2020

Nodule_me.exe

USER GUIDE

VERSION 1.1 - ENG

OVERVIEWS

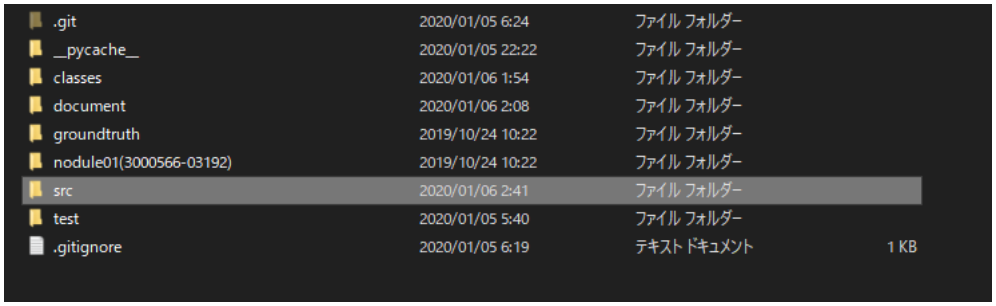
1. Install

1.1 download nodule me and unzip file.

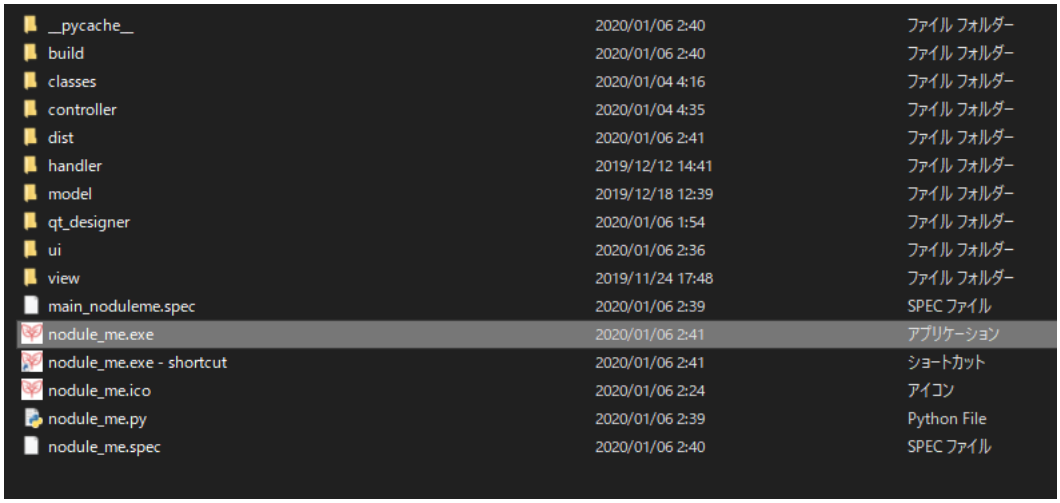
Please download nodule_me.zip at website.
Then you must unzip nodule_me.zip by unzip tools. (7-ZIP etc.)

1.2 open unzipped folder and find nodule_me.exe.

Find nodule_me.exe in unzipped nodule_me.zip file.
Place is folloing **nodule_me/src/nodule_me.exe**



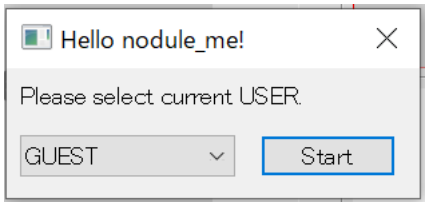
Double click to start Nodule me.
Please wait in a second to open the interface.



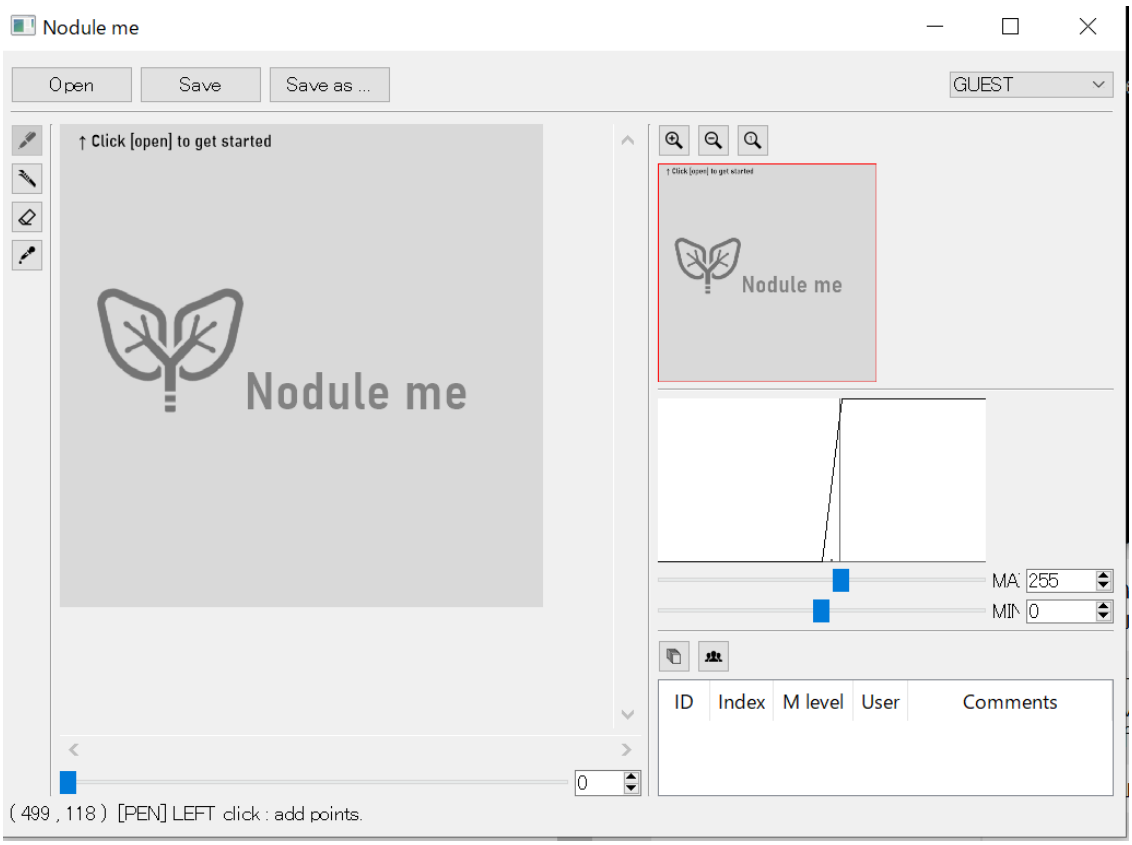
2. Start up

2.1 select current user.

Nodule me can use multi user. Please select your name in combo box.
(You can also change user later.)



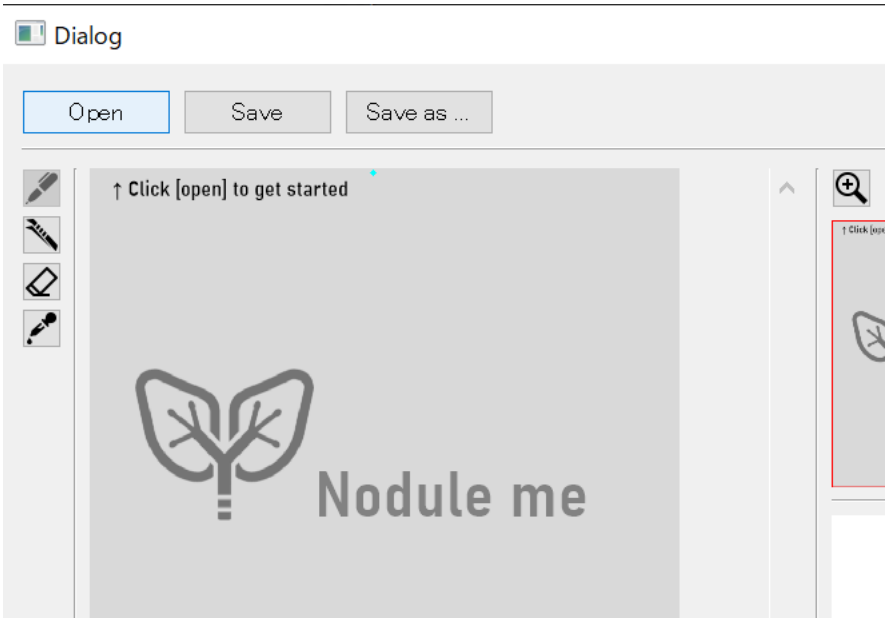
2.2 open main interface



3. Open DICOM data

3.1 click [Open] button

There is [Open] button at top left diagonal.
Please wait just a moment until new dialog will open.

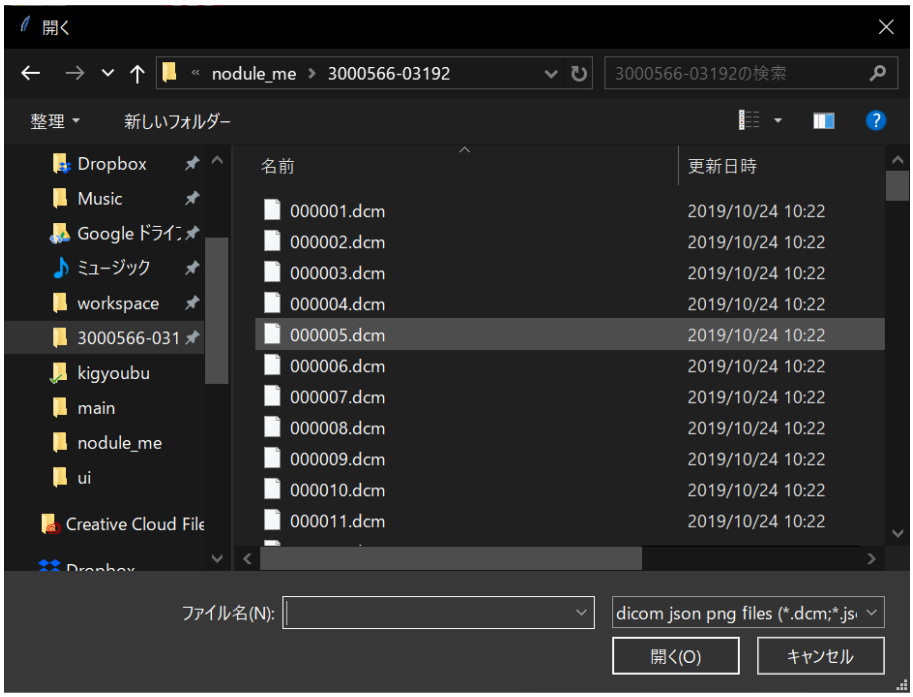


3.2 choose one of DICOM file.

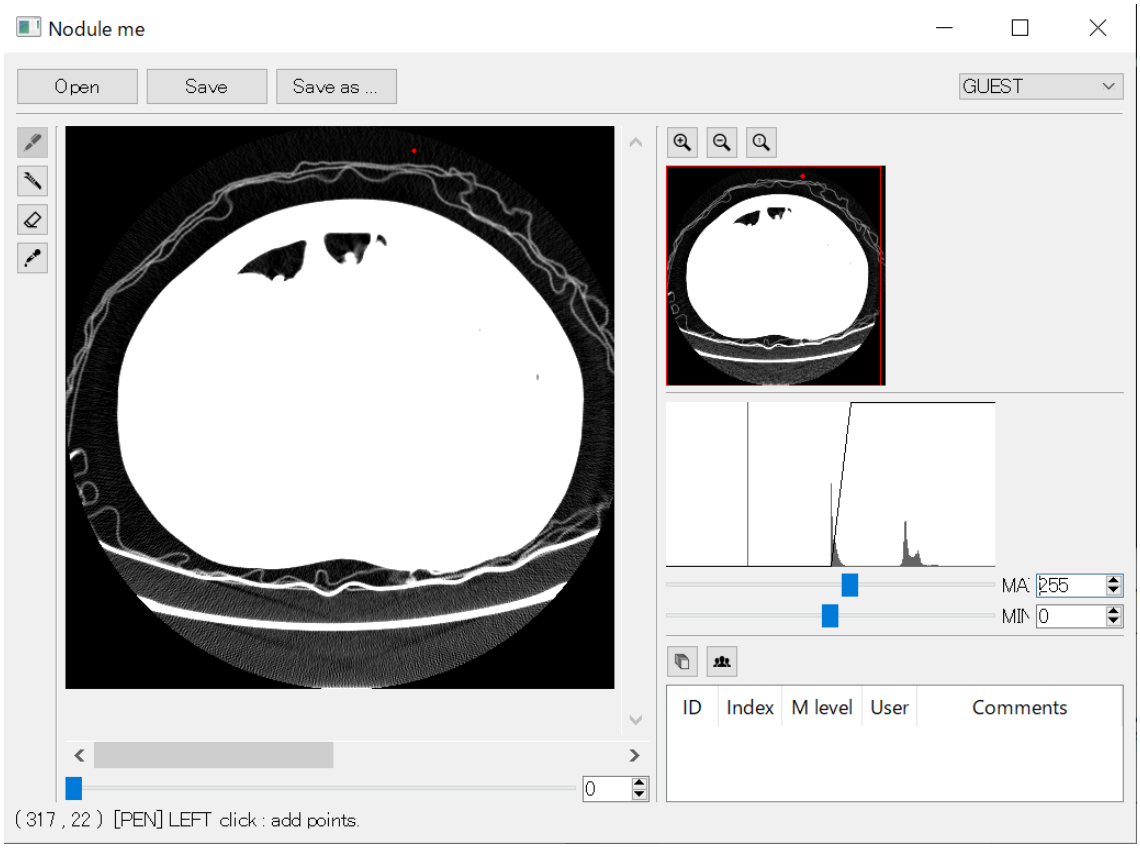
You select .dcm (DICOM) file.
→ Demo file is in nodule_me/nodule1(3000566-03192).
Please try if you don't have any .dcm data.

(Usually, one slice of CT scan images is associated with one .dcm file.
Whichever you choose .dcm file, you will have chosen all .dcm file in the folder.)

(You can also choose .png and .json file.)



3.3 open DICOM data.

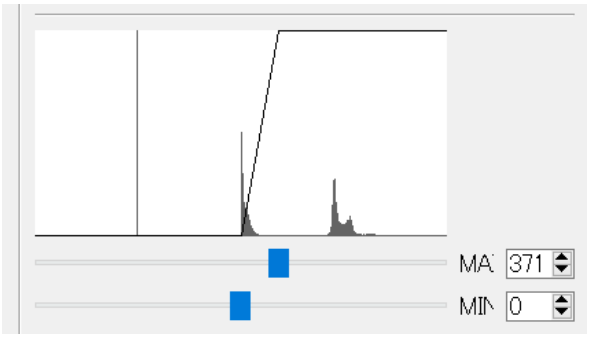


4. Contrast, Zoom and z-index.

- **Contrast Adjustment function**

Usually, DICOM data is 16bit but most display can only show 8bit.
Horizontal length is [-2024 2024] (max and min of DICOM pixel array).
Vertical length is [0 255] (max and min of display luminance).
Histogram show value of DICOM pixel array.

Please adjust contrast to your liking by moving below MAX/MIN slide bar.

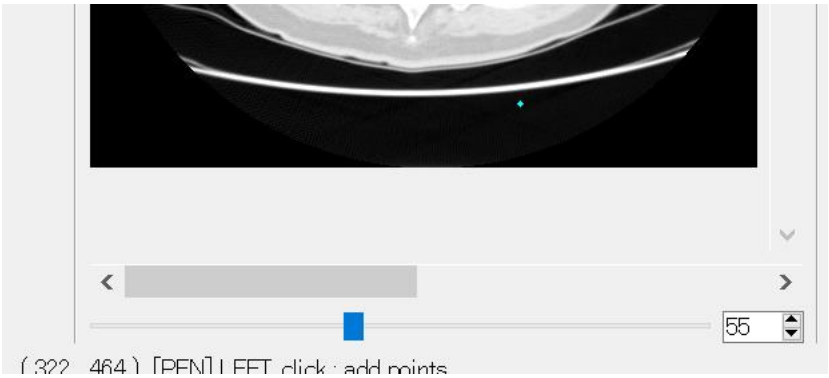


- **Zoom and Map function**

You can zoom up/down by pushing button or mouse rotate mouse wheel.
Also you can change area by dragging red square or scroll bar around canvas.

- **Z-index function**

Usually, CT-images is 3D volume data.
You can change z-index by index slide bar or spin box.



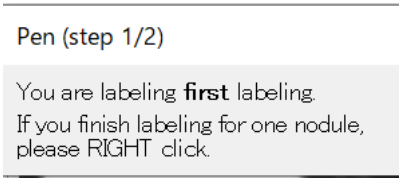
5. Labeling

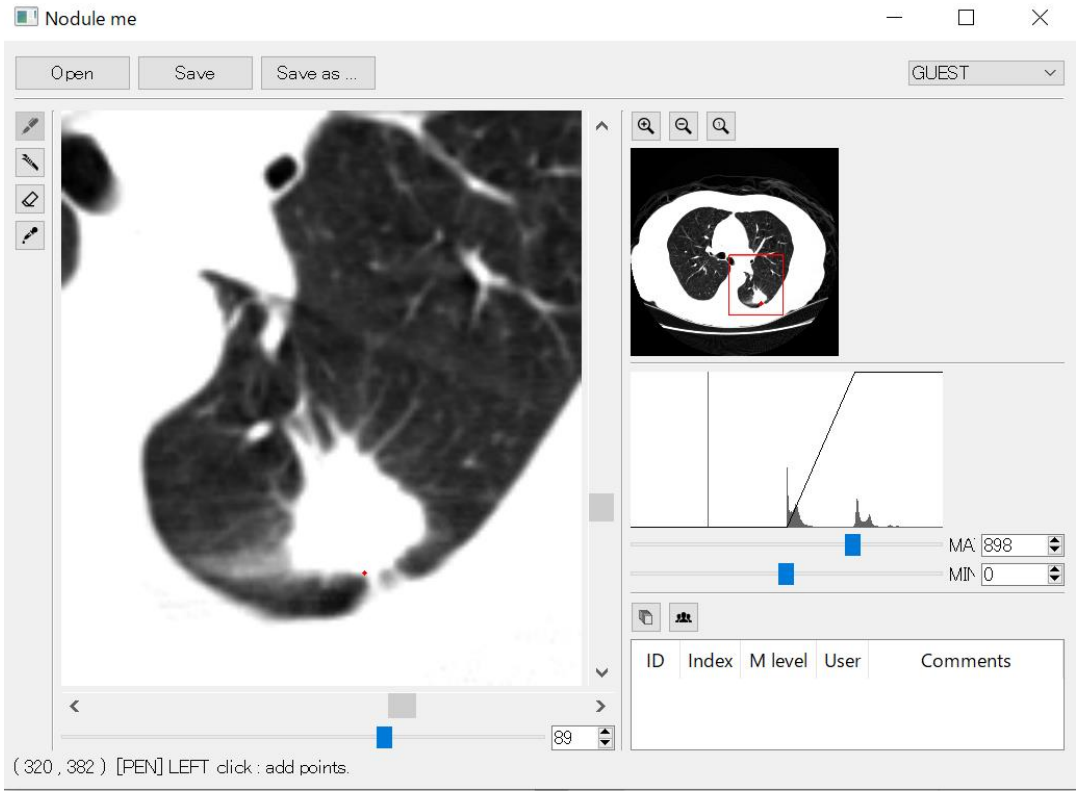
5.1 set [PEN] tool

If you don't close PEN, please select PEN tool.

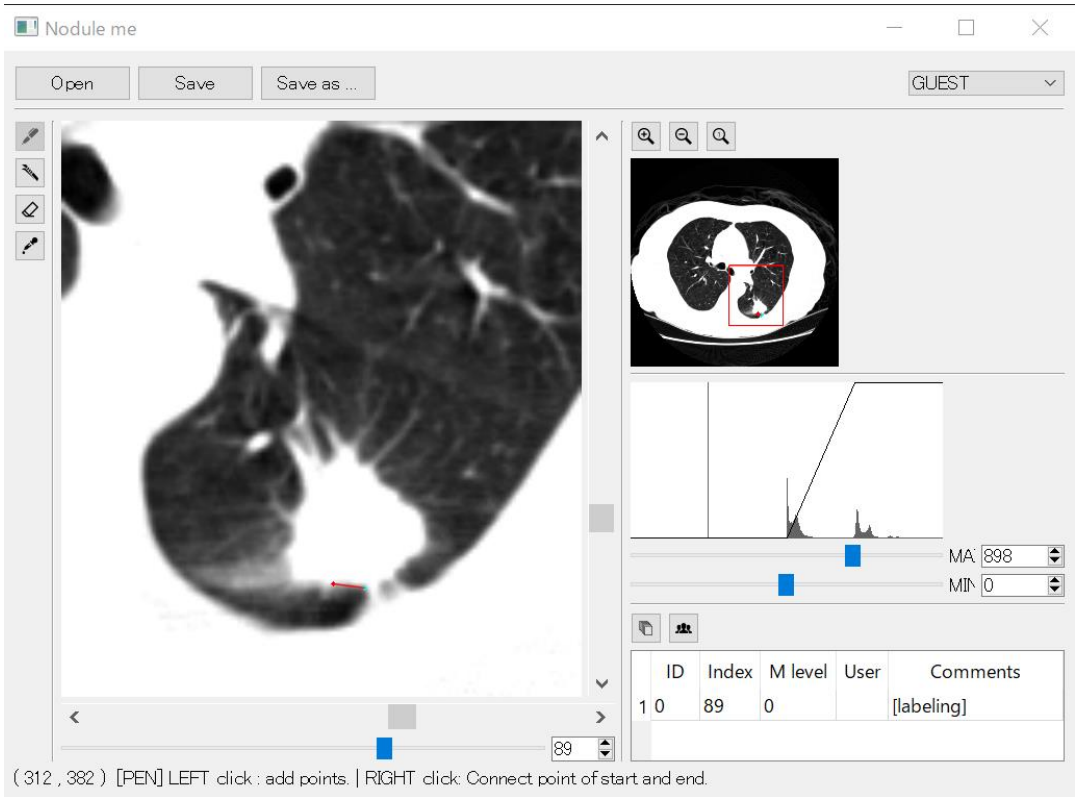
5.2 click canvas and add points of label.

When you find nodule, please start to label by click in canvas.
(After first pointing, pen (step1/2) dialog will be opened automatically following.)



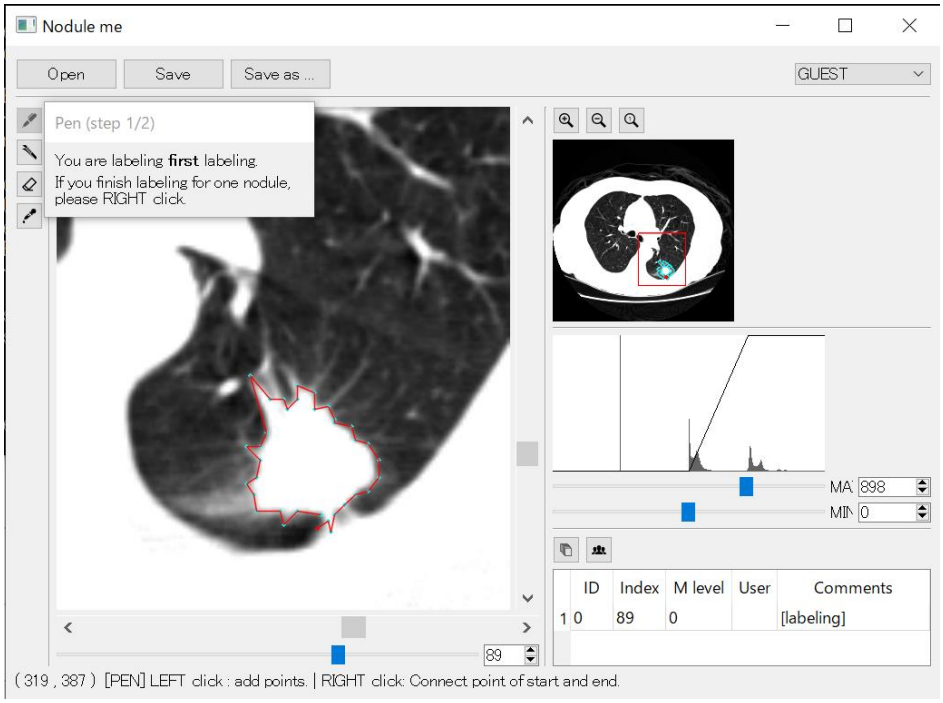


Please label nodule in one like this.

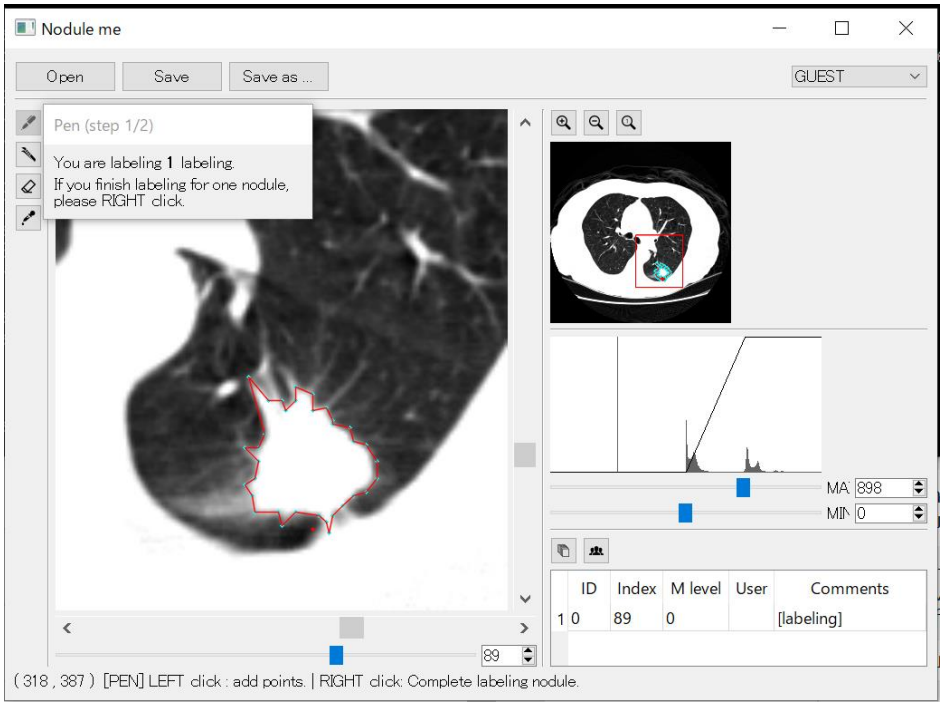


5.2 finish pointing of the slide.

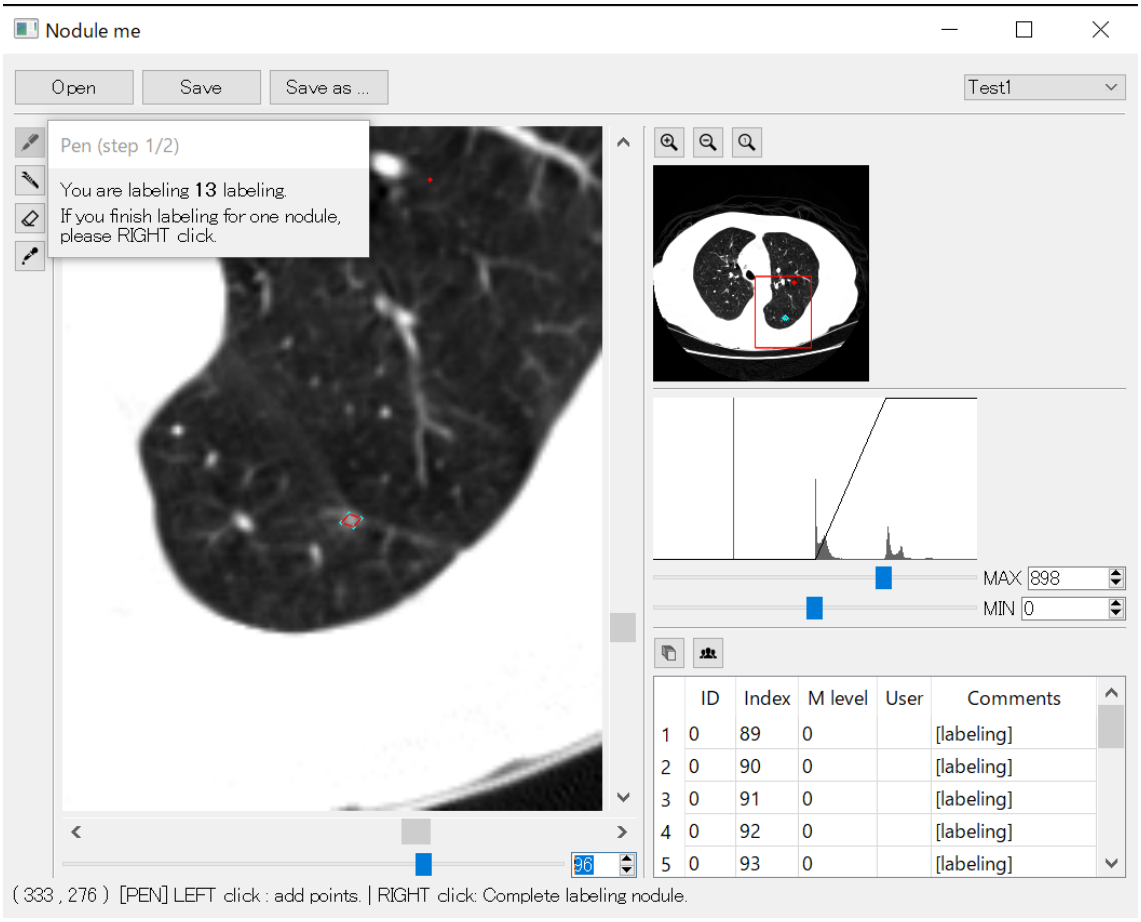
When you finish labeling in one slide, please **right ckick**.
The start and end of your points will be connected automatically
Temporarily, the label is saved but labeling has NOT completed yet.



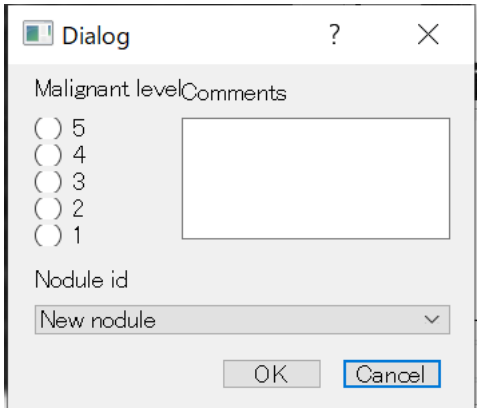
↓ right click



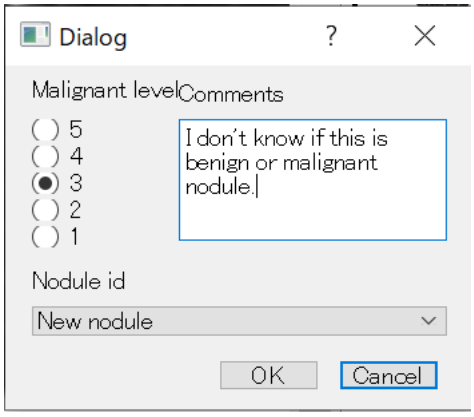
5.3 labeling all slices and finish labeling for one nodule



When you finish labeling all slices which contain one nodule, please **right click** again after right click. Dialog for information of nodule will be opened.



Please fill out [Malignant level].



5.4 complete labeling

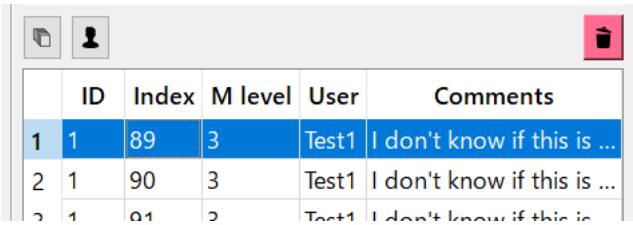
	ID	Index	M level	User	Comments
1	1	89	3	Test1	I don't know if this is ...
2	1	90	3	Test1	I don't know if this is ...
3	1	91	3	Test1	I don't know if this is ...
4	1	92	3	Test1	I don't know if this is ...
5	1	93	3	Test1	I don't know if this is ...
6	1	94	3	Test1	I don't know if this is ...
7	1	94	3	Test1	I don't know if this is ...
8	1	95	3	Test1	I don't know if this is ...
9	1	96	3	Test1	I don't know if this is ...
10	1	88	3	Test1	I don't know if this is ...
11	1	87	3	Test1	I don't know if this is ...
12	1	86	3	Test1	I don't know if this is ...
13	1	85	3	Test1	I don't know if this is ...

6. Label Table

6.1 Jump to selected label

You can jump the label you select.

After click label in list, area and index will be move to the label.



6.2 Switch filter [my]/[everyone]

my: Label table show only labels which labeled by you.

everyone: Label table show labels which labeled by everyone including you.

6.3 Switch filter [my]/[everyone]

one: Label table show only labels in current z-index.

all: Label table show labels in whole z-index.

6.4 Delete selected label

delete button: Delete selected label in list.

7. Tools

 PEN: add points of labels by click.

 PINSET: move points of labels by drag.

 ERASER: delete points by click.

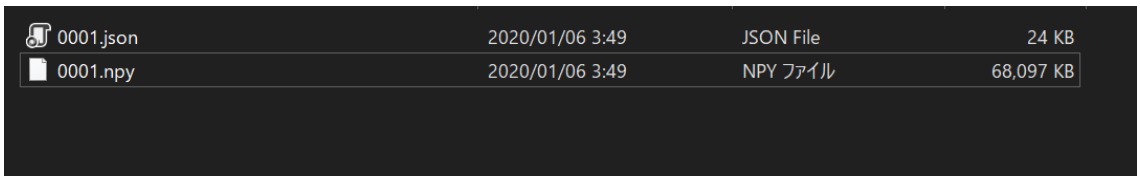
 INSERT TUBE: insert points between point and point of labels.

8. Save data

8.1 Name and save your label data

You can save your label data as .json file.
Please select place you save and name of your label file.

8.1 Complete to save your label data



.npy file is meta data for nodule_me.

.npy file includes pixel arrays of DICOM data.