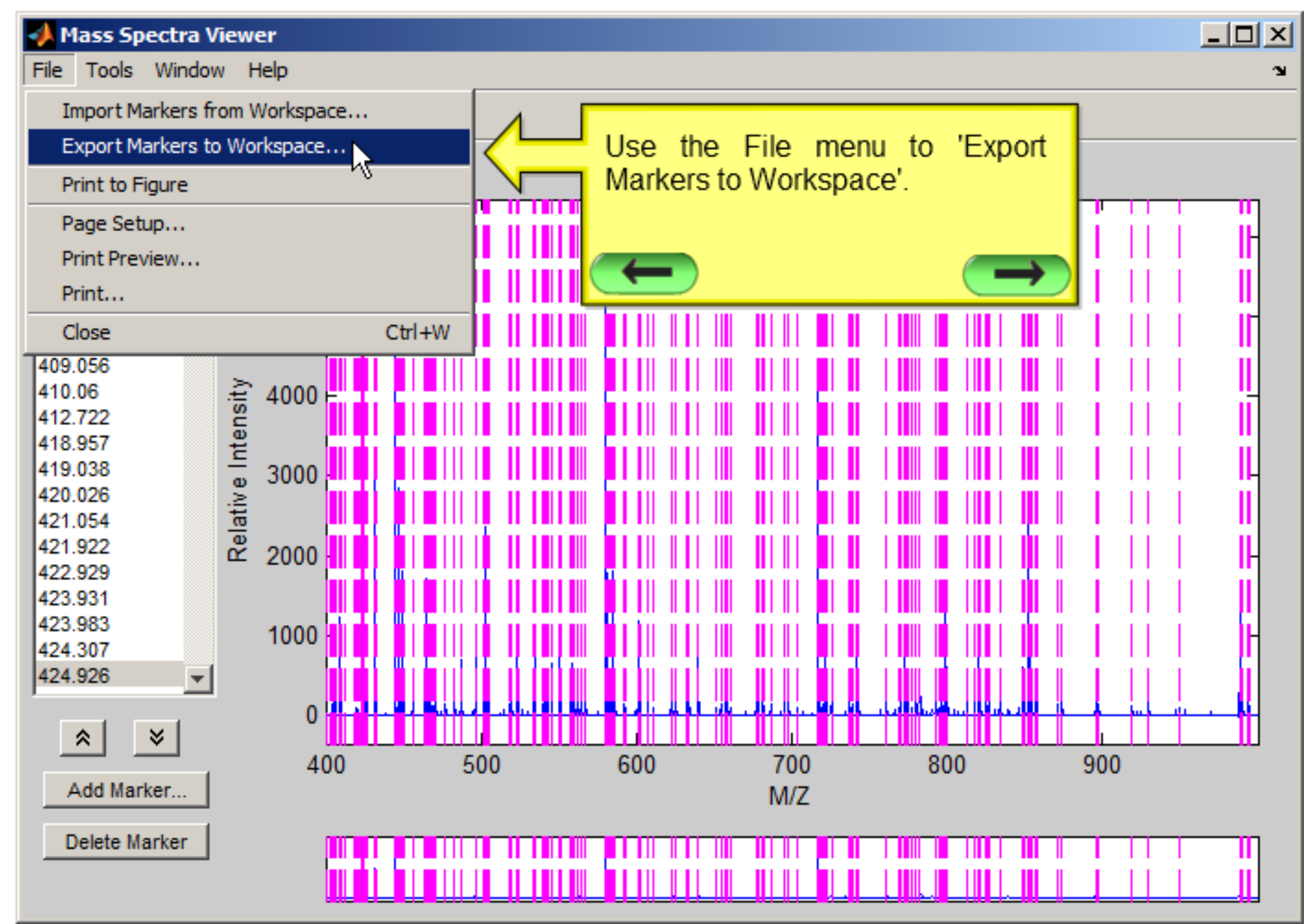
m/z : 400 1000



Command Window

New to MATLAB? Watch this [Video](#), see [Demos](#), or read [Getting Started](#).

fx >>



Labels exactmass

\Abbott_2015_Extracts\F

\Abbott_2015_04_21_Filt

\Abbott_2015_Extracts\F

\Abbott_2015_04_21_Filt

to plot

Min	Max
400.3...	994.1...

Command Window

New to MATLAB? Watch this [Video](#), see [Demos](#), or read [Getting Started](#).

fx >>

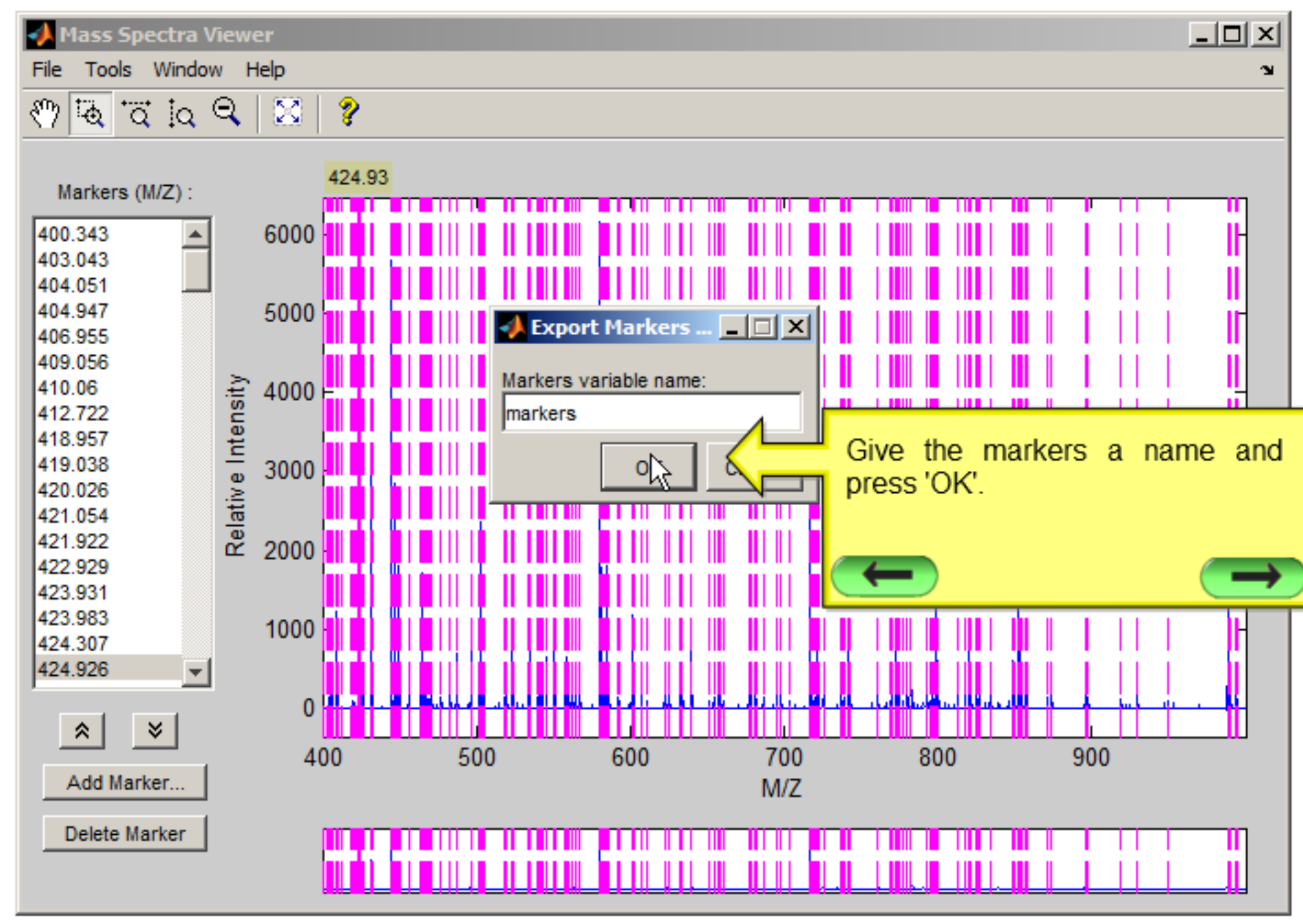
Labels exactmass

\Abbott_2015_Extracts\F

\Abbott_2015_04_21_Filt

\Abbott_2015_Extracts\F

\Abbott_2015_04_21_Filt



MSiReader v0.06 [Matlab]

Save your session using the 'Save' button.

SiReader 0.06 **W.M. KECK FTMS LABORATORY FOR HUMAN HEALTH RESEARCH**

Image Area = 1393.6 Intensity: Mean = 1.88198 StdDev = 22.601 Range = 0 to 397.332

Spots per Line: 260
Number of Lines: 134
Data loaded: HR2MSI mouse urinary bladder S096.imzML

Post Processing
 Noise Correction
BG File: none
Normalization: none
Reference peak: 519.14
Norm Cutoff: 1000

Appearance
Interpolation Type: linear
Order: 0
Edit Colormap

Instructions
2- Use the spectrum generator tool to plot peaks in the selected ROI.
3- The ROI can be moved in the image to generate another peaks plot.
4- Click the ROI tool again to exit and resume processing.

Heatmap Mode
 MSI File Data
 Custom Data [Load]

MS Navigation
m/z: 730.8996
m/z Window: 0.1 Da
Intensity: max of window
m/z Step: 0.01
Scale Override: 393.003
min: 0 max: 393.003

m/z: 400 1000

MSiReader v0.06 [Matlab R2011b 64-bit] 15:23:53 Tuesday, 2015.04.28

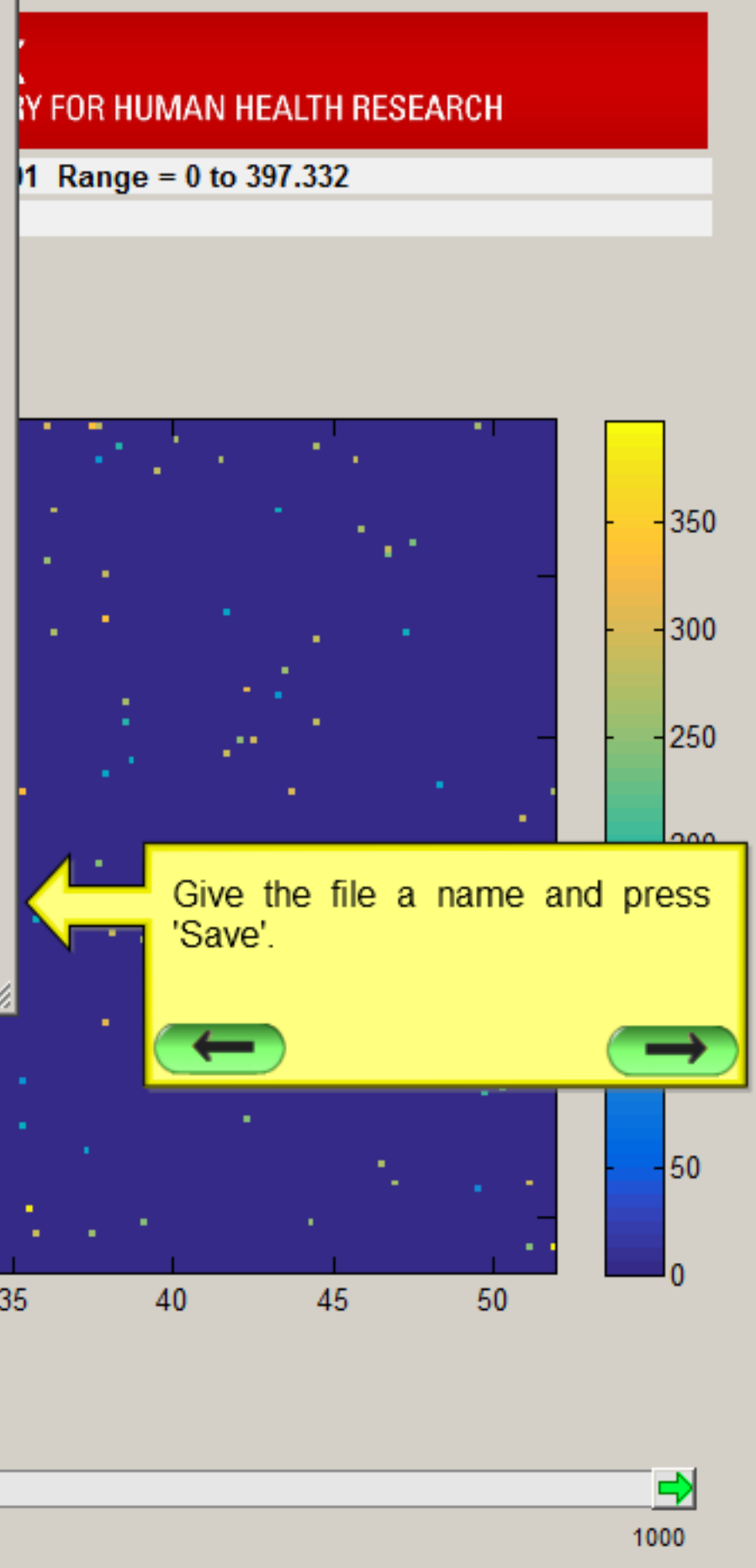
Save file name

Save in: **MATLAB**

Name	Date m...	Type	Size
mouseurinarybadderS096_nolinedimages	1/30/2015 1:19 PM	Microsoft Access...	1,142,36...
mouseurinarybadderS096	1/30/2015 9:25 AM	Microsoft Access...	614,166 KB
testimzMLdata2	1/29/2015 10:30...	Microsoft Access...	560,786 KB
testimzMLdata	1/20/2015 4:16 PM	Microsoft Access...	21,654 KB
PMMAPEG2000_05_8-07-14_shiftedcropped	11/6/2014 4:53 PM	Microsoft Access...	6,696 KB
PMMAPEG2000_02_8-07-14_shiftedcropped	11/6/2014 3:55 PM	Microsoft Access...	3,220 KB
PMMA5um10kv1000_1shiftedcropped	11/6/2014 3:28 PM	Microsoft Access...	6,187 KB
PEGPMMA20T02tempshifted	11/6/2014 3:14 PM	Microsoft Access...	9,003 KB
PEGPMMA20T02temp	11/6/2014 3:09 PM	Microsoft Access...	29,583 KB
NickQuickComparionLipids_LaterDatesToo_Neg	10/24/2014 2:26...	Microsoft Access...	41 KB
NickQuickComparionLipids_LaterDatesToo_Pos	10/24/2014 12:5...	Microsoft Access...	61 KB
NickQuickComparionLipids_Pos	10/23/2014 2:04...	Microsoft Access...	47 KB
NickQuickComparionLipids_Neg	10/23/2014 1:58...	Microsoft Access...	26 KB
NickColdStage201410_neg	10/22/2014 4:42...	Microsoft Access...	4 KB
NickColdStage201410_pos	10/22/2014 4:39...	Microsoft Access...	7 KB
EDRTestGTP	9/25/2014 4:19 PM	Microsoft Access...	27 KB
Slide2Spot2HSRDP	8/20/2014 11:23...	Microsoft Access...	4,244,74...
polymerdataforsyntheticsquare3dmatrix	6/19/2014 1:39 PM	Microsoft Access...	5,021 KB
testingdataformakingsyntheticimagesfromspectra	6/18/2014 4:05 PM	Microsoft Access...	10,986 KB
SAMChainLengthData	6/18/2014 3:31 PM	Microsoft Access...	8 KB

File name: Save Cancel

Save as type:

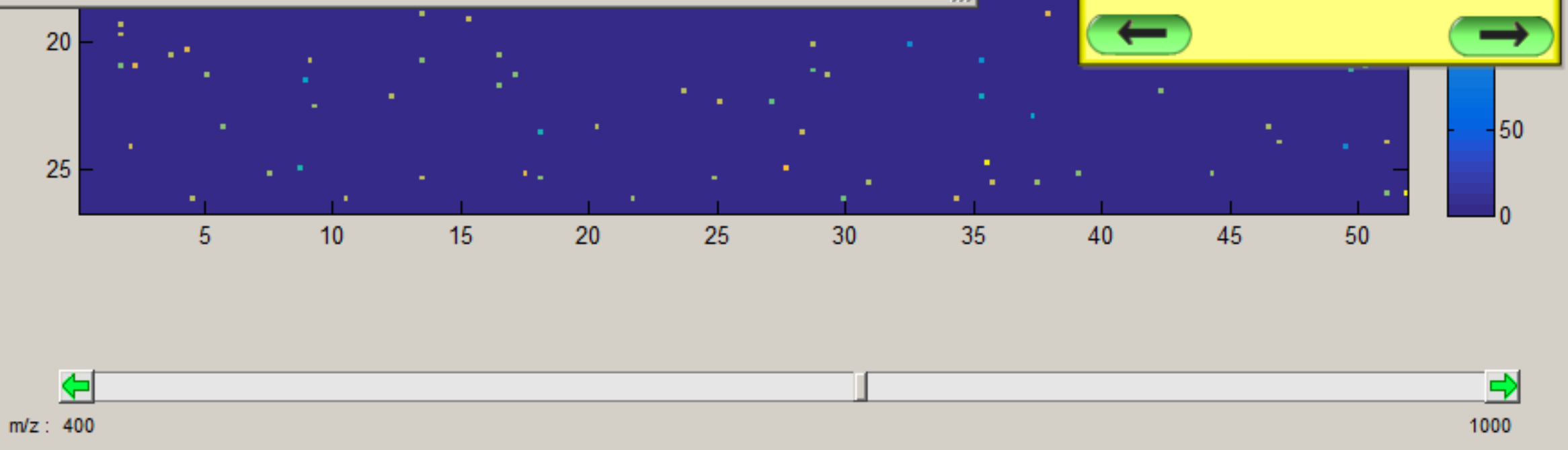


Edit Colormap

Instructions

- 2- Use the spectrum generator tool to plot peaks in the selected ROI.
- 3- The ROI can be moved in the image to generate another peaks plot.
- 4- Click the ROI tool again to exit and resume processing.

0 393.003



MSiReader v0.06 [Matlab R2011b 64-bit] 15:23:53 Tuesday, 2015.04.28

MSiReader 0.06

W.M. KECK
FTMS LABORATORY FOR HUMAN HEALTH RESEARCH

Image Area = 1393.6 Intensity: Mean = 1.88198 StdDev = 22.601 Range = 0 to 397.332

m/z Imaging Data

Spots per Line: 260 Spot Spacing: 200 um
Number of Lines: 134 Line Spacing: 200 um

Clear Data Data loaded: HR2MSI mouse urinary bladder S096.imzML

imzML File

Post Processing

Noise Correction
BG File: none

Normalization: none
Reference peak: 519.14
Norm Cutoff: 1000

Heatmap Mode

MSi File Data
 Custom Data

MS Navigation

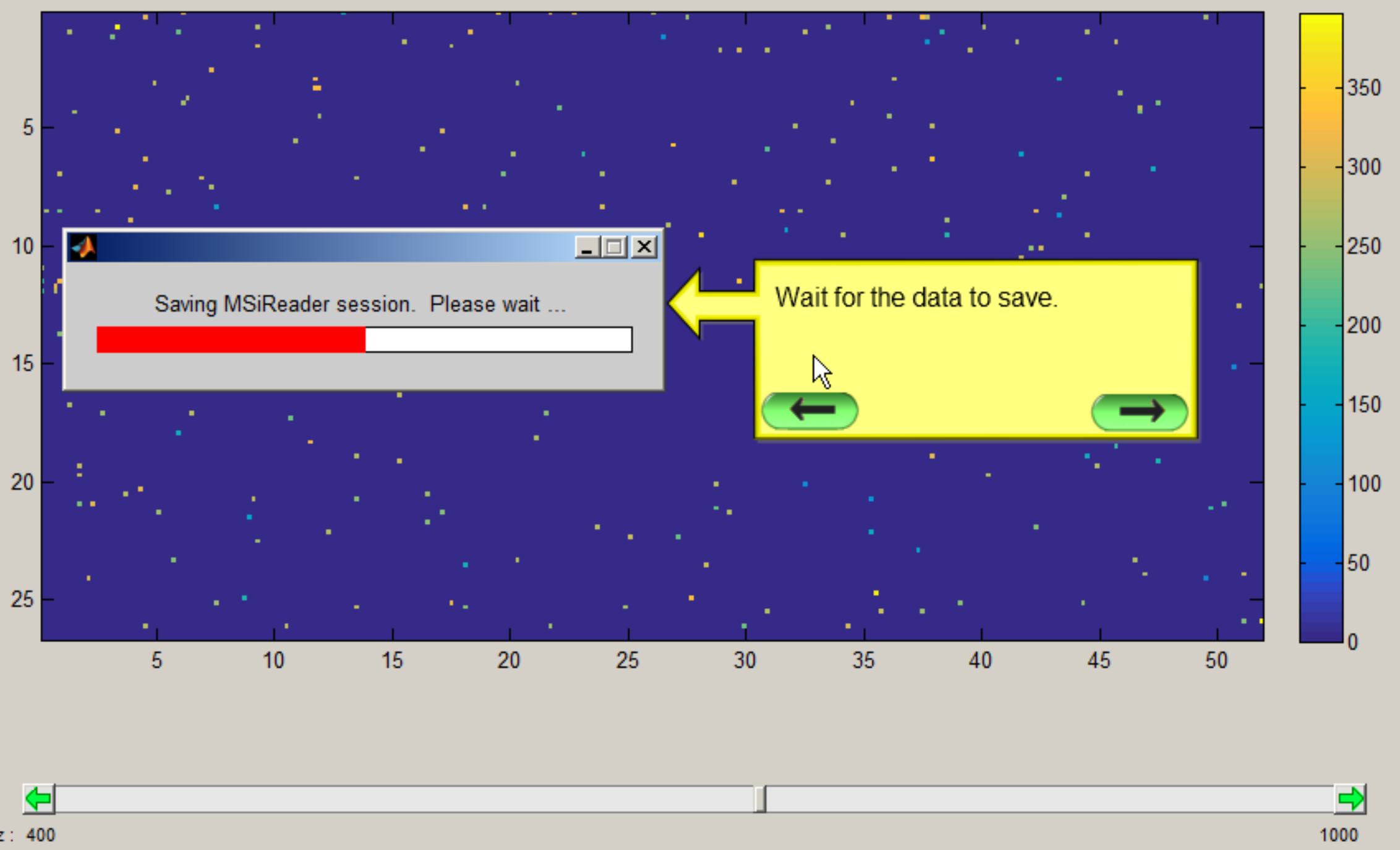
m/z: 730.8996
m/z Window: 0.1 Da
Intensity: max of window
m/z Step: 0.01
Scale Override: 393.003

Appearance

Interpolation Type: linear
Order: 0

- ### Instructions
- 2- Use the spectrum generator tool to plot peaks in the selected ROI.
 - 3- The ROI can be moved in the image to generate another peaks plot.
 - 4- Click the ROI tool again to exit and resume processing.

min: 0 max: 393.003



Make sure the MSi file and your peak list are loaded into the Matlab workspace.

The peak list will be in the workspace automatically if you saved it using the instructions in this tutorial.

To load the MSi file, type 'load <nameoffile>' at the Matlab Command Prompt. (<nameoffile> = the name you saved the MSiReader session as).

```
zcorrectorgui
clear;clc
zcorrectorgui
clear;clc
MSiReader
zcorrectorgui
clear;clc
zcorrectorgui
%-- 5/18/2015 10:55 AM --%
zcorrectorgui
cropimagesgui
clear;clc
autoloadbiffiles
cropimagesgui
clear;clc
imagegui
clc
load mouseurinarybadderS096
xlx
clc
```

Current Folder Workspace

Select data to plot

Name
MSi
markers

Command History

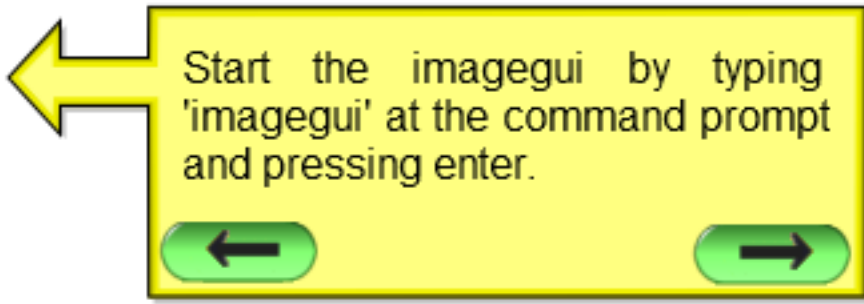
```
zcorrectorgui  
clear;clc  
zcorrectorgui  
clear;clc  
MSiReader  
zcorrectorgui  
clear;clc  
zcorrectorgui  
%-- 5/18/2015 10:55 AM --%  
zcorrectorgui  
cropimagesgui  
clear;clc  
autoloadbiffiles  
cropimagesgui  
clear;clc  
imagegui  
clc  
load mouseurinarybadderS096  
xlx  
clc
```

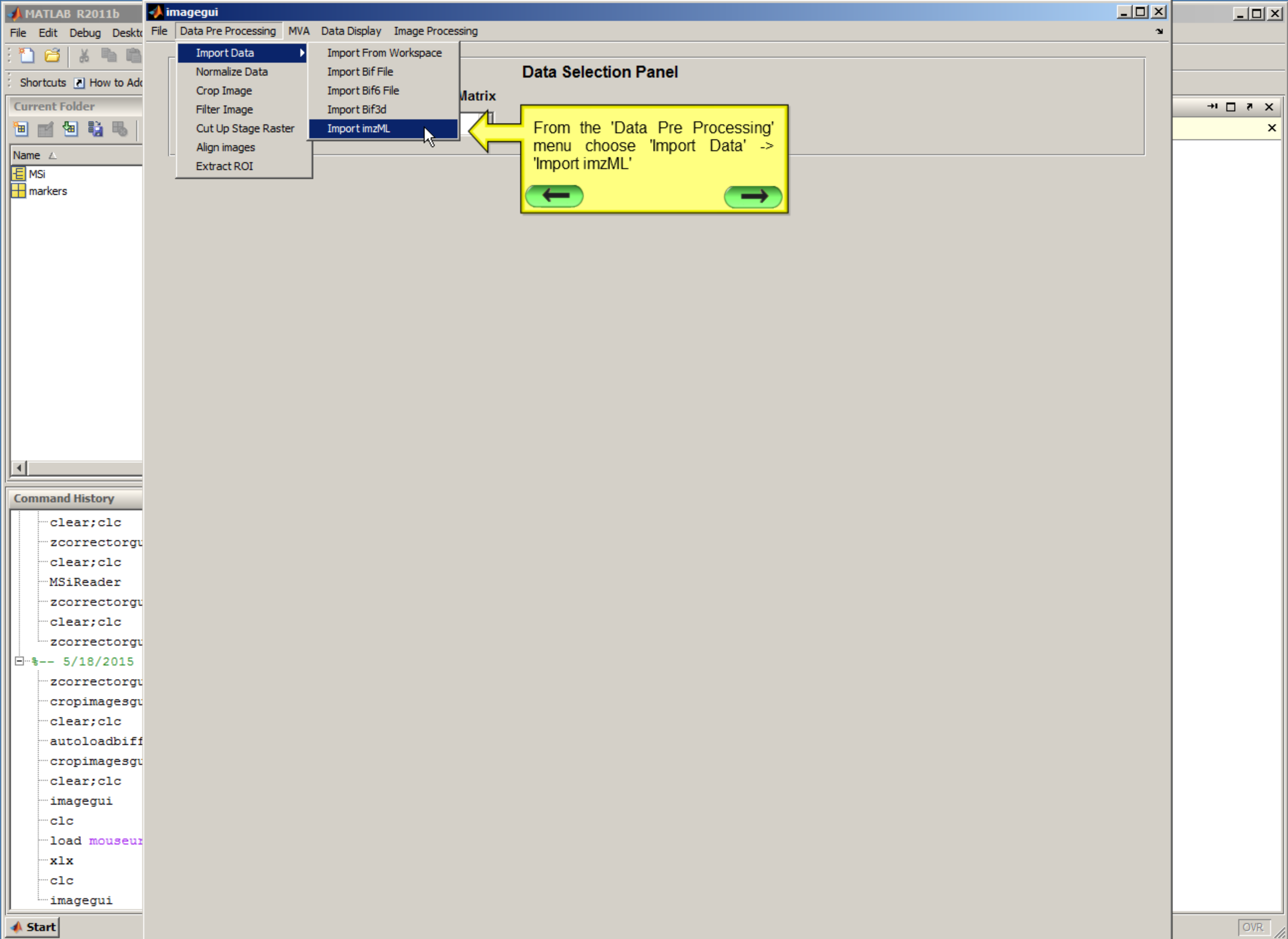
Command Window

New to MATLAB? Watch this [Video](#), see [Demos](#), or read [Getting Started](#).

```
f> >> imagegui
```

Start the imagegui by typing 'imagegui' at the command prompt and pressing enter.





- Import Data
 - Import From Workspace
 - Import Bif File
 - Import Bif6 File
 - Import Bif3d
 - Import imzML**
- Normalize Data
- Crop Image
- Filter Image
- Cut Up Stage Raster
- Align images
- Extract ROI

Data Selection Panel

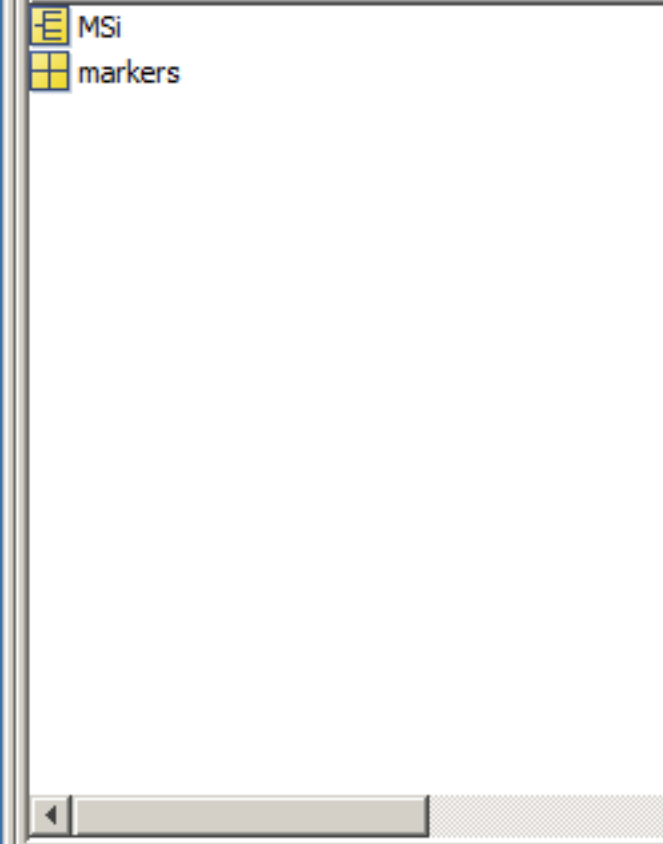
Matrix

From the 'Data Pre Processing' menu choose 'Import Data' -> 'Import imzML'



Command History

```
clear;clc
zcorrectorgu
clear;clc
MSiReader
zcorrectorgu
clear;clc
zcorrectorgu
5/18/2015
zcorrectorgu
cropimagesgu
clear;clc
autoloadbiff
cropimagesgu
clear;clc
imagegui
clc
load mouseu
xlx
clc
imagegui
```



```

MSiReader
zcorrectorgui
clear;clc
zcorrectorgui
5/18/2015 10:55 AM --%
zcorrectorgui
cropimagesgui
clear;clc
autoloadbiffiles
cropimagesgui
clear;clc
imagegui
clc
load mouseurinarybadder50
xlx
clc
imagegui
clc
guide imagegui
clc

```

Data Selection Panel

Name of Image Matrix:

Name of Variable Matrix:

Choose the data structure and peak/marker list from the drop down menus and press 'Load Data'

Data Structure:

Peak list:

- Choose one...
- MSi**

Load imzML Data

Close

Choose the MSi file with the data you want to load.

← →

MATLAB R2011b

File Edit Debug Desktop Window Help

Shortcuts How to Add What's New

Current Folder Workspace

Select data to

Name

- MSi
- markers

Command History

```
MSiReader  
zcorrectorgui  
clear;clc  
zcorrectorgui  
%-- 5/18/2015 10:55 AM --%  
zcorrectorgui  
cropimagesgui  
clear;clc  
autoloadbiffiles  
cropimagesgui  
clear;clc  
imagegui  
clc  
load mouseurinarybadder50  
xlx  
clc  
imagegui  
clc  
guide imagegui  
clc
```

imagegui

File Data Pre Processing MVA Data Display Image Processing

Data Selection Panel

Name of Image Matrix:

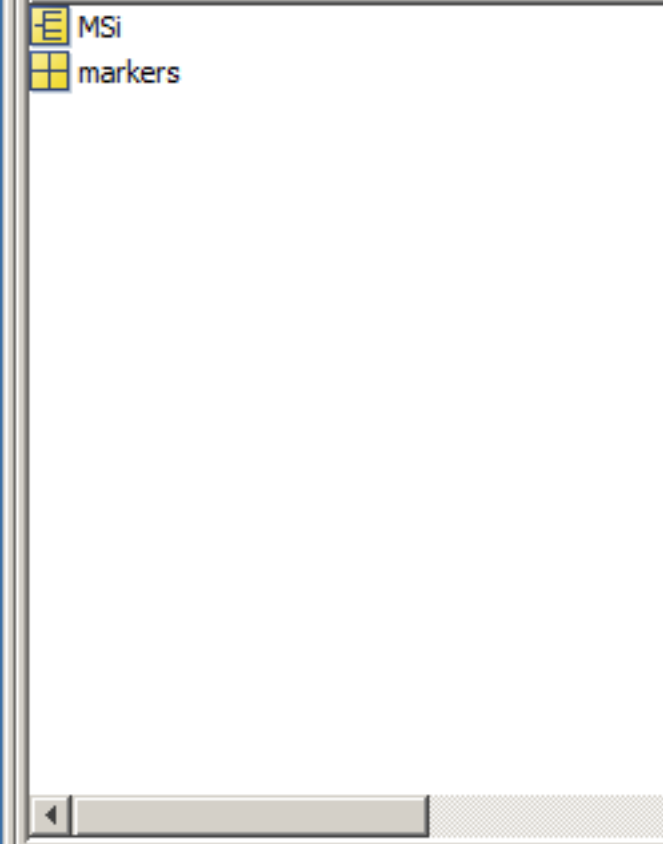
Name of Variable Matrix:

Choose the data structure and peak/marker list from the drop down menus and press 'Load Data'

Data Structure:

Peak list:

Choose the peak list file you want to use.



```
MSiReader
zcorrectorgui
clear;clc
zcorrectorgui
5/18/2015 10:55 AM --%
zcorrectorgui
cropimagesgui
clear;clc
autoloadbiffiles
cropimagesgui
clear;clc
imagegui
clc
load mouseurinarybadder50
xlx
clc
imagegui
clc
guide imagegui
clc
```

Data Selection Panel

Name of Image Matrix Name of Variable Matrix

Select Data Select Variables

Choose the data structure and peak/marker list from the drop down menus and press 'Load Data'

Data Structure Peak list
MSi markers

Load imzML Data

Close

Press the 'Load imzML Data' button.

← →

MATLAB R2011b
File Edit Debug Desktop Window Help

Shortcuts How to Add What's New

Current Folder Workspace

Name
MSi
markers

Command History

```
MSiReader  
zcorrectorgui  
clear;clc  
zcorrectorgui  
%-- 5/18/2015 10:55 AM --%  
zcorrectorgui  
cropimagesgui  
clear;clc  
autoloadbiffiles  
cropimagesgui  
clear;clc  
imagegui  
clc  
load mouseurinarybadder50  
xlx  
clc  
imagegui  
clc  
guide imagegui  
clc
```

Start

imagegui
File Data Pre Processing MVA Data Display Image Processing

Data Selection Panel

Name of Image Matrix:

Name of Variable Matrix:

Choose the data structure and peak/marker list from the drop down menus and press 'Load Data'

Data Structure: Peak list:

0% Progress
Loading imzML data...
Estimated time remaining: 00:09:59

Wait for the data to load in to the imagegui.

MATLAB R2011b
 File Edit Debug Desktop Window Help

Shortcuts How to Add What's New

Current Folder Workspace

Select data to plot

Name

- HR2MSI_mouse_urinary_bladder_S096
- HR2MSI_mouse_urinary_bladder_S096_sumofs
- HR2MSI_mouse_urinary_bladder_S096_totalco
- HR2MSI_mouse_urinary_bladder_S096peaks
- MSi
- markers

Command History

```

zcorrectorgui
clear;clc
MSiReader
zcorrectorgui
clear;clc
zcorrectorgui
5/18/2015 10:55 AM
zcorrectorgui
cropimagesgui
clear;clc
autoloadbiffiles
cropimagesgui
clear;clc
imagegui
clc
load mouseurinarybadderS09
xlsx
clc
imagegui
clc
  
```

imagegui
 File Data Pre Processing MVA Data Display Image Processing

Data Selection Panel

Name of Image Matrix: Name of Variable Matrix:

Load Selected Data

Image: **HR2MSI_mouse_urinary_bl**
 Variables: **HR2MSI_mouse_urinary_bl**

Variable List: 404.051, 404.947, 406.955, 409.056, 410.06, 412.723, 418.957, 420.026, 421.054, 421.922, 422.929, 423.983, 424.927, 426.083, 426.929, 429.118, 431.038

Variables to Plot: 406.955

Data (actual counts):

Add to Plot **Reset Plot**

Name for Combined Selected Variable Image:

Save Combined Variable Image

Close Panel

Create ext Figure **Save Plot to File**

Once the data is loaded, you can then select the data from the drop down menus at the top of the imagegui and carry out any function you choose.

See the other imagegui tutorials on our website for help on using the gui functions.
<http://www.nb.uw.edu/mvsa/multivariate-surface-analysis-homepage>

← →

MATLAB R2011b

File Edit Debug Desktop Window Help

Shortcuts How to Add What's New

Current Folder Workspace

Select data to plot

Name

- HR2MSI_mouse_urinary_bladder_S096
- HR2MSI_mouse_urinary_bladder_S096_sumofs
- HR2MSI_mouse_urinary_bladder_S096_totalco
- HR2MSI_mouse_urinary_bladder_S096peaks
- MSi
- markers

Command History

```

zcorrectorgui
clear;clc
MSiReader
zcorrectorgui
clear;clc
zcorrectorgui
5/18/2015 10:55 AM
zcorrectorgui
cropimagesgui
clear;clc
autoloadbiffiles
cropimagesgui
clear;clc
imagegui
clc
load mouseurinarybadderS09
xlsx
clc
imagegui
clc

```

imagegui

File Data Pre Processing MVA Data Display Image Processing

Data Selection Panel

Name of Image Matrix: HR2MSI_mouse...
 Name of Variable Matrix: HR2MSI_mouse_u...

Load Selected Data

Image: HR2MSI_mouse_urinary_bl...
 Variables: HR2MSI_mouse_urinary_bl...

Currently Selected Peaks

Browse all Peak Images

That ends this tutorial. Press the button on the left to go back to the previous step. Press the button on the right to start the tutorial over.

Please see the other imagegui tutorials for detailed information on how to use each function in the imagegui.

Variable List

- 404.051
- 404.947
- 406.955
- 409.056
- 410.06
- 412.723
- 418.957
- 420.026
- 421.054
- 421.922
- 422.929
- 423.983
- 424.927
- 426.083
- 426.929
- 429.118
- 431.038

Variables to Plot

- 406.955

Data (actual counts)

Add to Plot **Reset Plot**

Name for Combined Selected Variable Image

Save Combined Variable Image

Close Panel

Counts

Create ext Figure **Save Plot to File**