

LOCALIZE_FIBERS MATLAB App README

Mai-Anh Vu

5/31/2024

Howe Lab members: for compatibility with legacy code and formatting, please see Howe Lab Specifics on the last page.

Fiber location table

The purpose of this sequence of steps is to find the locations of your fibers, and match them to the grid. An output struct with crucial information will be generated, and has the following fields.

- info: the size, and location of your CT scan
- fiber_tops: intermediate information from the steps for localization of the fiber tops
- fiber_bottoms: intermediate information from the steps for localization of the fiber bottoms
- fiber_table_orig: same as below, with the information before manual editing
- **fiber_table**: this is the main output table. This will have a row for each fiber, and contains information about the coordinates for each fiber top and fiber bottom, as well as atlas labels

Before you begin

If you have a grid arrangement, and you want to map your recording locations to locations on the grid, you will want a matlab (.mat) file, which, when loaded, contains one field which provides the grid mapping of your fibers. There are 2 ways to do this:

1. One is a coordinate system. This is a matrix, where each row represents a fiber, and the columns represent row coordinates, column coordinates, and (optional) ID#. In this example to my right, column 1 contains the column# for each fiber. Column 2 contains the row#. Column 3 contains an ID# that I assigned ahead of time.

```
ans =  
  
     5     10      1  
     5     12      2  
     6     11      3  
     6     13      4  
     4      9      5  
     8     11      6  
     6      9      7  
     8      9      8  
     7      8      9  
     3      6     10  
     4      3     11  
     1      4     12  
     4      7     13  
     8     13     14  
     7     10     15  
     9     14     16  
    10     13     17  
     7     14     18  
    11     14     19  
    11     16     20  
    13     18     21  
    12     17     22  
    10     15     23  
    13     16     24  
    14     19     25  
    12     15     26  
    11     12     27  
    12     13     28  
    10      9     29  
    14     17     30  
    14     13     31  
    13     10     32  
     7     12     33  
    10     11     34
```

Before you begin (cont'd)

- The other options is a matrix that represents the layout of the grid. The values in the matrix are the ID# (you can use 1s if you don't have ID#s), and the locations are the actual row/column location in the grid arrangement. In my example below, fiber#64 is in row 1, column 2. Fiber#10 is in row 7, column 3.

```
ans =
```

0	64	0	69	0	0	0	0	0	0	0	0	0	0
73	0	70	0	59	0	0	0	0	0	0	0	0	0
0	38	0	11	0	65	0	0	0	0	0	0	0	0
12	0	36	0	67	0	66	0	58	0	0	0	0	0
0	39	0	37	0	68	0	63	0	60	0	0	0	0
0	0	10	0	40	0	62	0	61	0	54	0	0	0
0	0	42	13	0	57	0	56	0	48	0	55	0	0
0	0	41	0	35	0	9	0	46	0	71	0	53	0
0	0	0	5	0	7	0	8	0	29	0	51	0	0
0	0	0	0	1	0	15	0	47	0	52	0	32	0
0	0	0	0	0	3	0	6	0	34	0	50	0	49
0	0	0	0	2	0	33	0	72	0	27	0	45	0
0	0	0	0	0	4	0	14	0	17	0	28	0	31
0	0	0	0	0	0	18	0	16	0	19	0	43	0
0	0	0	0	0	0	0	0	0	23	0	26	0	44
0	0	0	0	0	0	0	0	0	0	20	0	24	0
0	0	0	0	0	0	0	0	0	0	0	22	0	30
0	0	0	0	0	0	0	0	0	0	0	0	21	0
0	0	0	0	0	0	0	0	0	0	0	0	0	25

Before you begin (cont'd)

Note: If you don't have a grid arrangement, but you have some reference of what the grid tops should look like (a coordinate file like #1) or just an image you want to use, you can use that too.

LOCALIZE_FIBERS

Click to locate your CT.

This button would be for to locate the in-progress localization file if you want to resume an unfinished localization.

Then click load

Locate CT path to registered CT .tif file

Locate inprog path to inprog.mat file (optional)

Load

1. IDENTIFY FIBER TOPS (opens separate app)

2. REFINE FIBER TOPS & ASSIGN LABELS (opens separate app)

3. IDENTIFY FIBER AREA (opens separate app)

4. MAP FIBER TIPS

Multifiber separation algorithm

☒ watershed ☐ GMM

5. CHECK MULTIFIBERS (opens separate app)

6. ADD ATLAS INFO & SAVE FINAL OUTPUT (opens separate app)

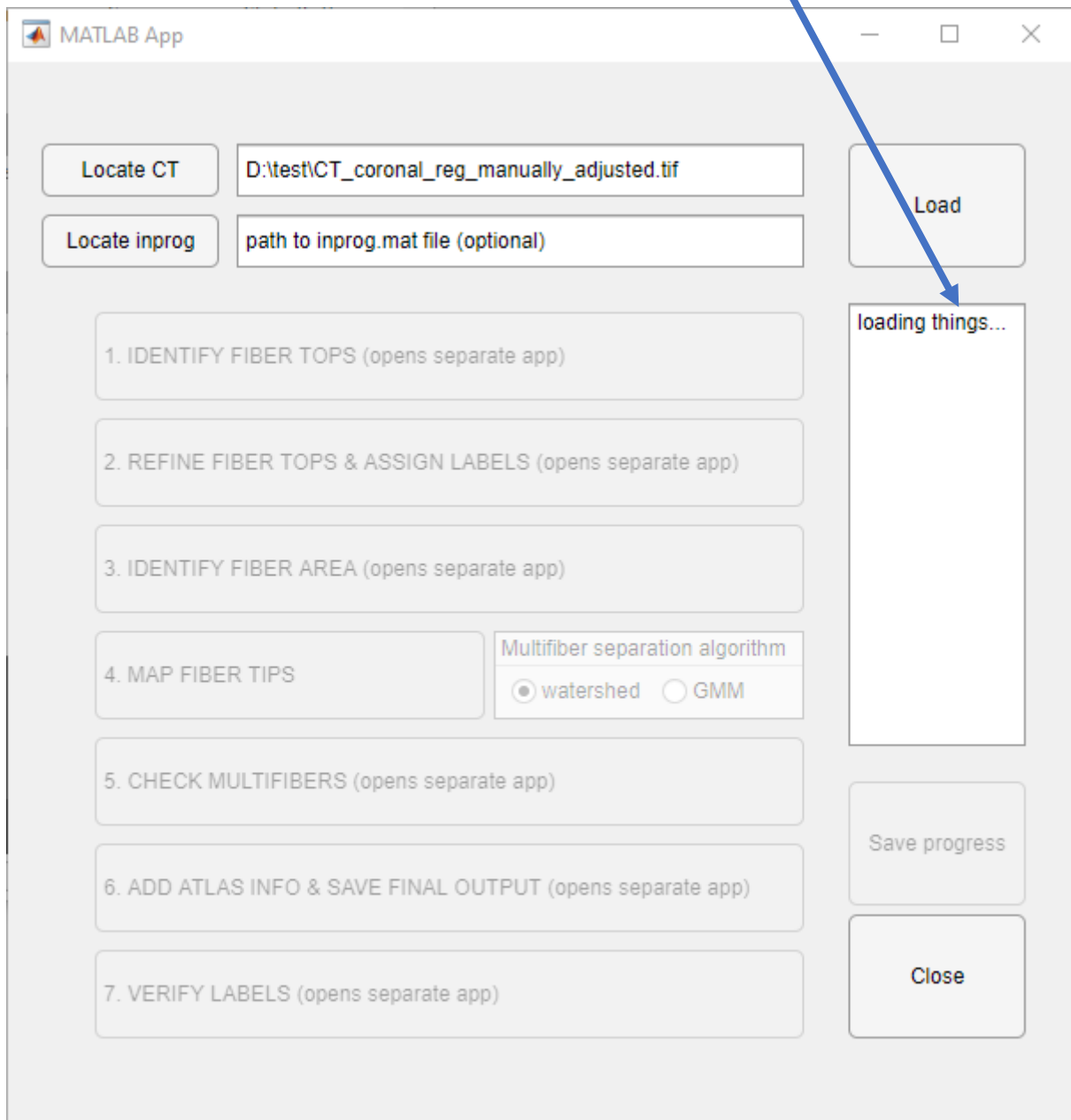
7. VERIFY LABELS (opens separate app)

Save progress

Close

LOCALIZE_FIBERS

This text window will keep you updated.



The image shows a MATLAB App window titled "MATLAB App". The interface is designed for a fiber localization process. It features a series of steps on the left, each in a light gray box:

- 1. IDENTIFY FIBER TOPS (opens separate app)
- 2. REFINE FIBER TOPS & ASSIGN LABELS (opens separate app)
- 3. IDENTIFY FIBER AREA (opens separate app)
- 4. MAP FIBER TIPS
- 5. CHECK MULTIFIBERS (opens separate app)
- 6. ADD ATLAS INFO & SAVE FINAL OUTPUT (opens separate app)
- 7. VERIFY LABELS (opens separate app)

Step 4 is expanded, showing a "Multifiber separation algorithm" section with two radio buttons: "watershed" (selected) and "GMM".

At the top, there are two input fields with associated buttons:

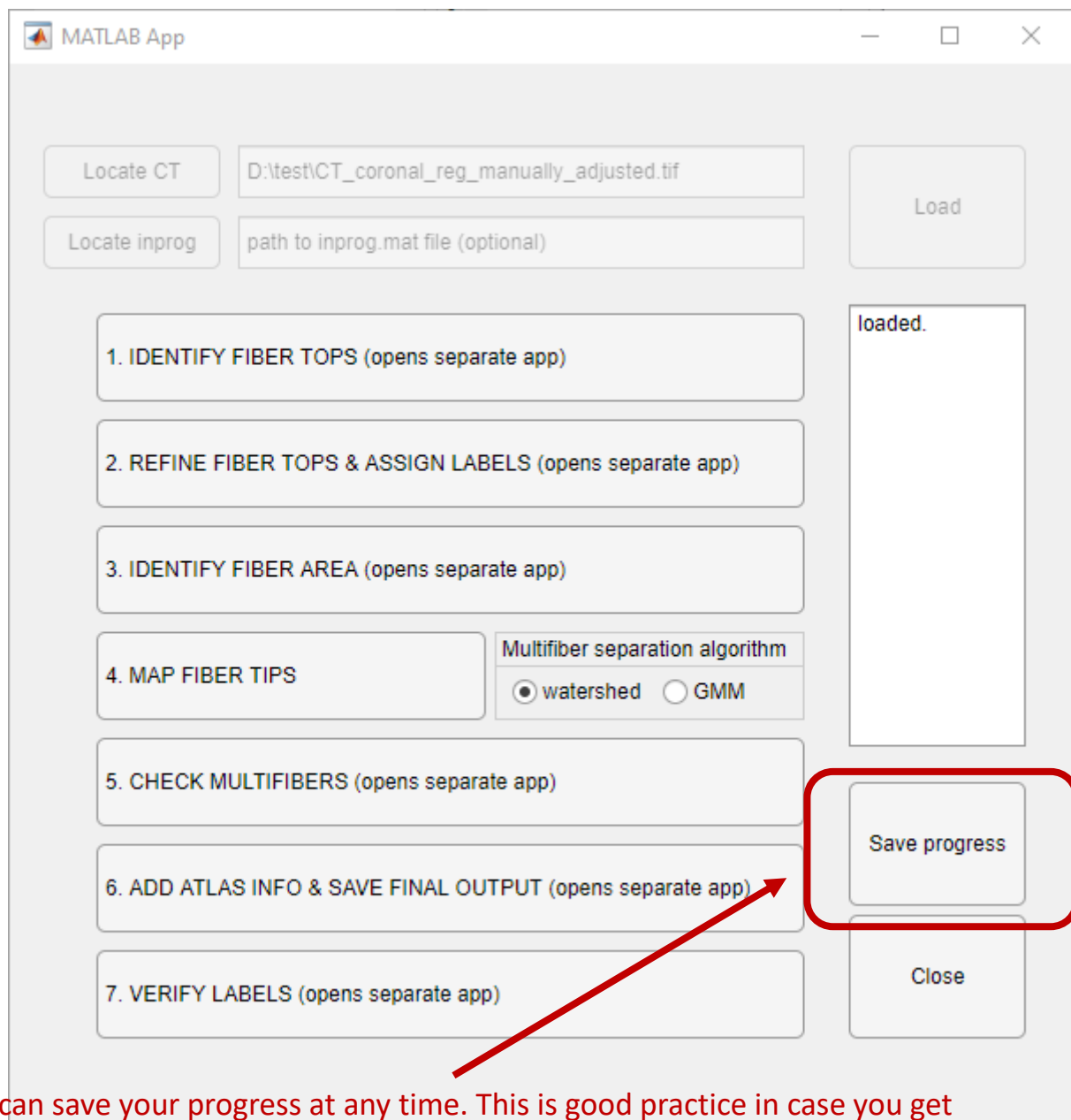
- "Locate CT" button next to a text field containing "D:\test\CT_coronal_reg_manually_adjusted.tif".
- "Locate inprog" button next to a text field containing "path to inprog.mat file (optional)".

On the right side, there are three buttons: "Load", "Save progress", and "Close".

A blue arrow points from the text "This text window will keep you updated." to a text area on the right that contains the text "loading things...".

LOCALIZE_FIBERS

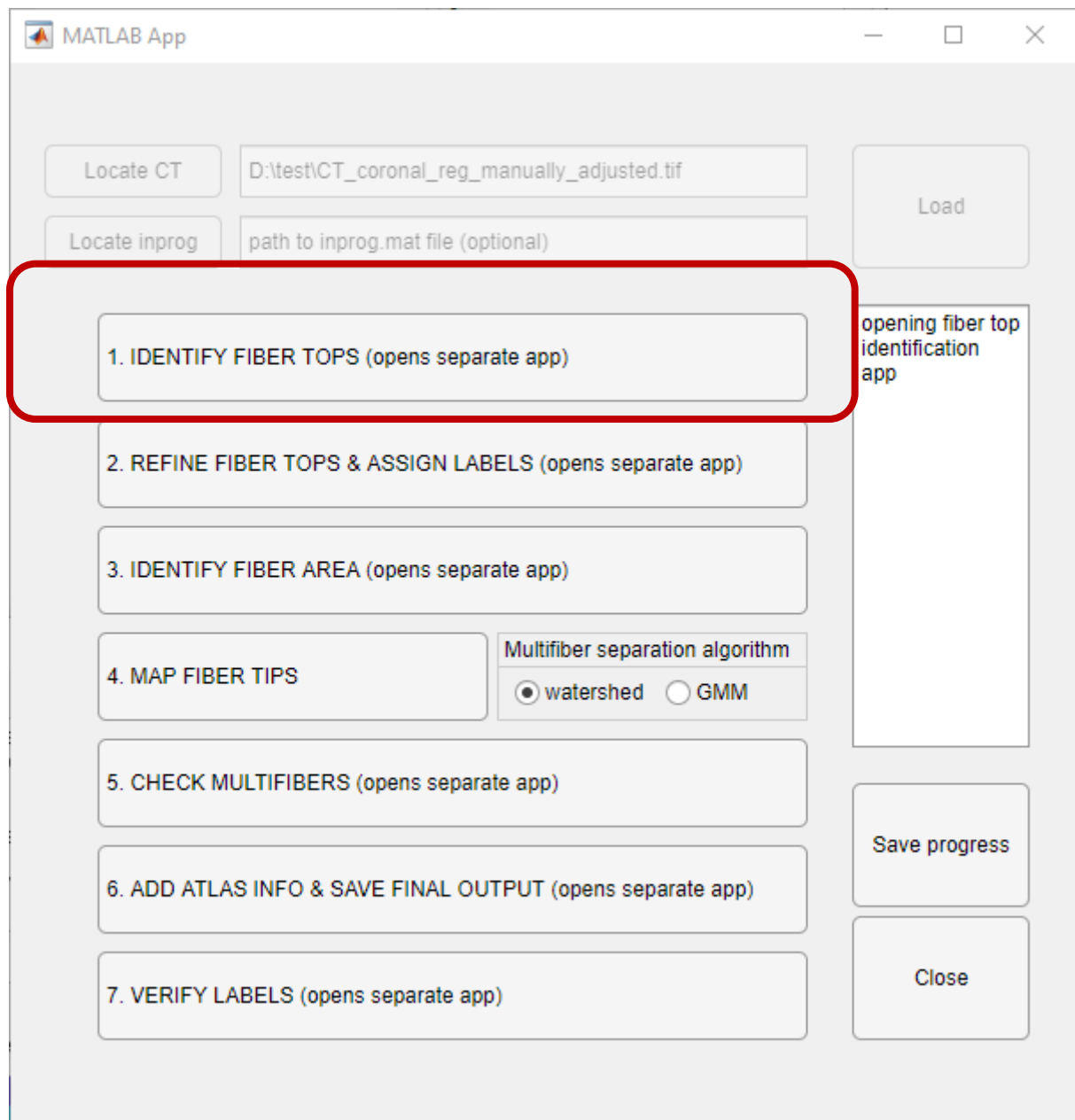
Now you'll go through the steps in order.



The image shows a MATLAB App window titled "MATLAB App". The interface includes several input fields and buttons. At the top, there are two input fields: "Locate CT" with the value "D:\test\CT_coronal_reg_manually_adjusted.tif" and "Locate inprog" with the value "path to inprog.mat file (optional)". To the right of these is a "Load" button. Below the input fields is a vertical list of seven steps, each in a button-like box: "1. IDENTIFY FIBER TOPS (opens separate app)", "2. REFINE FIBER TOPS & ASSIGN LABELS (opens separate app)", "3. IDENTIFY FIBER AREA (opens separate app)", "4. MAP FIBER TIPS", "5. CHECK MULTIFIBERS (opens separate app)", "6. ADD ATLAS INFO & SAVE FINAL OUTPUT (opens separate app)", and "7. VERIFY LABELS (opens separate app)". To the right of the steps is a text area labeled "loaded.". Below the text area is a "Save progress" button, which is highlighted with a red rounded rectangle. A red arrow points from the "Save progress" button to step 6. Below the "Save progress" button is a "Close" button. To the right of step 4 is a section titled "Multifiber separation algorithm" with two radio buttons: "watershed" (selected) and "GMM".

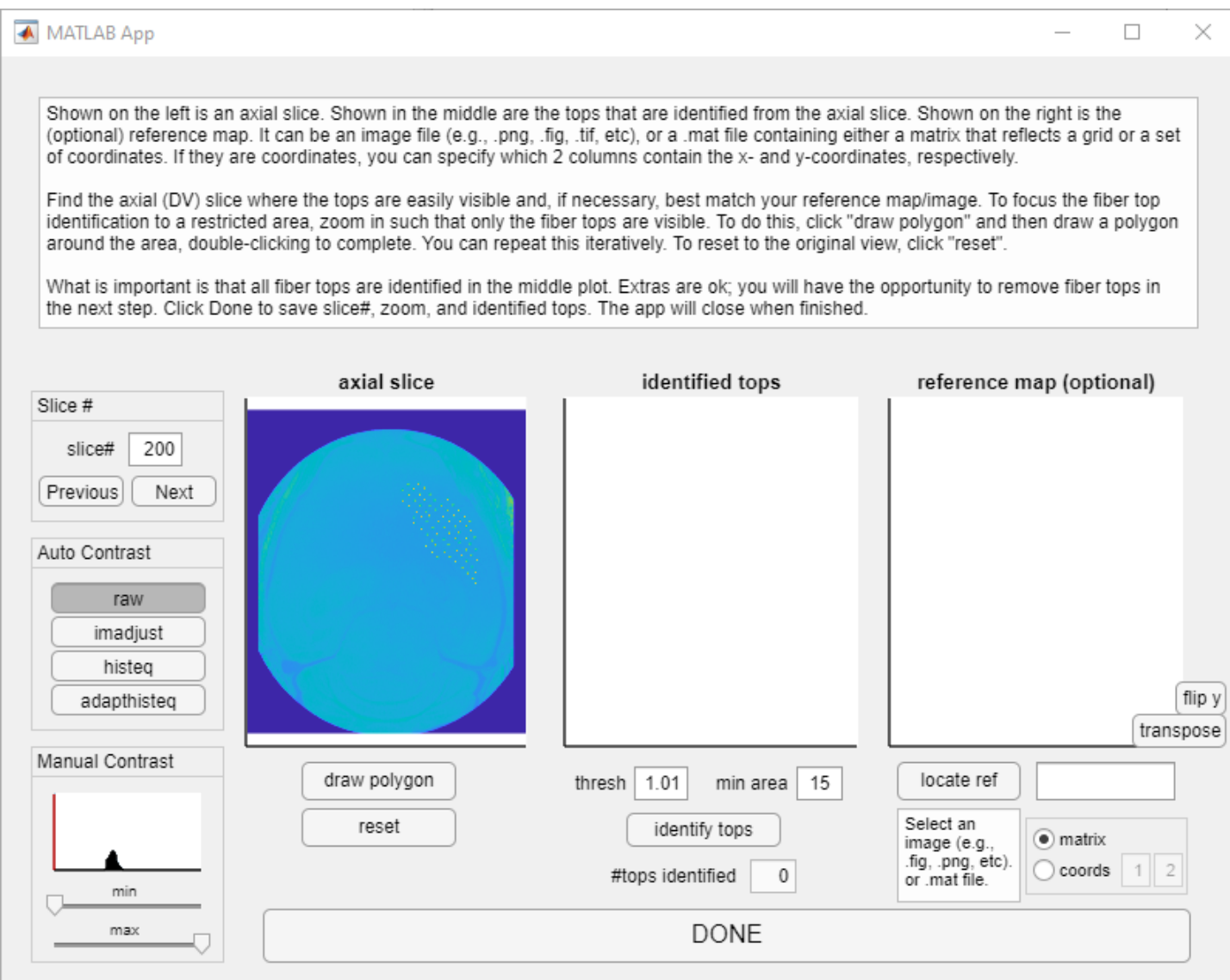
You can save your progress at any time. This is good practice in case you get interrupted, or you run into issues at a step. You'll be able to pick up where you left off. This will be name something like `___in_prog.mat`, and after step 6, it will be named `____localized_fibers.mat`

IDENTIFY FIBER TOPS

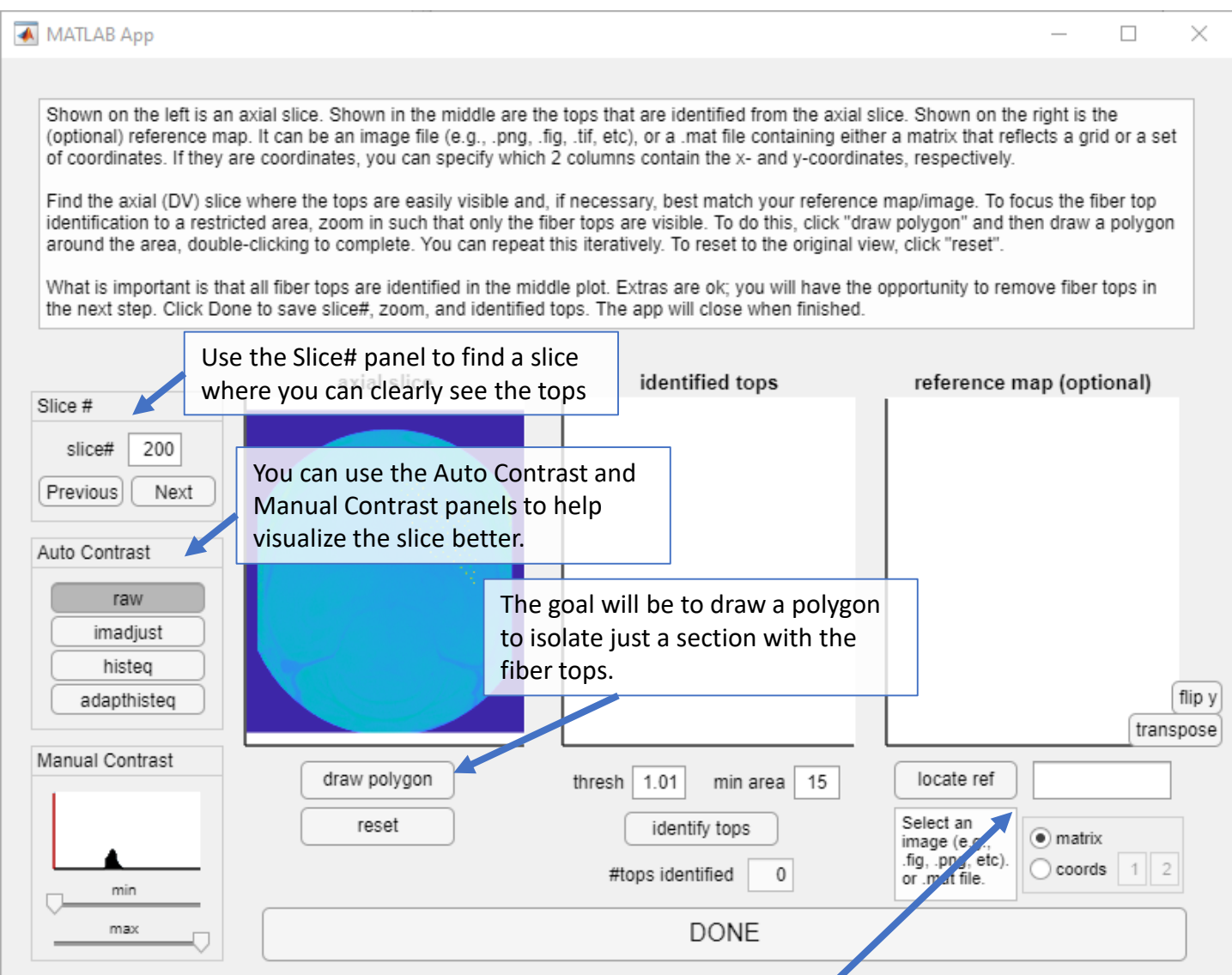


IDENTIFY FIBER TOPS

Eventually, we'll map each fiber top to each fiber bottom. The objective of this app is to locate your fiber tops.




IDENTIFY FIBER TOPS



This is where you can load the reference mentioned in the "Before you begin" section. If it's an image file, it'll automatically display. If it's a .mat file, specify if it's a matrix arrangement or a coordinate file. You can specify which columns of the coordinate file contain the x-, and y-coordinates, respectively.

IDENTIFY FIBER TOPS

 MATLAB App

Shown on the left is an axial slice. Shown in the middle are the tops that are identified from the axial slice. Shown on the right is the (optional) reference map. It can be an image file (e.g., .png, .fig, .tif, etc), or a .mat file containing either a matrix that reflects a grid or a set of coordinates. If they are coordinates, you can specify which 2 columns contain the x- and y-coordinates, respectively.


Find the axial (DV) slice where the tops are easily visible and, if necessary, best match your reference map/image. To focus the fiber top identification to a restricted area, zoom in such that only the fiber tops are visible. To do this, click "draw polygon" and then draw a polygon around the area, double-clicking to complete. You can repeat this iteratively. To reset to the original view, click "reset".

What is important is that all fiber tops are identified in the middle plot. Extras are ok; you will have the opportunity to remove fiber tops in the next step. Click Done to save slice#, zoom, and identified tops. The app will close when finished.

axial slice **identified tops** **reference map (optional)**

Slice #
slice# 200
Previous Next

Auto Contrast
raw
imadjust
histeq
adapthisteq

Manual Contrast

min
max

draw polygon
reset

axial slice


axial slice

axial slice

flip y
transpose

matrix
ords 1 2

IDENTIFY FIBER TOPS

 MATLAB App

Shown on the left is an axial slice. Shown in the middle are the tops that are identified from the axial slice. Shown on the right is the (optional) reference map. It can be an image file (e.g., .png, .fig, .tif, etc), or a .mat file containing either a matrix that reflects a grid or a set of coordinates. If they are coordinates, you can specify which 2 columns contain the x- and y-coordinates, respectively.

Find the axial (DV) slice where the tops are easily visible and, if necessary, best match your reference map/image. To focus the fiber top identification to a restricted area, zoom in such that only the fiber tops are visible. To do this, click "draw polygon" and then draw a polygon around the area, double-clicking to complete. You can repeat this iteratively. To reset to the original view, click "reset".

What is important is that all fiber tops are identified in the middle plot. Extras are ok; you will have the opportunity to remove fiber tops in the next step. Click Done to save slice#, zoom, and identified tops. The app will close when finished.

axial slice **identified tops** **reference map (optional)**

Slice #
slice# 180
Previous Next

Auto Contrast
raw
imadjust
histeq
adapthisteq

Manual Contrast
min
max

draw polygon
reset

thresh 1.01 min area 15
identify tops
#tops identified 73

locate ref D:\test\top_grid
Select an image (e.g., .fig, .png, etc), or .mat file.
☒ matrix
☐ coords 1 2

flip y
transpose

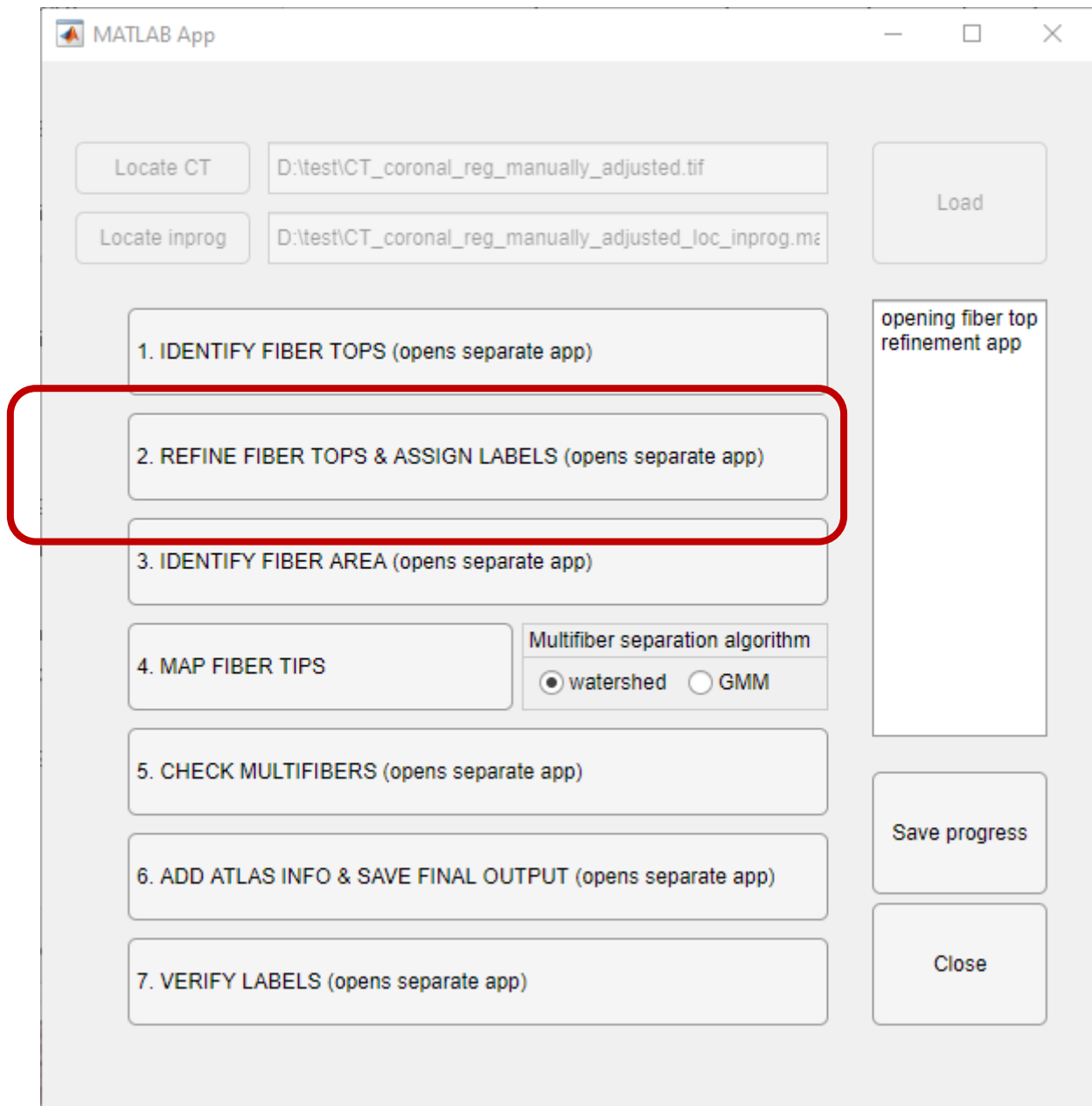
DONE

Now click identify tops. The #tops identified will be shown. You can adjust the threshold or minimum area to get better results. You may also need to pick a different slice, draw a different polygon, and identify tops again.

I can compare this to the reference I loaded that has my design. They match.

Click DONE when satisfied


REFINE FIBER TOPS & ASSIGN LABELS



REFINE FIBER TOPS & ASSIGN LABELS

Here you can refine the tops. You cannot add tops, but you can delete tops.

If you have your fibers arranged in a grid, and want to assign each fiber top to a grid location, you can do that too.

 MATLAB App

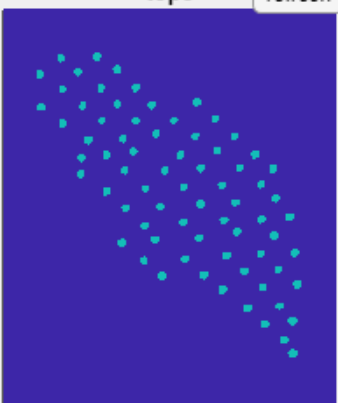
The primary goal in this step is to delete any identified fiber tops as necessary, and if desired, to assign labels to the fiber tops. You may assign up to 3 numeric labels for each fiber top (e.g., for a grid arrangement, you might want to assign columns and rows). Shown in the table is the top_num identifier, and the labels, which are manually editable. The top_num number labels are arbitrarily assigned, and you won't be able to change them, though you can create a new identifier as one of the other labels. The columns are sortable.

Shown on the left are the tops identified in the last step. To select fiber tops, you can click one of the selection options, or you can select the fibers of interest in the top_num column of the table. The selected tops will appear in the selection #s field (which you can also edit to select fibers). Selected fibers will be highlighted in the table and on the plot.

As in the last step, the right axes will show the (optional) reference map. As in the previous step, it can be an image file, a matrix (e.g., for a grid-like arrangement), or an array of coordinates. You can specify which columns contain which coordinates, and alternate ID (set to 0 if you don't have an alternate ID). If you have a grid arrangement (matrix, or as row and column coordinates), you can check the "assign grid" box to generate an automatic assignment, which you can then manually edit as necessary.

tops

refresh



selection #s

select single top

select multiple: line

select multiple: polygon

reset all

reference map (optional)

locate ref

☒ matrix

☐ coords:

1

Label1/x/col

2

Label2/y/row

3

Label3/ID

☐ assign grid

flip y

transpose


top_ID	Label1	Label2	Label3
1	NaN	NaN	N
2	NaN	NaN	N
3	NaN	NaN	N
4	NaN	NaN	N
5	NaN	NaN	N
6	NaN	NaN	N
7	NaN	NaN	N
8	NaN	NaN	N
9	NaN	NaN	N
10	NaN	NaN	N
11	NaN	NaN	N
12	NaN	NaN	N
13	NaN	NaN	N

delete

DONE

REFINE FIBER TOPS & ASSIGN LABELS

There are 3 ways to select fiber(s). You can enter numbers in the selection #s window. You can click a button to select a single top, multiple tops by drawing a line through them, or multiple tops by drawing a polygon around them. You can also select tops by clicking the numbers in the top_ID column. The whole row will be selected

 MATLAB App

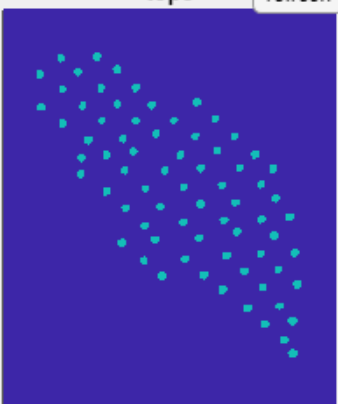
The primary goal in this step is to delete any identified fiber tops as necessary, and if desired, to assign labels to the fiber tops. You may assign up to 3 numeric labels for each fiber top (e.g., for a grid arrangement, you might want to assign columns and rows). Shown in the table is the top_num identifier, and the labels, which are manually editable. The top_num number labels are arbitrarily assigned, and you won't be able to change them, though you can create a new identifier as one of the other labels. The columns are sortable.

Shown on the left are the tops identified in the last step. To select fiber tops, you can click one of the selection options, or you can select the fibers of interest in the top_num column of the table. The selected tops will appear in the selection #s field (which you can also edit to select fibers). Selected fibers will be highlighted in the table and on the plot.

As in the last step, the right axes will show the (optional) reference map. As in the previous step, it can be an image file, a matrix (e.g., for a grid-like arrangement), or an array of coordinates. You can specify which columns contain which coordinates, and alternate ID (set to 0 if you don't have an alternate ID). If you have a grid arrangement (matrix, or as row and column coordinates), you can check the "assign grid" box to generate an automatic assignment, which you can then manually edit as necessary.

tops

refresh



selection #s

select single top

select multiple: line

select multiple: polygon

reset all

reference map (optional)

locate ref

☒ matrix

☐ coords:

1

Label1/x/col

2

Label2/y/row

3

Label3/ID

☐ assign grid

flip y

transpose

top_ID	Label1	Label2	Label3
1	NaN	NaN	N
2	NaN	NaN	N
3	NaN	NaN	N
4	NaN	NaN	N
5	NaN	NaN	N
6	NaN	NaN	N
7	NaN	NaN	N
8	NaN	NaN	N
9	NaN	NaN	N
10	NaN	NaN	N
11	NaN	NaN	N
12	NaN	NaN	N
13	NaN	NaN	N

delete

DONE

REFINE FIBER TOPS & ASSIGN LABELS

Here in this example, I've loaded my reference, and specified that it is a matrix (see slide 4). Note that "flip y" and "transpose" just apply to the display, and don't change the grid assignment.

To generate first-pass automatic grid location assignments, check the "assign grid" box. You'll see that the columns for grid_col, grid_row, and ID automatically populate.

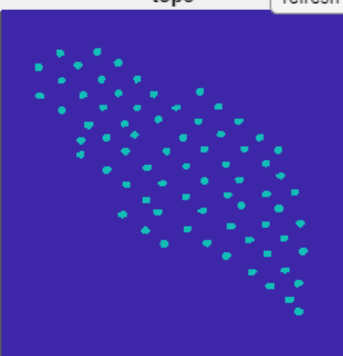
MATLAB App

The primary goal in this step is to delete any identified fiber tops as necessary, and if desired, to assign labels to the fiber tops. You may assign up to 3 numeric labels for each fiber top (e.g., for a grid arrangement, you might want to assign columns and rows). Shown in the table is the top_num identifier, and the labels, which are manually editable. The top_num number labels are arbitrarily assigned, and you won't be able to change them, though you can create a new identifier as one of the other labels. The columns are sortable.

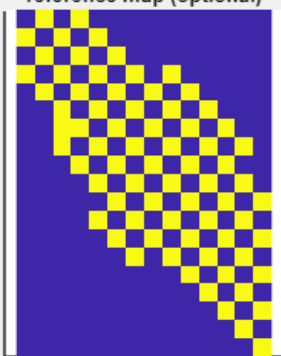
Shown on the left are the tops identified in the last step. To select fiber tops, you can click one of the selection options, or you can select the fibers of interest in the top_num column of the table. The selected tops will appear in the selection #s field (which you can also edit to select fibers). Selected fibers will be highlighted in the table and on the plot.

As in the last step, the right axes will show the (optional) reference map. As in the previous step, it can be an image file, a matrix (e.g., for a grid-like arrangement), or an array of coordinates. You can specify which columns contain which coordinates, and alternate ID (set to 0 if you don't have an alternate ID). If you have a grid arrangement (matrix, or as row and column coordinates), you can check the "assign grid" box to generate an automatic assignment, which you can then manually edit as necessary.

tops refresh



reference map (optional)



flip y
transpose

selection #s

select single top

select multiple: line

select multiple: polygon

reset all

locate ref

☒ matrix ☐ coords:

1

Label1/x/col

2

Label2/y/row

3

Label3/ID

☒ assign grid

top_ID	grid_col	grid_row	ID	
1	1	2	73	▲
2	1	4	12	
3	2	1	64	
4	2	3	38	
5	2	5	39	
6	3	2	70	
7	3	7	42	
8	3	8	41	
9	3	4	36	
10	3	6	10	
11	4	1	69	
12	4	3	11	
13	4	5	37	
14	4	7	12	▼

delete

DONE

REFINE FIBER TOPS & ASSIGN LABELS

Now you need to manually verify that these are correct. In this example, I start with the grid columns but sorting the grid_col column (click the heading). Now I select the rows (remember: click in the top_ID column to make a selection) that correspond with column 1. The fibers will be highlighted in the identified tops (first image), and if applicable, the reference map will display the columns/rows highlighted.

MATLAB App

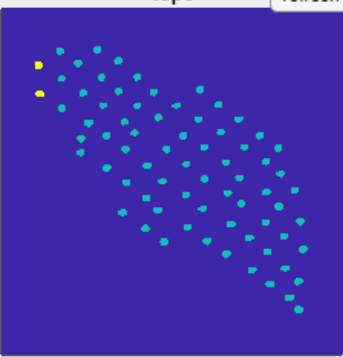
The primary goal in this step is to delete any identified fiber tops as necessary, and if desired, to assign labels to the fiber tops. You may assign up to 3 numeric labels for each fiber top (e.g., for a grid arrangement, you might want to assign columns and rows). Shown in the table is the top_num identifier, and the labels, which are manually editable. The top_num number labels are arbitrarily assigned, and you won't be able to change them, though you can create a new identifier as one of the other labels. The columns are sortable.

Shown on the left are the tops identified in the last step. To select fiber tops, you can click one of the selection options, or you can select the fibers of interest in the top_num column of the table. The selected tops will appear in the selection #s field (which you can also edit to select fibers). Selected fibers will be highlighted in the table and on the plot.

As in the last step, the right axes will show the (optional) reference map. As in the previous step, it can be an image file, a matrix (e.g., for a grid-like arrangement), or an array of coordinates. You can specify which columns contain which coordinates, and alternate ID (set to 0 if you don't have an alternate ID). If you have a grid arrangement (matrix, or as row and column coordinates), you can check the "assign grid" box to generate an automatic assignment, which you can then manually edit as necessary.

tops

refresh



reference map (optional)

locate ref

D:\test\top_grid2.mat

☒ matrix

☐ coords:

1

Label1/x/col

2

Label2/y/row

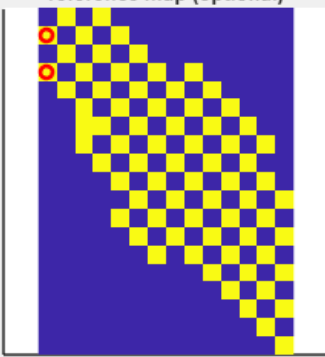
3

Label3/ID

☒ assign grid

flip y

transpose



top_ID	grid_col	grid_row	ID
1	1	2	73
2	1	4	12
3	2	1	64
4	2	3	38
5	2	5	39
6	3	2	70
7	3	7	42
8	3	8	41
9	3	4	36
10	3	6	10
11	4	1	69
12	4	3	11
13	4	5	37
14	4	7	12

delete

DONE

If you want to change the column or row assignment of any of the fibers, click in the grid_col or grid_row box you want to change, and edit the number. Clicking delete will delete the tops corresponding to the highlighted rows.

REFINE FIBER TOPS & ASSIGN LABELS

Go through all the columns

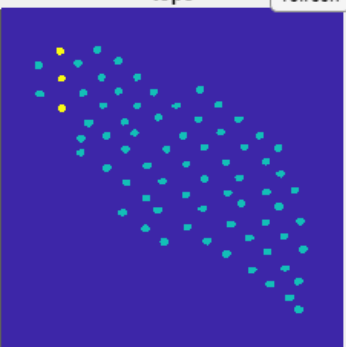
MATLAB App

The primary goal in this step is to delete any identified fiber tops as necessary, and if desired, to assign labels to the fiber tops. You may assign up to 3 numeric labels for each fiber top (e.g., for a grid arrangement, you might want to assign columns and rows). Shown in the table is the top_num identifier, and the labels, which are manually editable. The top_num number labels are arbitrarily assigned, and you won't be able to change them, though you can create a new identifier as one of the other labels. The columns are sortable.

Shown on the left are the tops identified in the last step. To select fiber tops, you can click one of the selection options, or you can select the fibers of interest in the top_num column of the table. The selected tops will appear in the selection #s field (which you can also edit to select fibers). Selected fibers will be highlighted in the table and on the plot.

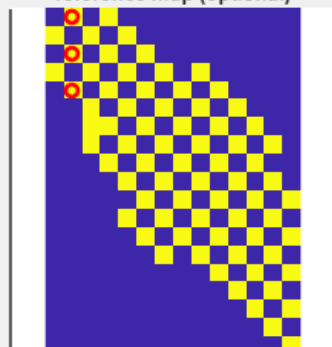
As in the last step, the right axes will show the (optional) reference map. As in the previous step, it can be an image file, a matrix (e.g., for a grid-like arrangement), or an array of coordinates. You can specify which columns contain which coordinates, and alternate ID (set to 0 if you don't have an alternate ID). If you have a grid arrangement (matrix, or as row and column coordinates), you can check the "assign grid" box to generate an automatic assignment, which you can then manually edit as necessary.

tops refresh



selection #s

reference map (optional)



☒ matrix ☐ coords:

☒ assign grid

top_ID	grid_col	grid_row	ID	
1	1	2	73	
2	1	4	12	
3	2	1	64	
4	2	3	38	
5	2	5	39	
6	3	2	70	
7	3	7	42	
8	3	8	41	
9	3	4	36	
10	3	6	10	
11	4	1	69	
12	4	3	11	
13	4	5	37	
14	4	7	12	

REFINE FIBER TOPS & ASSIGN LABELS

And also the rows. To easily look at rows, sort the grid_row column.

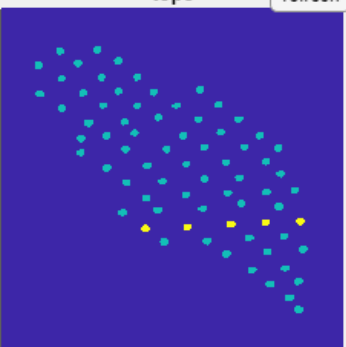
MATLAB App

The primary goal in this step is to delete any identified fiber tops as necessary, and if desired, to assign labels to the fiber tops. You may assign up to 3 numeric labels for each fiber top (e.g., for a grid arrangement, you might want to assign columns and rows). Shown in the table is the top_num identifier, and the labels, which are manually editable. The top_num number labels are arbitrarily assigned, and you won't be able to change them, though you can create a new identifier as one of the other labels. The columns are sortable.

Shown on the left are the tops identified in the last step. To select fiber tops, you can click one of the selection options, or you can select the fibers of interest in the top_num column of the table. The selected tops will appear in the selection #s field (which you can also edit to select fibers). Selected fibers will be highlighted in the table and on the plot.

As in the last step, the right axes will show the (optional) reference map. As in the previous step, it can be an image file, a matrix (e.g., for a grid-like arrangement), or an array of coordinates. You can specify which columns contain which coordinates, and alternate ID (set to 0 if you don't have an alternate ID). If you have a grid arrangement (matrix, or as row and column coordinates), you can check the "assign grid" box to generate an automatic assignment, which you can then manually edit as necessary.

tops refresh



selection #s: 25,38,50,59,72

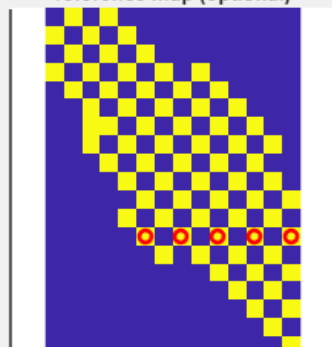
select single top

select multiple: line

select multiple: polygon

reset all

reference map (optional)



locate ref: D:\test\top_grid2.mat

☒ matrix ☐ coords:

1

Label1/x/col

2

Label2/y/row

3

Label3/ID

☒ assign grid

flip y transpose

top_ID	grid_col	grid_row ↑	ID
69	14	11	49
18	5	12	2
29	7	12	33
41	9	12	72
53	11	12	27
64	13	12	45
25	6	13	4
38	8	13	14
50	10	13	17
59	12	13	28
72	14	13	31
32	7	14	18
44	9	14	16

delete

DONE

Click done when you are satisfied.

REFINE FIBER TOPS & ASSIGN LABELS

Here's an example of what the reference map would look like if you loaded a set of coordinates instead.

MATLAB App

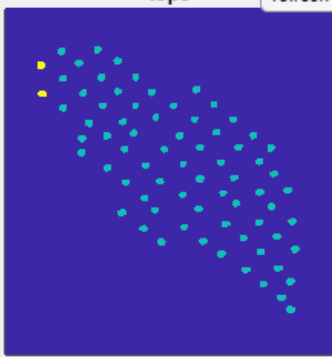
The primary goal in this step is to delete any identified fiber tops as necessary, and if desired, to assign labels to the fiber tops. You may assign up to 3 numeric labels for each fiber top (e.g., for a grid arrangement, you might want to assign columns and rows). Shown in the table is the top_num identifier, and the labels, which are manually editable. The top_num number labels are arbitrarily assigned, and you won't be able to change them, though you can create a new identifier as one of the other labels. The columns are sortable.

Shown on the left are the tops identified in the last step. To select fiber tops, you can click one of the selection options, or you can select the fibers of interest in the top_num column of the table. The selected tops will appear in the selection #s field (which you can also edit to select fibers). Selected fibers will be highlighted in the table and on the plot.

As in the last step, the right axes will show the (optional) reference map. As in the previous step, it can be an image file, a matrix (e.g., for a grid-like arrangement), or an array of coordinates. You can specify which columns contain which coordinates, and alternate ID (set to 0 if you don't have an alternate ID). If you have a grid arrangement (matrix, or as row and column coordinates), you can check the "assign grid" box to generate an automatic assignment, which you can then manually edit as necessary.

tops

refresh



selection #s

1,2

select single top

select multiple: line

select multiple: polygon

reset all

reference map (optional)

locate ref

D:\test\top_coords.m

☐ matrix

☒ coords:

1

Label1/x/col

2

Label2/y/row

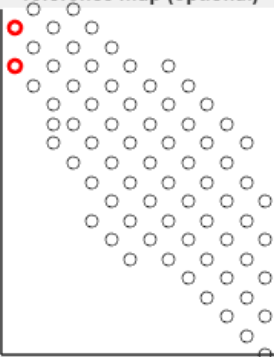
3

Label3/ID

☒ assign grid

flip y

transpose



top_ID	grid_col	grid_row	ID
1	1	2	73
2	1	4	12
3	2	1	64
4	2	3	38
5	2	5	39
6	3	2	70
7	3	7	42
8	3	8	41
9	3	4	36
10	3	6	10
11	4	1	69
12	4	3	11
13	4	5	37
14	4	7	12

delete

DONE

IDENTIFY FIBER AREA

MATLAB App

Locate CT: D:\test\CT_coronal_reg_manually_adjusted.tif

Locate inprog: path to inprog.mat file (optional)

Load

1. IDENTIFY FIBER TOPS (opens separate app)

2. REFINE FIBER TOPS & ASSIGN LABELS (opens separate app)

3. IDENTIFY FIBER AREA (opens separate app)

4. MAP FIBER TIPS

Multifiber separation algorithm:
☒ watershed ☐ GMM

5. CHECK MULTIFIBERS (opens separate app)

6. ADD ATLAS INFO & SAVE FINAL OUTPUT (opens separate app)

7. VERIFY LABELS (opens separate app)

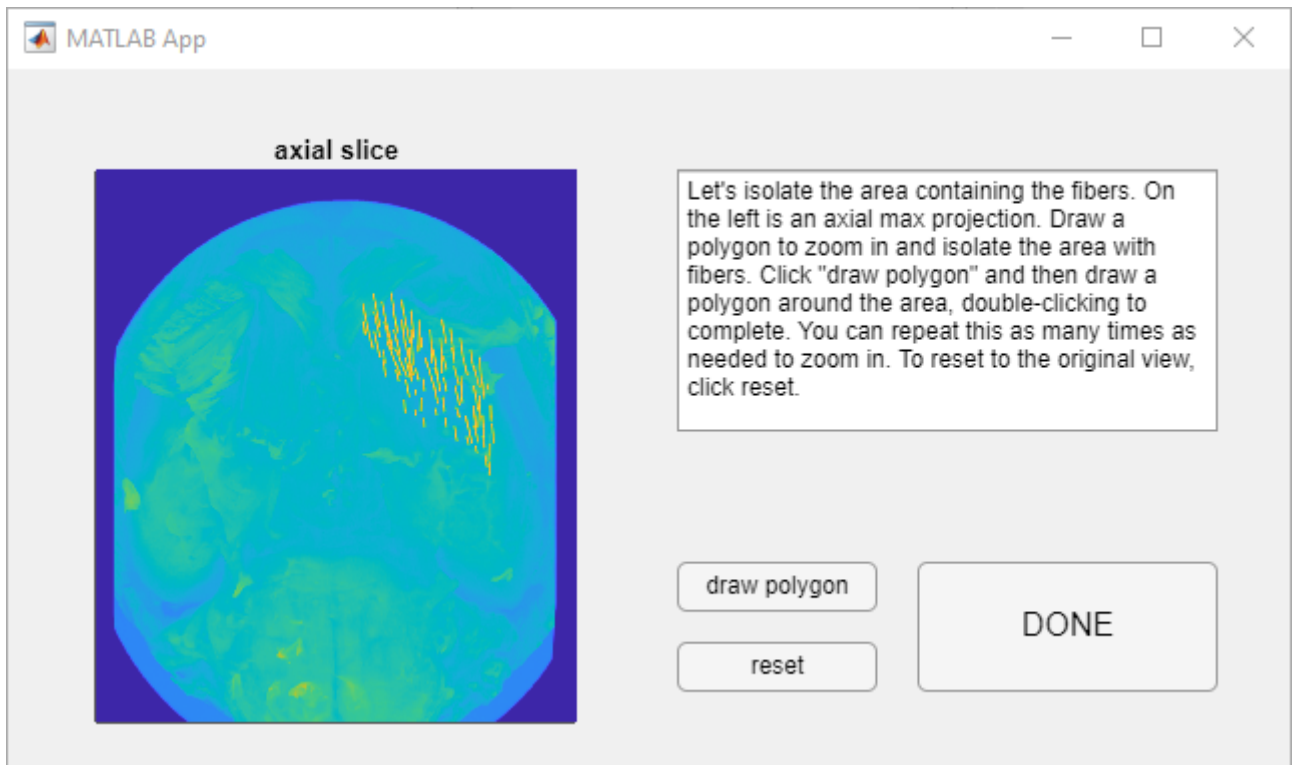
opening fiber area identification app

Save progress

Close

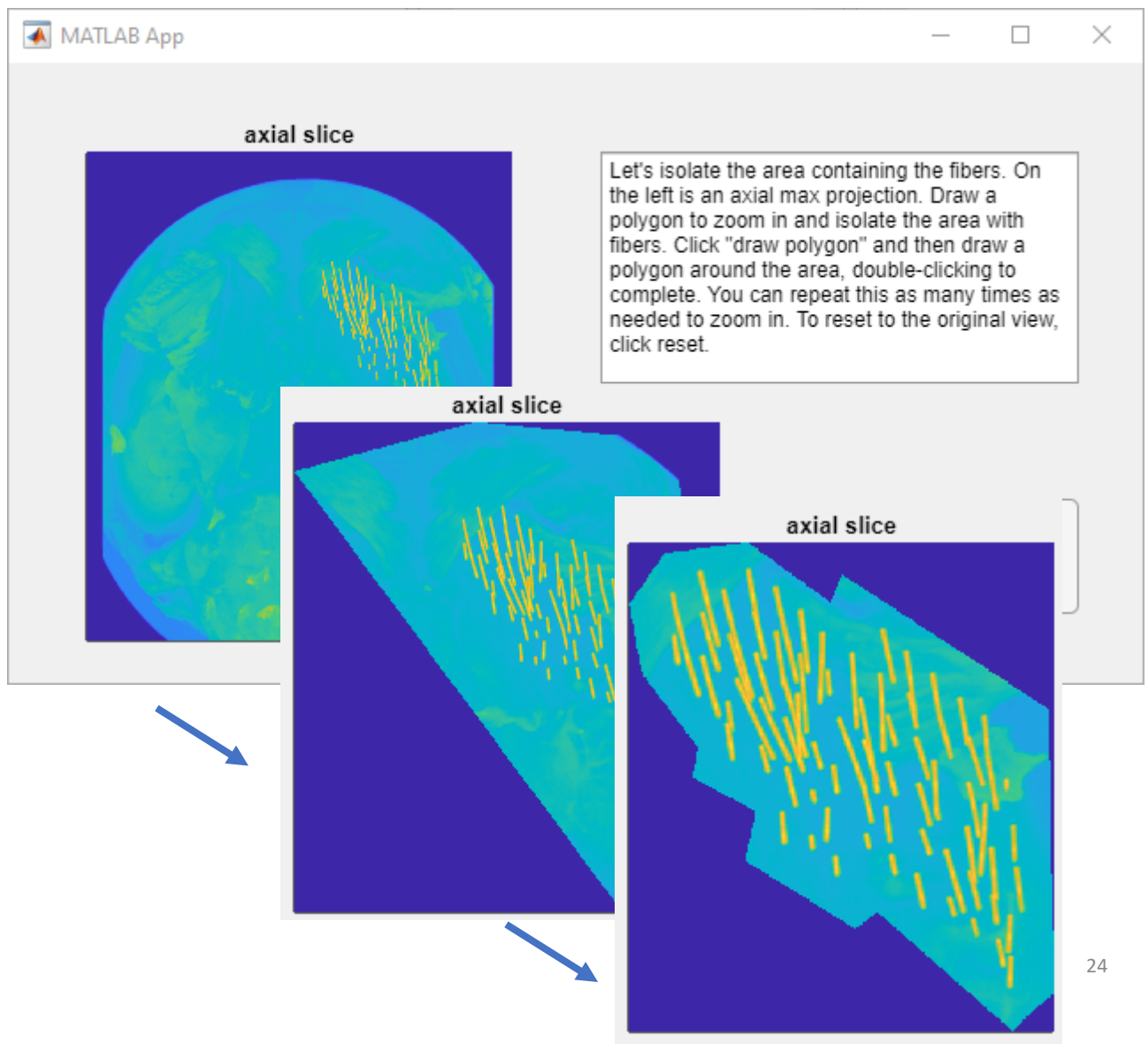
IDENTIFY FIBER AREA

We will eventually be automatically detecting fibers based on brightness. To make that search easier, we will restrict the detection area axially based on where we know fibers are, based on the maximum projection. Use the draw polygon button to isolate this area. Repeat as necessary. You can reset. Click done when you are satisfied



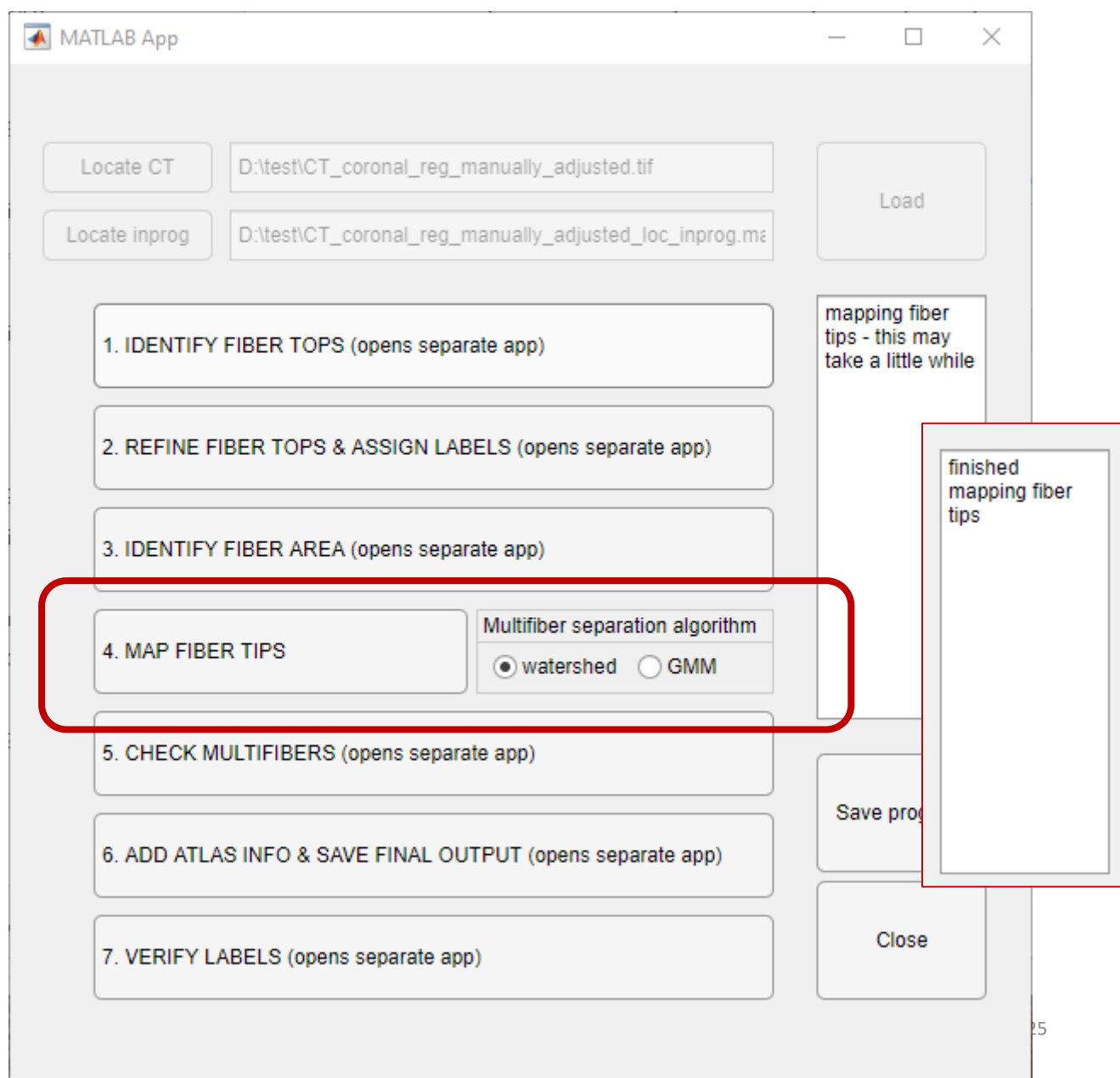
IDENTIFY FIBER AREA

We will eventually be automatically detecting fibers based on brightness. To make that search easier, we will restrict the detection area axially based on where we know fibers are, based on the maximum projection. Use the draw polygon button to isolate this area. Repeat as necessary. You can reset. Click done when you are satisfied



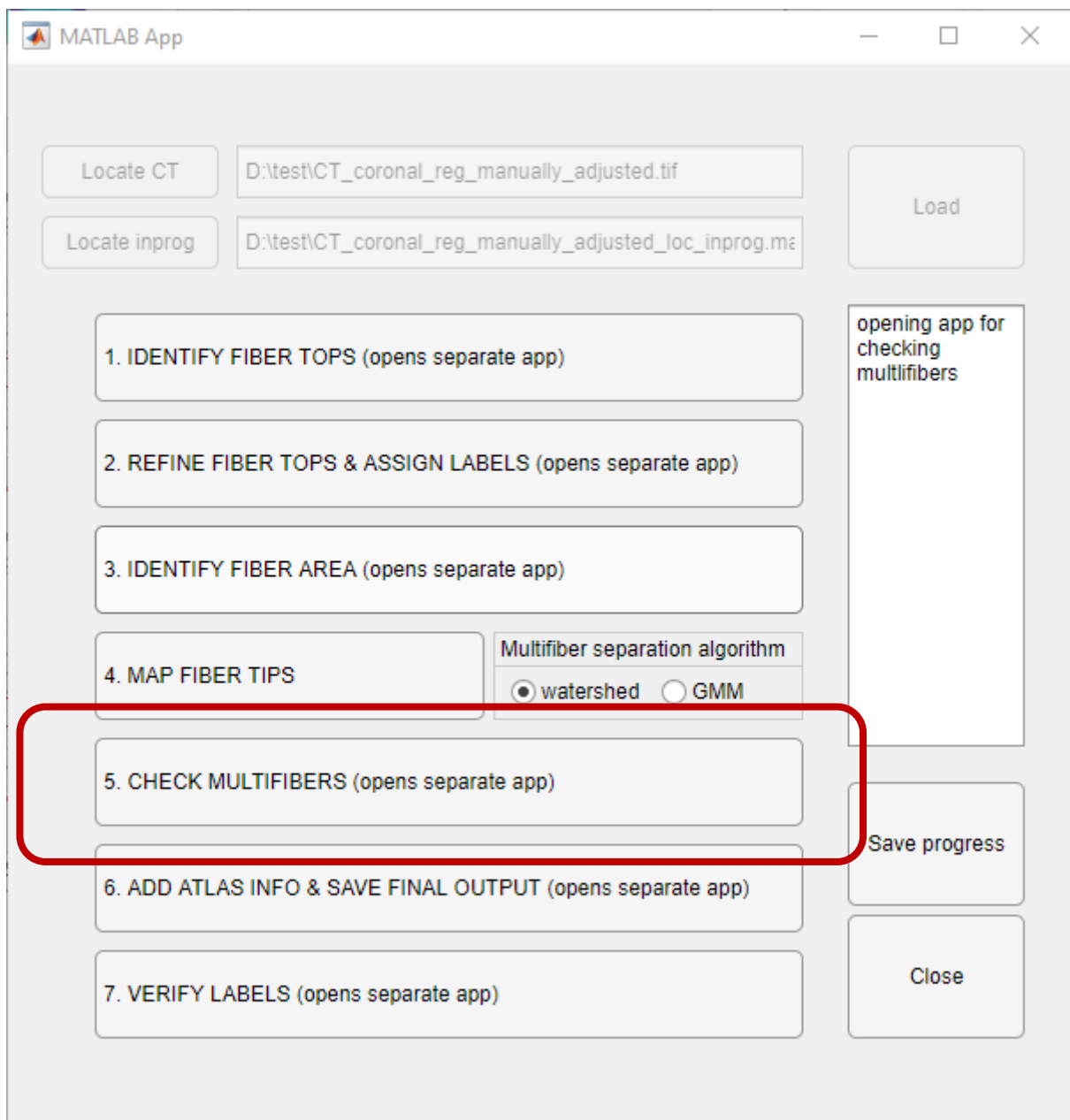
MAP FIBER TIPS

Now it's time to automatically detect the fibers and map them to your identified tops. For separating any fibers that are touching ("multifibers"), you can choose between the watershed (see Vu et al., 2024) and gaussian mixture models (this might entail some trial and error). This does not open a separate app. You will be notified when it is finished.

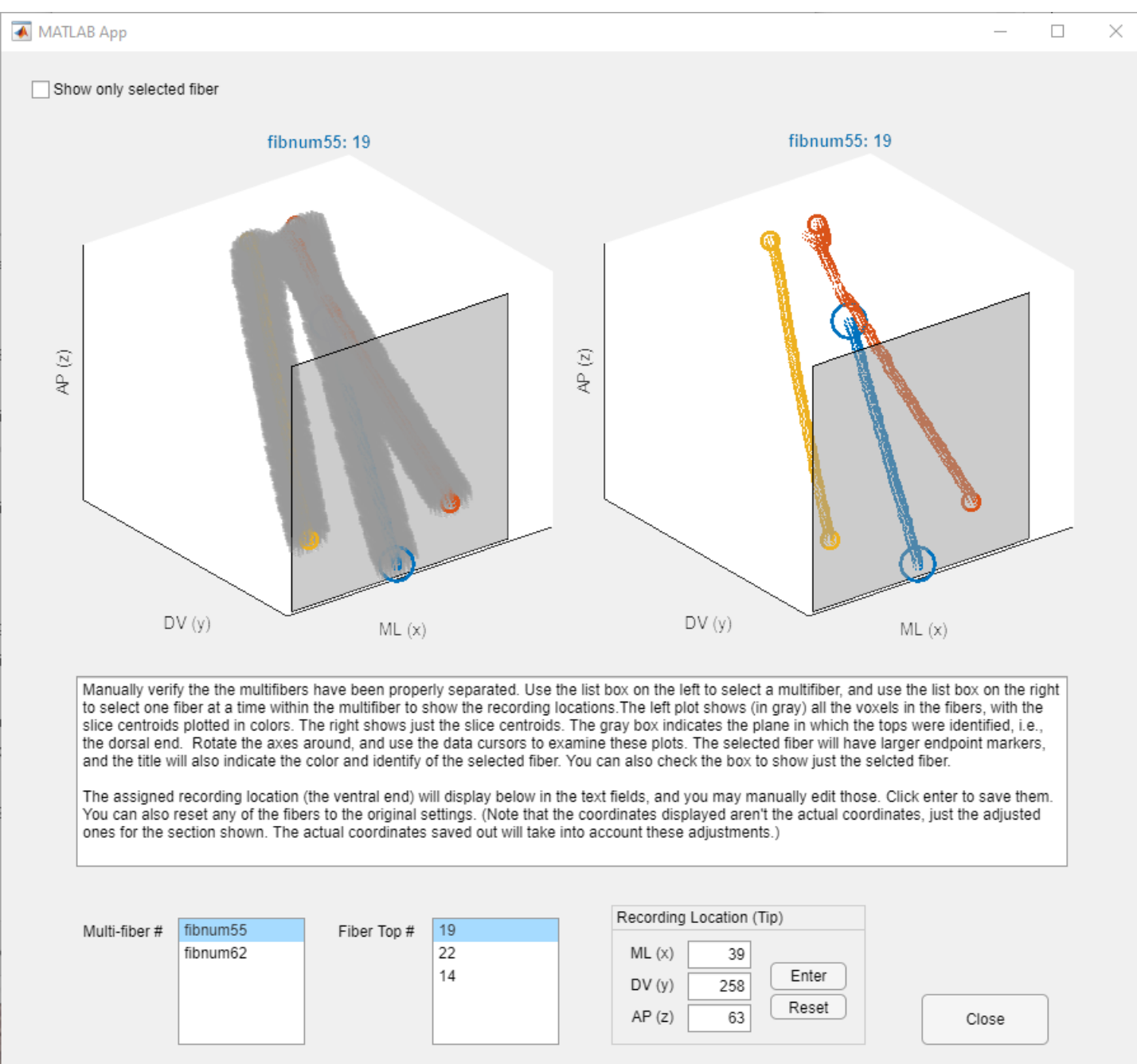


CHECK MULTIFIBERS

Fibers that are touching get initially lumped together as a single fiber. The mapping step includes an automatic separation of them, but it's not perfect and you'll need to manually check the separation, and refine as necessary.

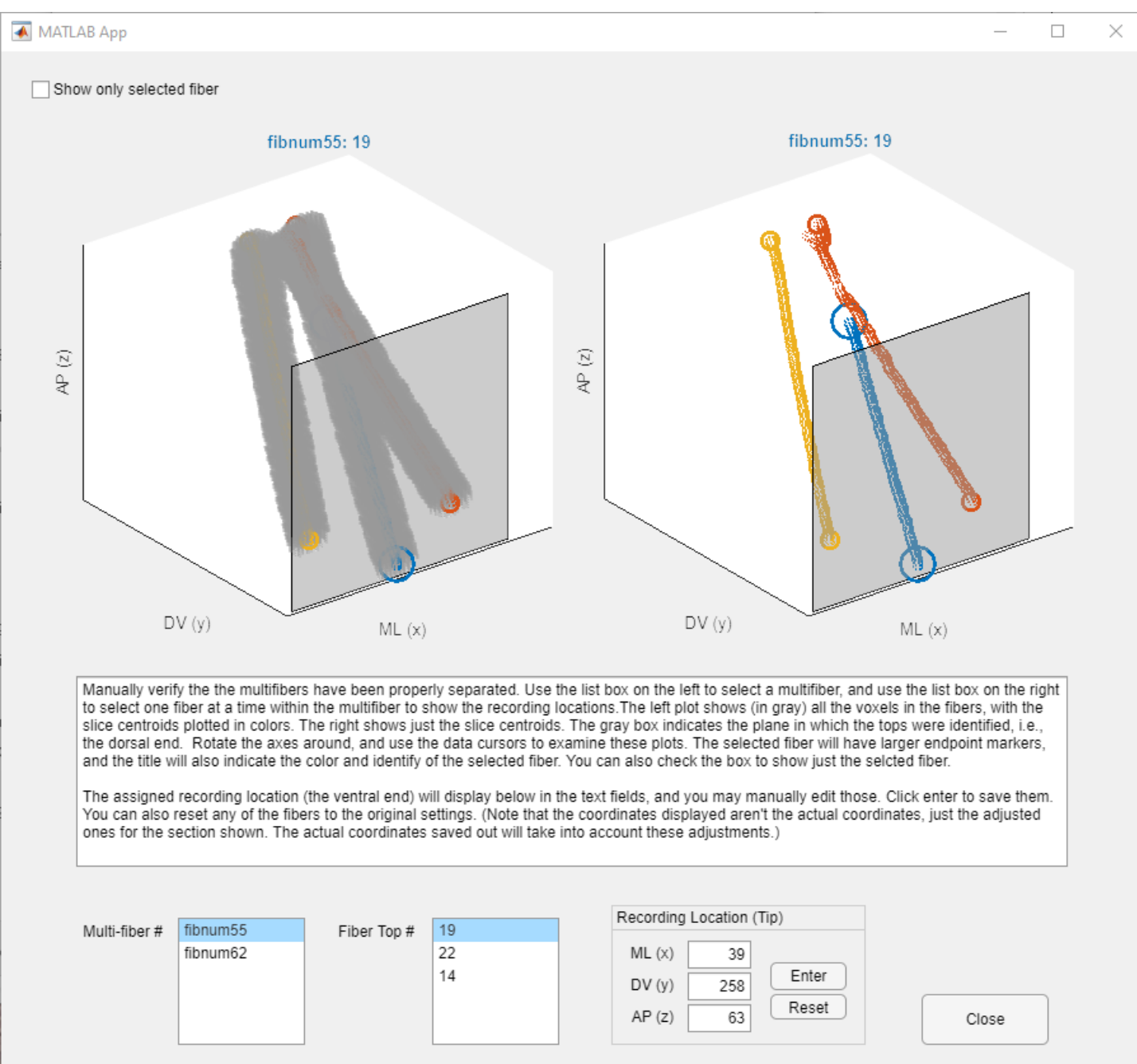


CHECK MULTIFIBERS



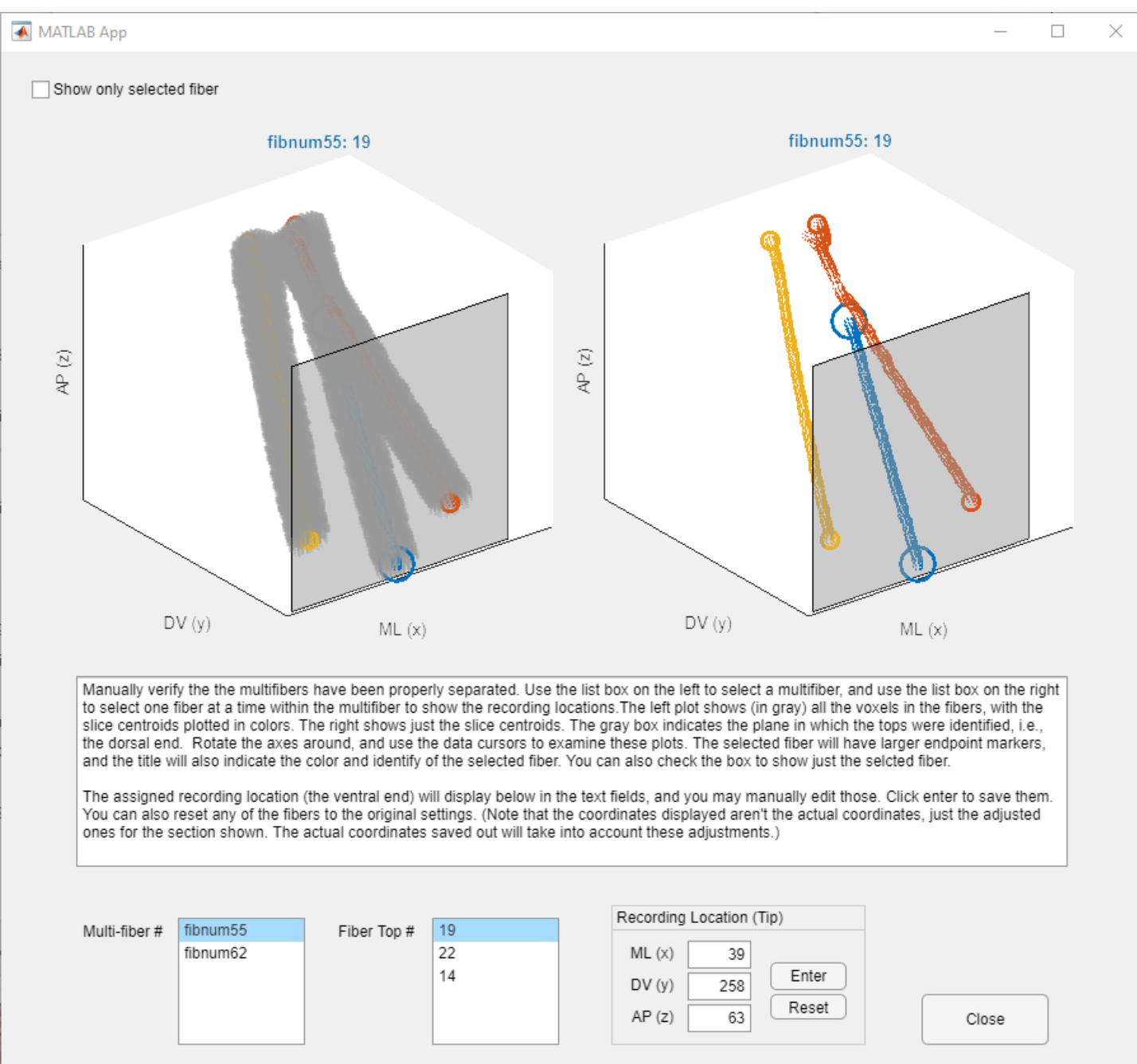
The left menu contains the multifibers (fiber bottom #), and the right menu contains the fiber top #s that belong in this multifiber (these identification numbers themselves are automatically assigned in previous steps).

CHECK MULTIFIBERS



The left hand figure shows (in gray) all the voxels in this multifiber. Plotted in color (both plots) are what was automatically identified as the centroids of those cross sections.

CHECK MULTIFIBERS



The selected fiber will have larger circles at the endpoints, and the coordinates of the location are displayed. The title of the plots show the selection and its corresponding color.

CHECK MULTIFIBERS

MATLAB App

☒ Show only selected fiber

fibnum55: 19

AP (z)

DV (y)

ML (x)

fibnum55: 19

AP (z)

DV (y)

ML (x)

Manually verify the the multifibers have been properly separated. Use the list box on the left to select a multifiber, and use the list box on the right to select one fiber at a time within the multifiber to show the recording locations. The left plot shows (in gray) all the voxels in the fibers, with the slice centroids plotted in colors. The right shows just the slice centroids. The gray box indicates the plane in which the tops were identified, i.e., the dorsal end. Rotate the axes around, and use the data cursors to examine these plots. The selected fiber will have larger endpoint markers, and the title will also indicate the color and identify of the selected fiber. You can also check the box to show just the selcted fiber.

The assigned recording location (the ventral end) will display below in the text fields, and you may manually edit those. Click enter to save them. You can also reset any of the fibers to the original settings. (Note that the coordinates displayed aren't the actual coordinates, just the adjusted ones for the section shown. The actual coordinates saved out will take into account these adjustments.)

Multi-fiber #

fibnum55
fibnum62

Fiber Top #

19
22
14

Recording Location (Tip)

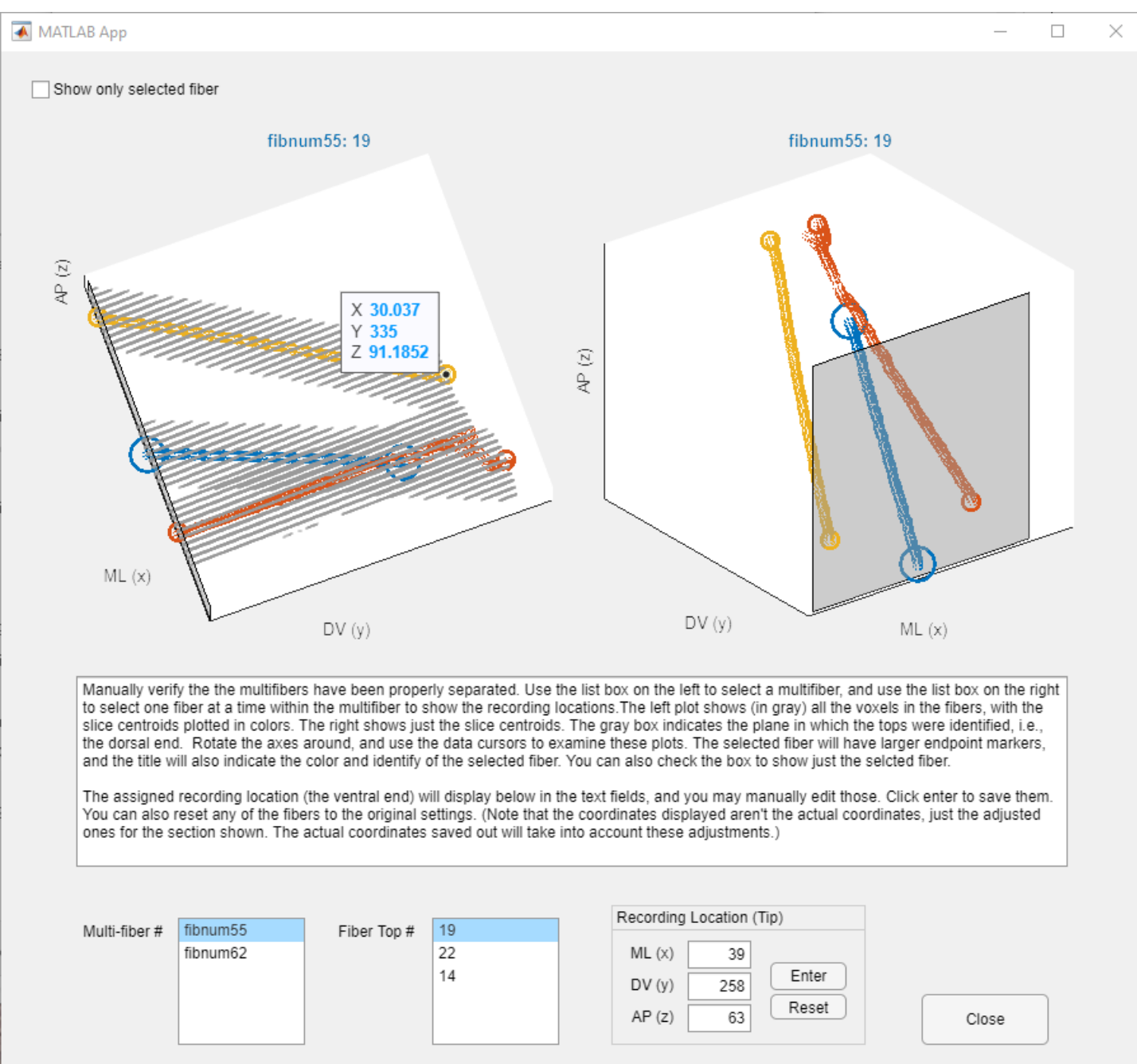
ML (x) 39
DV (y) 258
AP (z) 63

Enter
Reset

Close

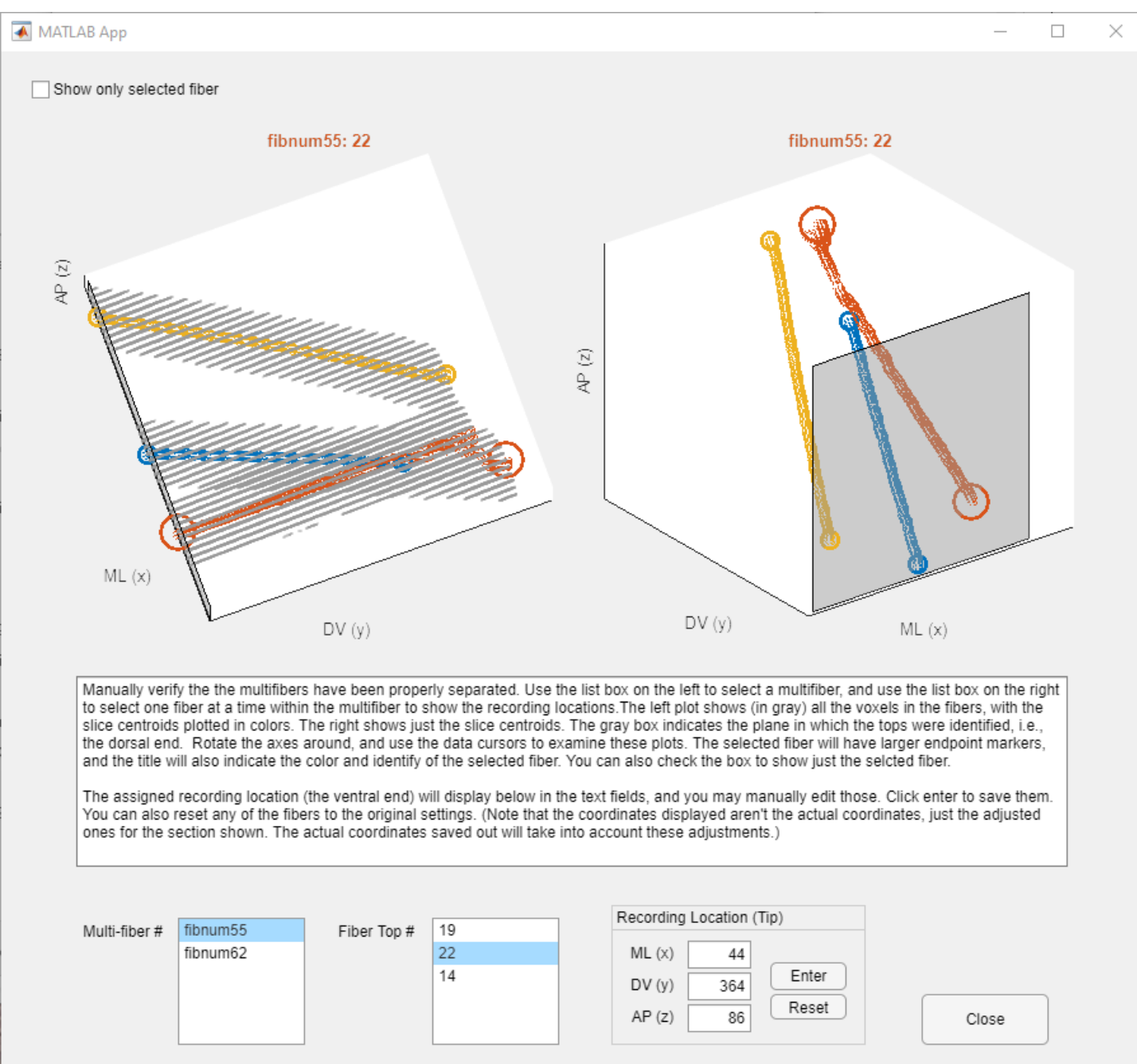
Checking the box allows you to just display the selected fiber

CHECK MULTIFIBERS



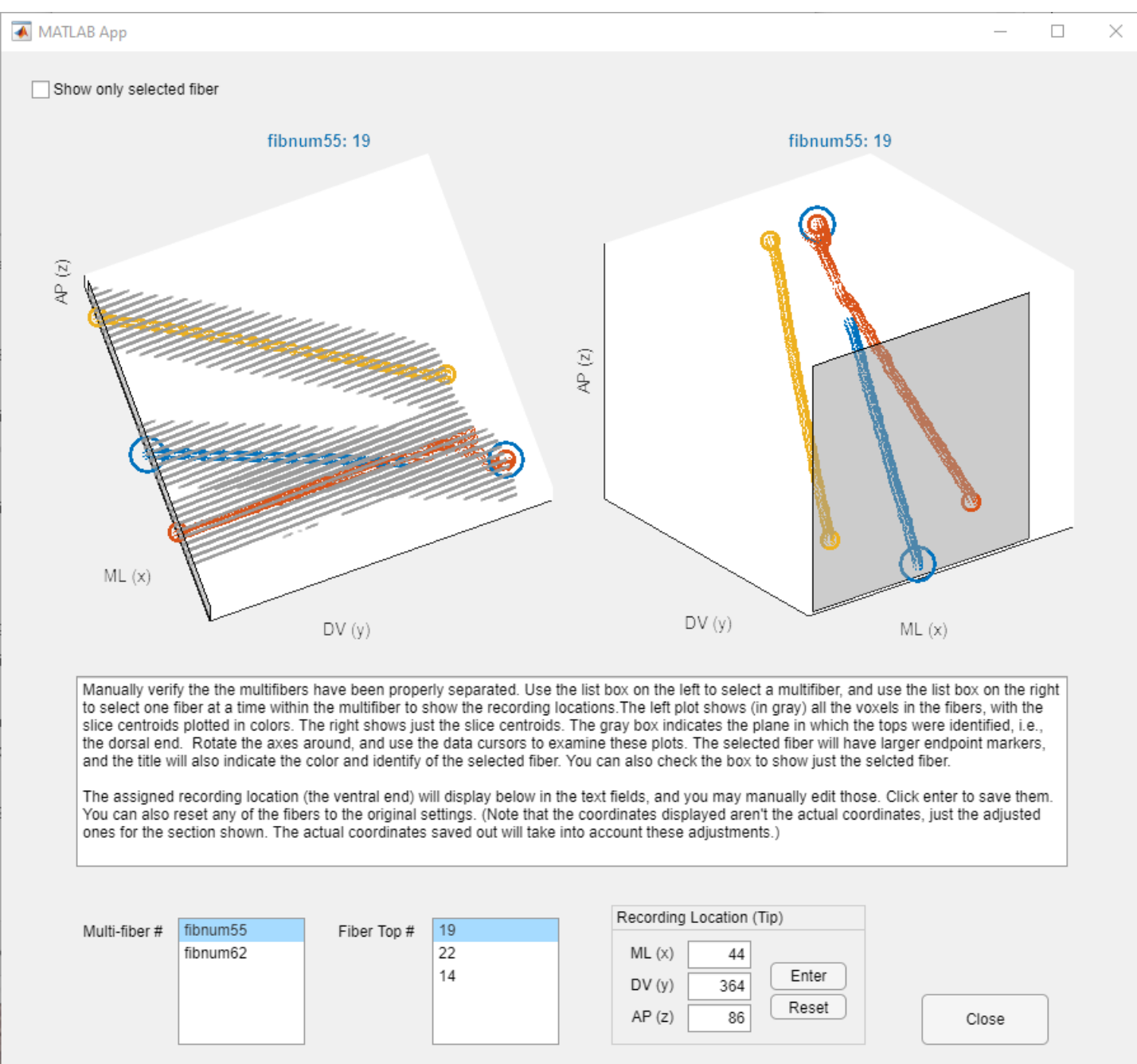
Use the plot tools (however near the title to see tools to rotate, pan, zoom, or reset the view. Swivel the plots around to see whether you agree. Clicking will display coordinates of your clicked point. In this case, we see that the blue and orange endpoints where incorrectly identified.

CHECK MULTIFIBERS



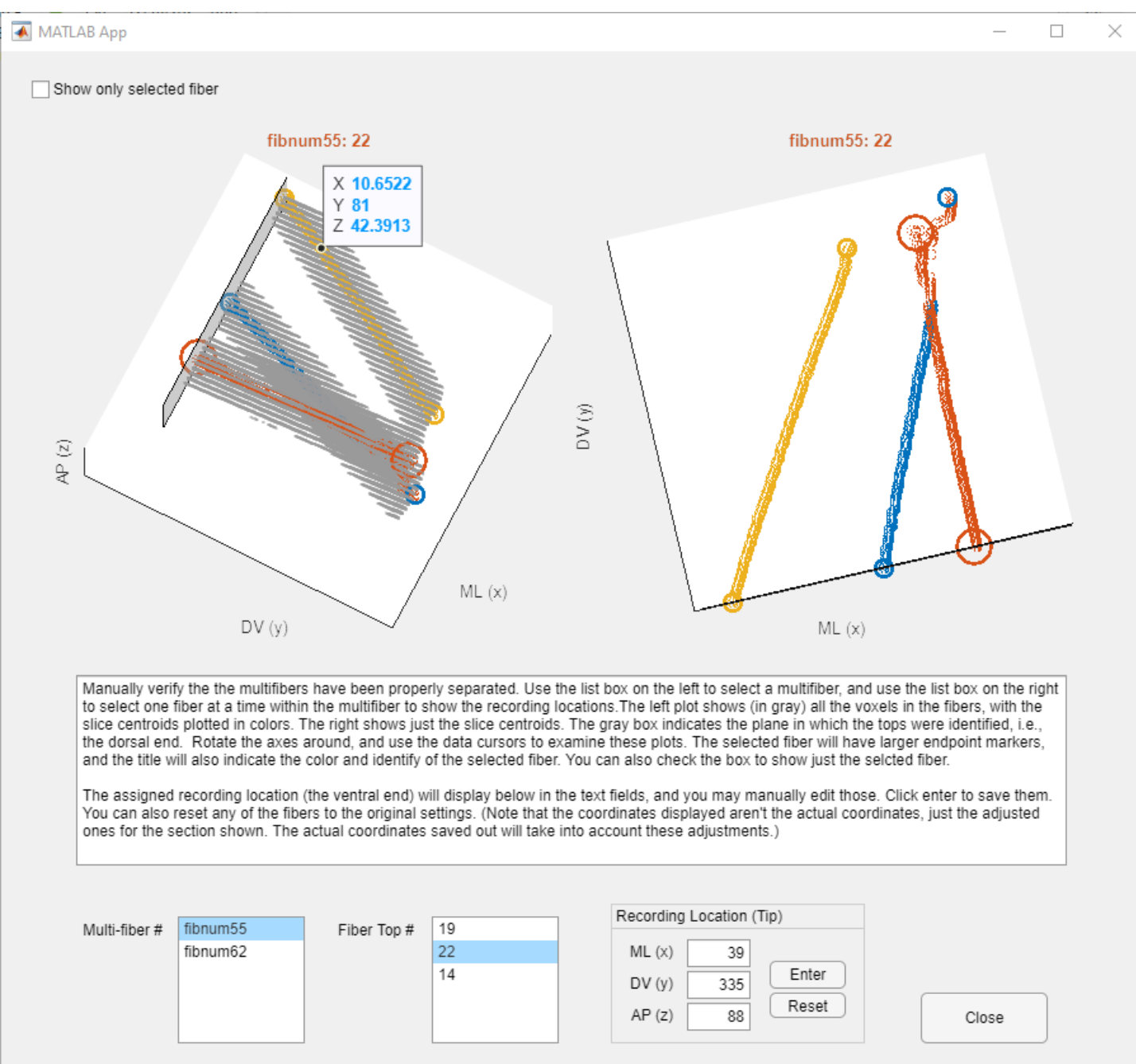
The orange endpoint should be the blue endpoint, so we click the orange fiber to note those coordinates.

CHECK MULTIFIBERS



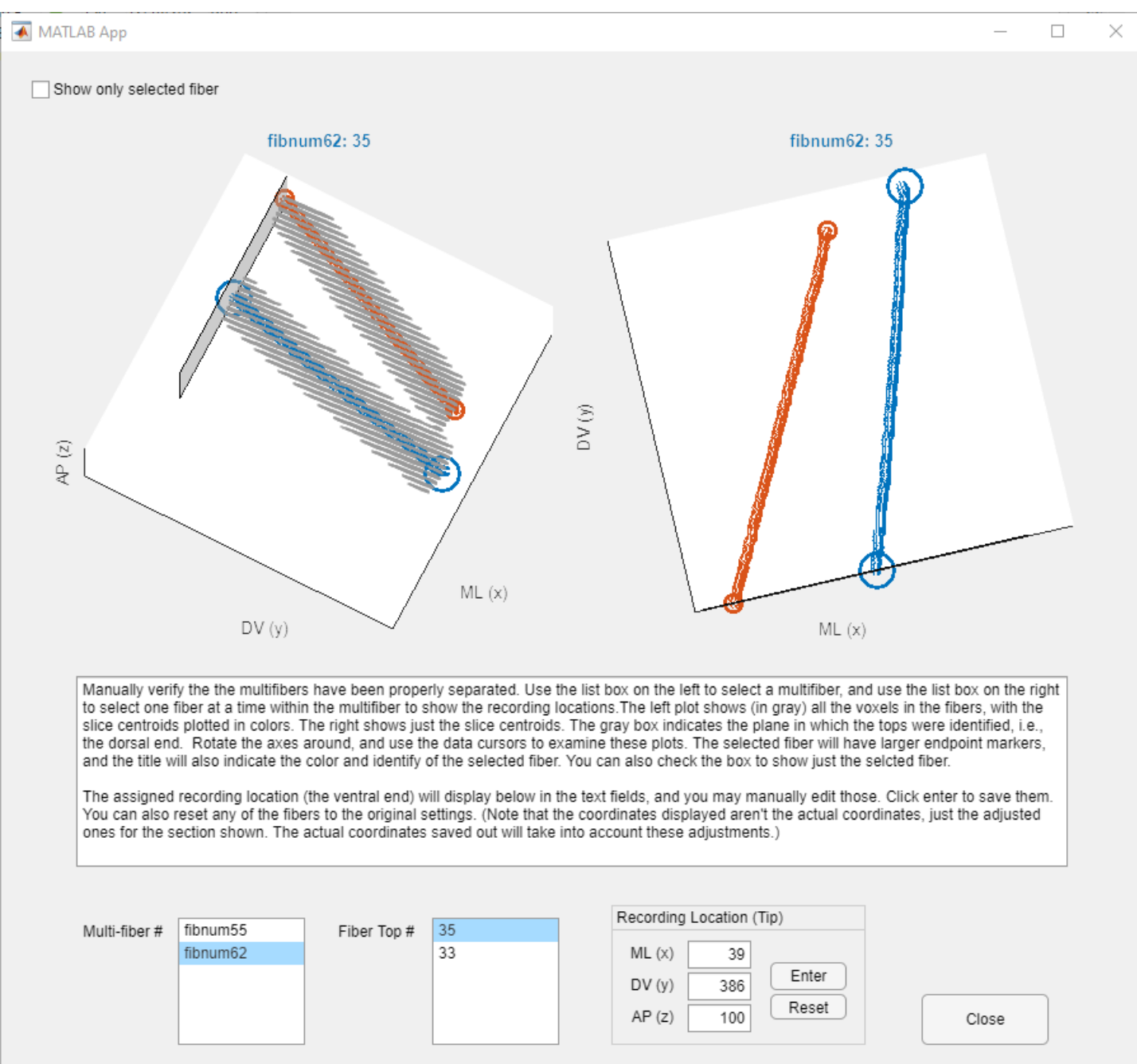
Now we go back to the blue fiber, enter those coordinates, and click “Enter”. The plot is updated.

CHECK MULTIFIBERS



Now we want to change the orange endpoint. Click around in the left plot until you find what is the endpoint (I moved the data cursor here so as not to occlude the end). Enter those coordinates, and click Enter.

CHECK MULTIFIBERS



We can see here the second multifiber was properly separated. Once you're finished, click Close to return to the main fiber localization app.

ADD ATLAS INFO & SAVE

Now that you're satisfied with the identification and mapping of fiber tops and bottoms, it's time to assign them to the atlas (see Vu et al., 2024 for atlas references).

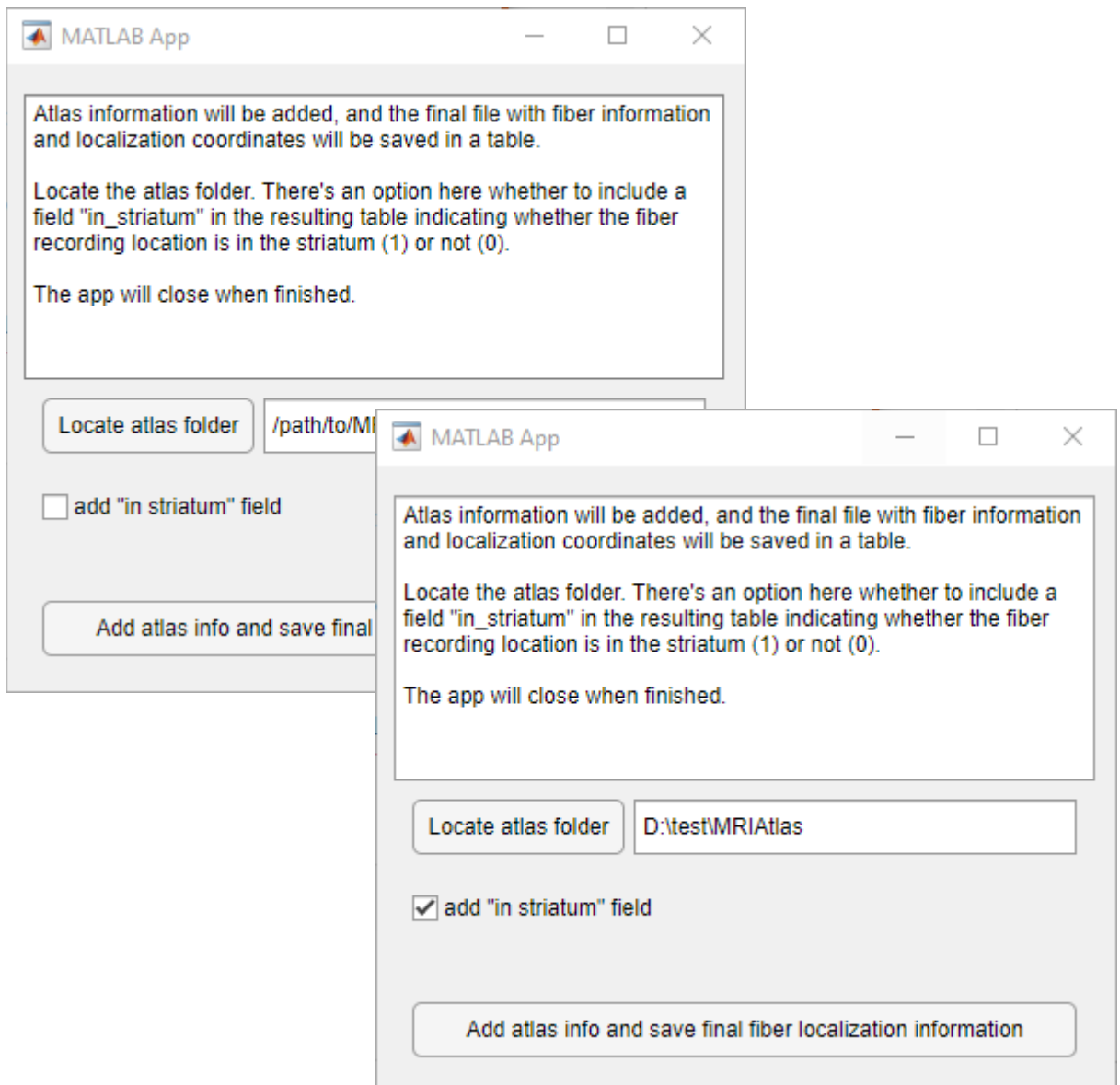
The image shows a MATLAB App window titled "MATLAB App". The interface includes several input fields and buttons. At the top, there are two input fields: "Locate CT" with the path "D:\test\CT_coronal_reg_manually_adjusted.tif" and "Locate inprog" with the path "D:\test\CT_coronal_reg_manually_adjusted_loc_inprog.m". To the right of these is a "Load" button. Below these are seven numbered steps in a vertical list:

1. IDENTIFY FIBER TOPS (opens separate app)
2. REFINE FIBER TOPS & ASSIGN LABELS (opens separate app)
3. IDENTIFY FIBER AREA (opens separate app)
4. MAP FIBER TIPS
5. CHECK MULTIFIBERS (opens separate app)
6. ADD ATLAS INFO & SAVE FINAL OUTPUT (opens separate app)
7. VERIFY LABELS (opens separate app)

Step 4 has a sub-section titled "Multifiber separation algorithm" with two radio buttons: "watershed" (selected) and "GMM". To the right of the steps is a large text area containing the text "opening app for saving atlas info". At the bottom right, there are two buttons: "Save progress" and "Close". A red rectangular box highlights step 6 and the "Save progress" button.

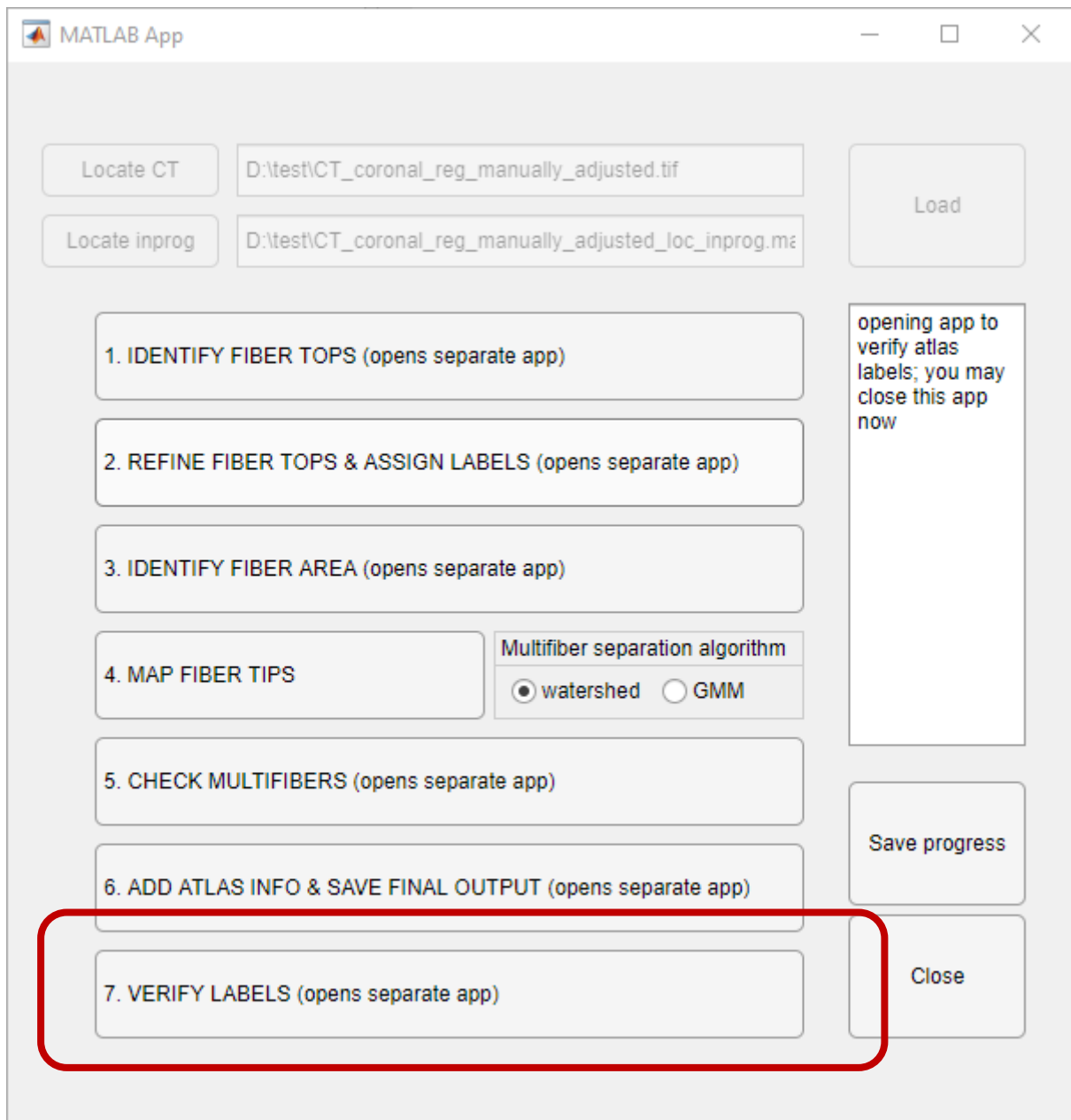
ADD ATLAS INFO & SAVE

Locate your atlas folder. In Vu et al., 2024, we were only looking in striatum, so built in is a filter for that, which will output a column in the resulting table with 1 and 0 indicating whether the recording location is in the striatum. You may opt into that as well. This app saves and closes automatically when finished. Note that it may take a while.



VERIFY LABELS

Now it's time to manually verify that assigned labels. This will open a separate app **verify_atlas_labels.mlapp**. You can run this externally as well and don't need to go through this LOCALIZE_FIBERS app. You can close this app now.



VERIFY LABELS

Locate the atlas folder, as well as the fiber file that was saved in the previous step. The loading may take a little while

MATLAB App

Locate atlas folder

/path/to/MRIAtlas

Locate fiber file

/path/to/fibers.mat

OK

Fiber #

1

2

3

4

5

Coronal

DV

ML

AP

0

Click

ML

Axial

AP

ML

DV

0

Click

ML

Sagittal

DV

AP

ML

0

Click

AP

Fiber counts

keep

0

reject

0

unsure

0

Atlas view

☒ structural

☐ labels

Currently Assigned Location

AP index

0

ML index

0

DV index

0

☒ keep

☐ reject

☐ unsure

Reset to original

Candidate Alternate Location

AP index

0

ML index

0

DV index

0

Save new label

☐ save with new indices

Save

VERIFY LABELS

When the files are loaded, the Fiber # menu will populate (use this menu to select fibers), and some images will pop up. The top row shows the CT with your selected fiber tip highlighted. The bottom row shows the atlas, and you can toggle between the structural view (shown) and the label view (next slide)

MATLAB App

Locate atlas folder
D:\test\WMRIAtlas

Locate fiber file
D:\test\CT_coronal_

OK

The CT registration won't be perfect, so in some cases (when your recording location is near an anatomical boundary, for example), you may disagree with the assigned atlas label. Click through the fibers from the listbox to manually verify these labels. If you disagree with a label, click "click" in one of the atlas views, and then click a point in the atlas that you believe is more suitable for your recording location. The new alternative label (and location) will show up in the box at the bottom right. You can then opt to save the new label. You can also opt to save the new location itself. You can always reset the fiber back to its original location and label. You can view the structural atlas, or the segmented atlas using the Atlas view panel, and you can move through the slices using the Slice panel. The keep/reject/unsure categorization at the bottom is an optional feature that may be useful. You can click Save as often as you wish.

Fiber #

26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48

Coronal

DV

ML

AP 532

Axial

AP

ML

345

Sagittal

DV

AP

ML 832

Fiber counts

keep 73
reject 0
unsure 0

Atlas view

☒ structural
☐ labels

Click

Click

Click

Currently Assigned Location

Caudoputamen

Caudoputamen- intermediate, dorsolateral, intermedial dorsal

AP index 532 ML index 832 DV index 345

☒ keep ☐ reject ☐ unsure

Reset to original

Candidate Alternate Location

Caudoputamen

Caudoputamen- intermediate, dorsolateral, intermedial dorsal

AP index 532 ML index 832 DV index 345

Save new label ☐ save with new indices

Save

VERIFY LABELS

Atlas label view

MATLAB App

Locate atlas folder
D:\test\WRIAtlas

Locate fiber file
D:\test\CT_coronal_

OK

The CT registration won't be perfect, so in some cases (when your recording location is near an anatomical boundary, for example), you may disagree with the assigned atlas label. Click through the fibers from the listbox to manually verify these labels. If you disagree with a label, click "click" in one of the atlas views, and then click a point in the atlas that you believe is more suitable for your recording location. The new alternative label (and location) will show up in the box at the bottom right. You can then opt to save the new label. You can also opt to save the new location itself. You can always reset the fiber back to its original location and label. You can view the structural atlas, or the segmented atlas using the Atlas view panel, and you can move through the slices using the Slice panel. The keep/reject/unsure categorization at the bottom is an optional feature that may be useful. You can click Save as often as you wish.

Fiber #

47
48
49
50
51
52
53
54
55
56
57
58
59
60
61
62
63
64
65
66
67
68
69
70

Coronal

DV
ML
AP 678

Axial

AP
ML
257

Sagittal

DV
AP
ML 903

Fiber counts

keep 73
reject 0
unsure 0

Atlas view

☐ structural
☒ labels

Currently Assigned Location

Primary somatosensory area barrel field layer 6a

Primary somatosensory cortex, barrel field, layer 6a

AP index 678 ML index 903 DV index 257

☒ keep ☐ reject ☐ unsure

Reset to original

Candidate Alternate Location

Caudoputamen

Caudoputamen- caudal, dorsal

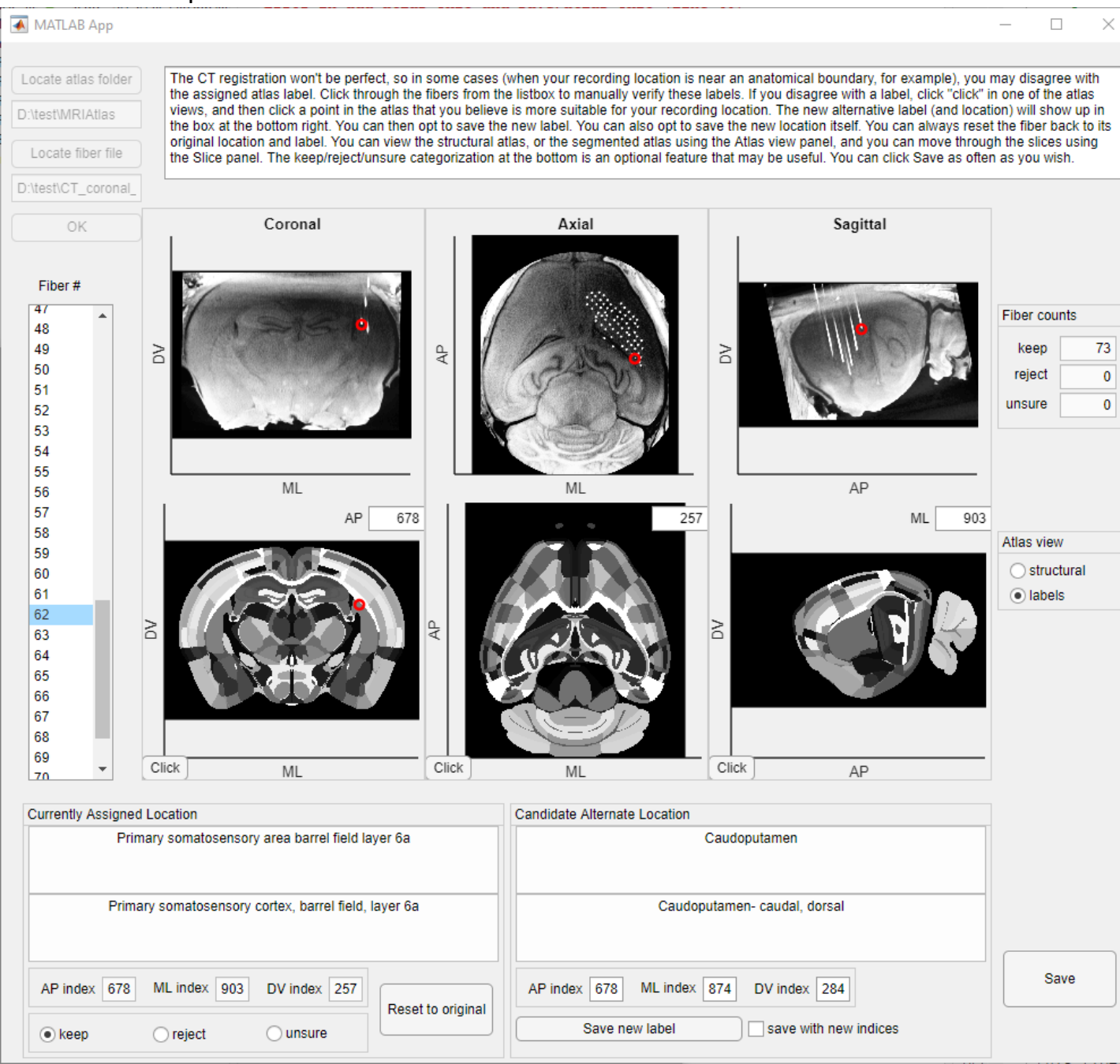
AP index 678 ML index 874 DV index 284

Save new label ☐ save with new indices

Save

VERIFY LABELS

The bottom left panel shows the currently assigned location. You'll see atlas labels as well as the location. There is also an optional feature that lets you decide whether to keep or reject each fiber. This will add a column to the output table where 1 means keep, 0 means reject, and 0.5 means you're unsure. Running totals are shown in the Fiber counts panel.



VERIFY LABELS

Let's say in this example, you disagree with the original label. Here I clicked "Click" in the Coronal view on the atlas slice, and clicked what I think more accurately captures my fiber location. You can see in the bottom right panel the new labels and coordinate.

MATLAB App

Locate atlas folder
D:\test\WRIAtlas

Locate fiber file
D:\test\CT_coronal_

OK

The CT registration won't be perfect, so in some cases (when your recording location is near an anatomical boundary, for example), you may disagree with the assigned atlas label. Click through the fibers from the listbox to manually verify these labels. If you disagree with a label, click "click" in one of the atlas views, and then click a point in the atlas that you believe is more suitable for your recording location. The new alternative label (and location) will show up in the box at the bottom right. You can then opt to save the new label. You can also opt to save the new location itself. You can always reset the fiber back to its original location and label. You can view the structural atlas, or the segmented atlas using the Atlas view panel, and you can move through the slices using the Slice panel. The keep/reject/unsure categorization at the bottom is an optional feature that may be useful. You can click Save as often as you wish.

Fiber #

47
48
49
50
51
52
53
54
55
56
57
58
59
60
61
62
63
64
65
66
67
68
69
70

Coronal

DV

ML

AP 678

Click

Axial

ML

257

Click

AP

DV

ML 903

Click

Fiber counts

keep 73
reject 0
unsure 0

Atlas view

☒ structural
☐ labels

Currently Assigned Location

Primary somatosensory area barrel field layer 6a

Primary somatosensory cortex, barrel field, layer 6a

AP index 678 ML index 903 DV index 257

☒ keep ☐ reject ☐ unsure

Reset to original

Candidate Alternate Location

Caudoputamen

Caudoputamen- caudal, dorsal

AP index 678 ML index 874 DV index 284

Save new label ☐ save with new indices

Save

VERIFY LABELS

If you agree with the new label, you can save the new label. You can also opt to save the new coordinates too. If you want to preserve the spatial relationships of these fiber locations (note: in this registered atlas space) but want to just edit the anatomical label (as may be appropriate just due to individual differences in brain morphology), you can opt out of saving the new indices, and just save the label itself.

MATLAB App

Locate atlas folder
D:\test\WRIAtlas

Locate fiber file
D:\test\CT_coronal_

OK

The CT registration won't be perfect, so in some cases (when your recording location is near an anatomical boundary, for example), you may disagree with the assigned atlas label. Click through the fibers from the listbox to manually verify these labels. If you disagree with a label, click "click" in one of the atlas views, and then click a point in the atlas that you believe is more suitable for your recording location. The new alternative label (and location) will show up in the box at the bottom right. You can then opt to save the new label. You can also opt to save the new location itself. You can always reset the fiber back to its original location and label. You can view the structural atlas, or the segmented atlas using the Atlas view panel, and you can move through the slices using the Slice panel. The keep/reject/unsure categorization at the bottom is an optional feature that may be useful. You can click Save as often as you wish.

Fiber #

47
48
49
50
51
52
53
54
55
56
57
58
59
60
61
62
63
64
65
66
67
68
69
70

Coronal

DV

ML

AP

678

Axial

ML

257

AP

903

Fiber counts

keep 73
reject 0
unsure 0

Atlas view

☒ structural
☐ labels

Click

Click

Click

Currently Assigned Location

Primary somatosensory area barrel field layer 6a

Primary somatosensory cortex, barrel field, layer 6a

AP index 678 ML index 903 DV index 257

☒ keep ☐ reject ☐ unsure

Reset to original

Candidate Alternate Location

Caudoputamen

Caudoputamen- caudal, dorsal

AP index 678 ML index 874 DV index 284

Save new label ☐ save with new indices

Save

VERIFY LABELS

Save as often as you wish. Close the app when finished. Note that the original fiber table generated in the prior step is saved in the output in a field called `fiber_table_orig`. Any changes you've done in this app are reflected in the `fiber_table` field.

Locate atlas folder

D:\test\WRIAtlas

Locate fiber file

D:\test\CT_coronal_

OK

Fiber #

47

48

49

50

51

52

53

54

55

56

57

58

59

60

61

62

63

64

65

66

67

68

69

70

Coronal

DV

ML

AP

678

Click

ML

Axial

AP

ML

257

Click

ML

S

🔍

🖱️

🔍

🏠

DV

AP

ML

903

Click

AP

Fiber counts

keep

73

reject

0

unsure

0

Atlas view

☒ structural

☐ labels

Currently Assigned Location

Primary somatosensory area barrel field layer 6a

Primary somatosensory cortex, barrel field, layer 6a

AP index

678

ML index

903

DV index

257

☒ keep

☐ reject

☐ unsure

Reset to original

Candidate Alternate Location

Caudoputamen

Caudoputamen- caudal, dorsal

AP index

678

ML index

874

DV index

284

Save new label

☐ save with new indices

Save

HOWE LAB SPECIFICS

What's different?	What to do?
The naming convention of the fields in the output localized fiber table is different.	<p>To create a version of the fiber table with the same naming conventions as before, see <code>howelab_table_labels.m</code>.</p> <p>Note: there will be some additional fields that we did not used to have.</p>
The “in_striatum” field doesn't automatically get populated unless you specify.	<p>Enable the “add in striatum field” option in the ADD ATLAS INFO & SAVE step.</p> <p>In the VERIFY LABELS step, use the “keep/reject/unsure” fields. This used to be “in striatum? yes/no/maybe”. Then during analysis, you can use a conjunction of the “in_striatum” and “keep” fields as applicable.</p>