

Nodule_me.exe

USER GUIDE

VERSION 1.2 - ENG

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1. Install

1.1 download nodule me and unzip file.

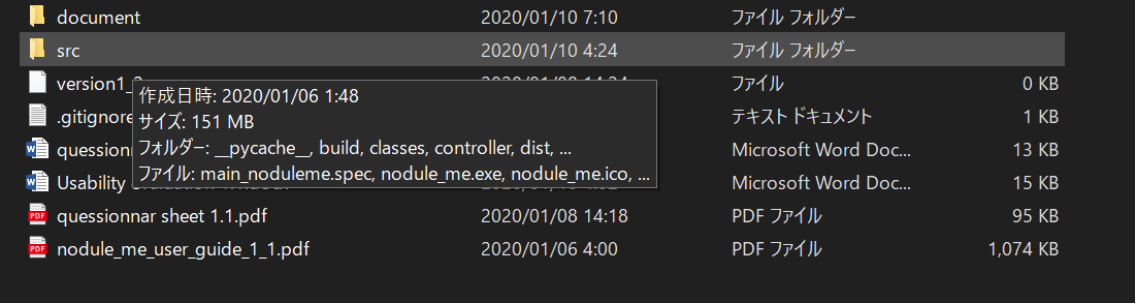
Please download [nodule_me.zip](#) at website.

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.

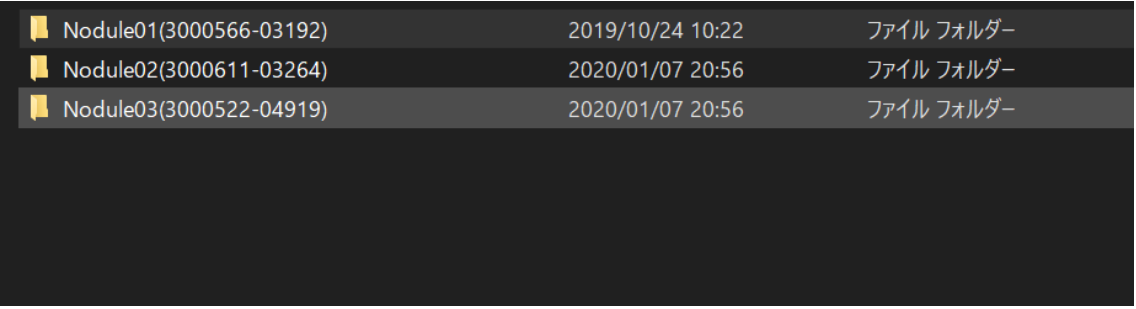
Location is **nodule_me/src/nodule_me.exe**



Item	Created	Type	Size
document	2020/01/10 7:10	ファイル フォルダー	
src	2020/01/10 4:24	ファイル フォルダー	
version1	2020/01/06 1:48	ファイル	0 KB
.gitignore	サイズ: 151 MB	テキスト ドキュメント	1 KB
question	フォルダー: __pycache__, build, classes, controller, dist, ...	Microsoft Word Doc...	13 KB
Usability	ファイル: main_noduleme.spec, nodule_me.exe, nodule_me.ico, ...	Microsoft Word Doc...	15 KB
questionnar sheet 1.1.pdf	2020/01/08 14:18	PDF ファイル	95 KB
nodule_me_user_guide_1_1.pdf	2020/01/06 4:00	PDF ファイル	1,074 KB

Double click to start Nodule me.

Please wait in a second to open the interface.

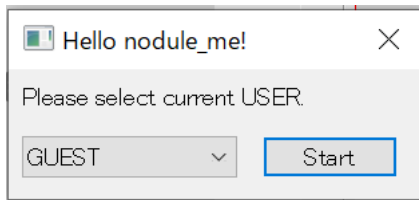


Item	Created	Type
Nodule01(3000566-03192)	2019/10/24 10:22	ファイル フォルダー
Nodule02(3000611-03264)	2020/01/07 20:56	ファイル フォルダー
Nodule03(3000522-04919)	2020/01/07 20:56	ファイル フォルダー

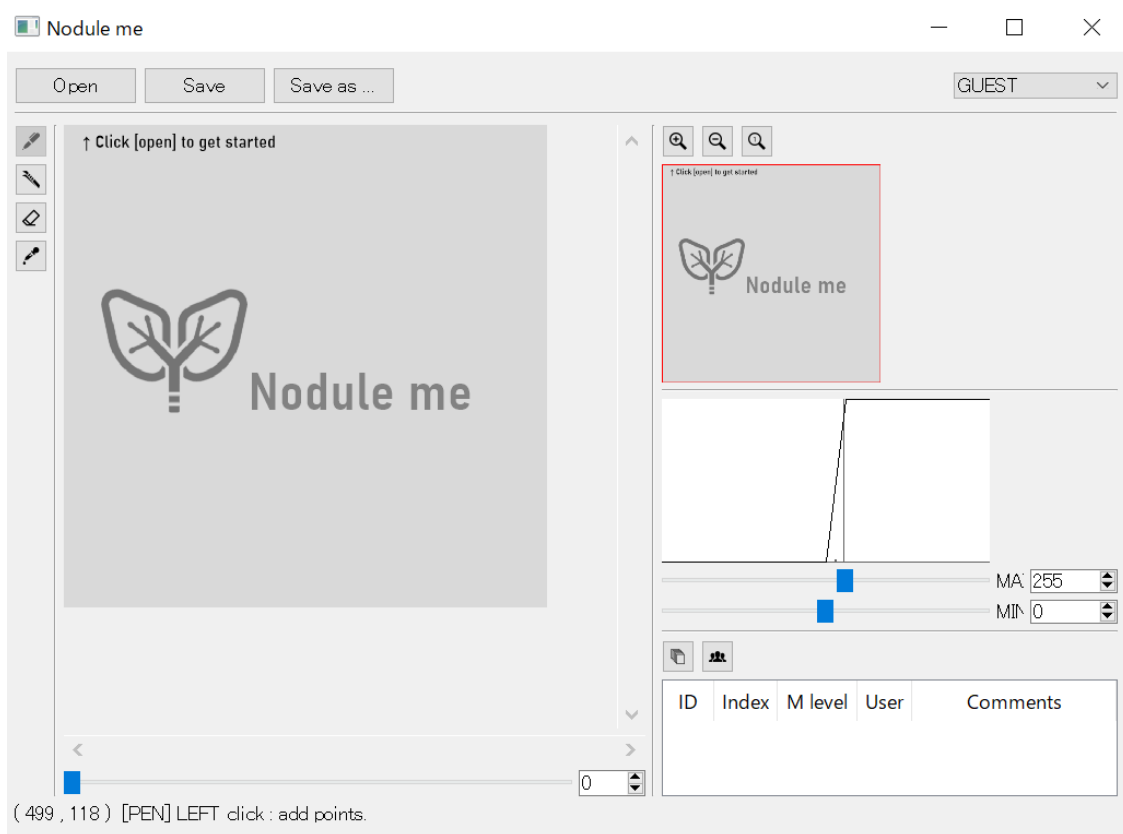
2. Start up

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

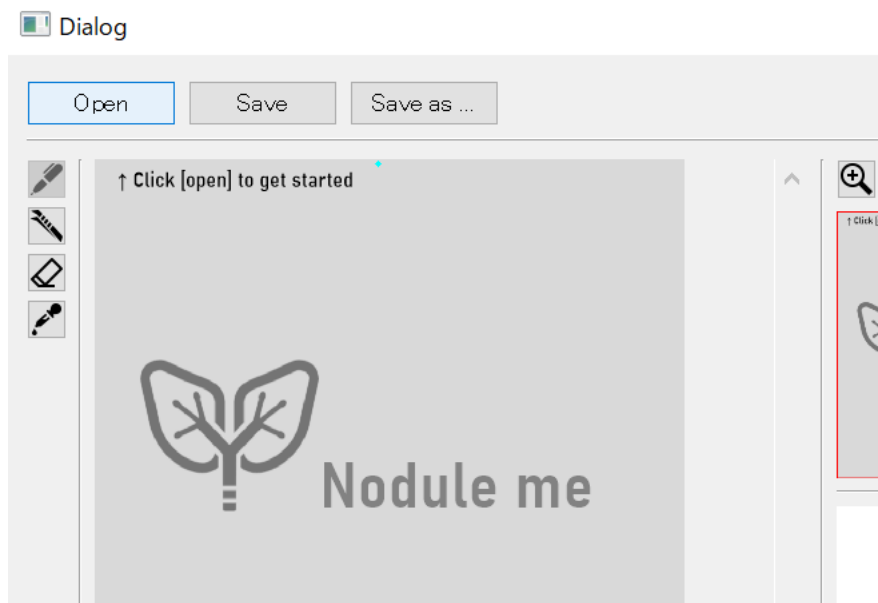


3. Open DICOM data

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.

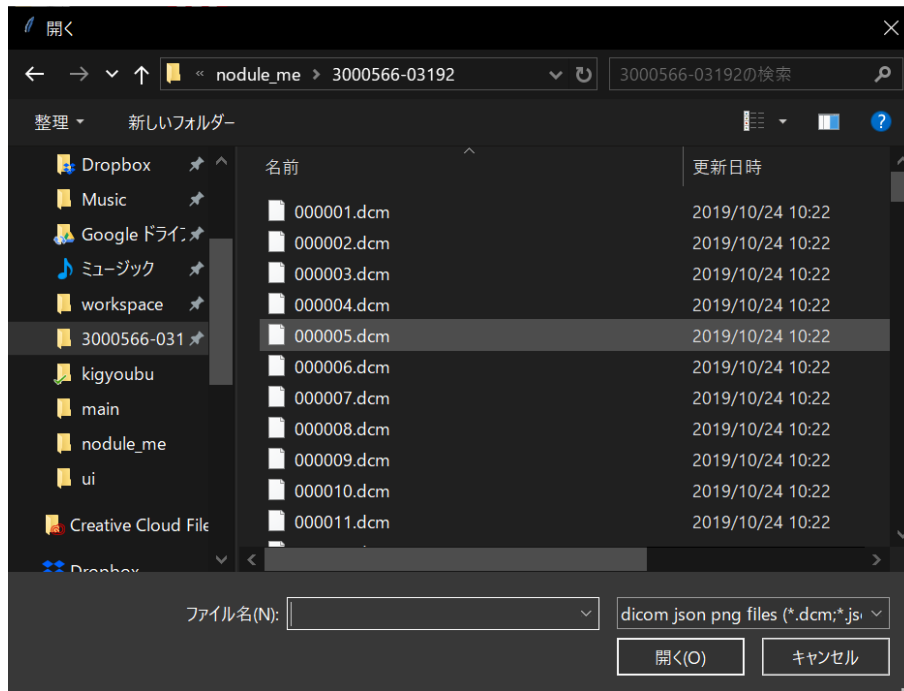
You select .dcm (DICOM) file.

→ Demo file is in **nodule_me_sample.zip**

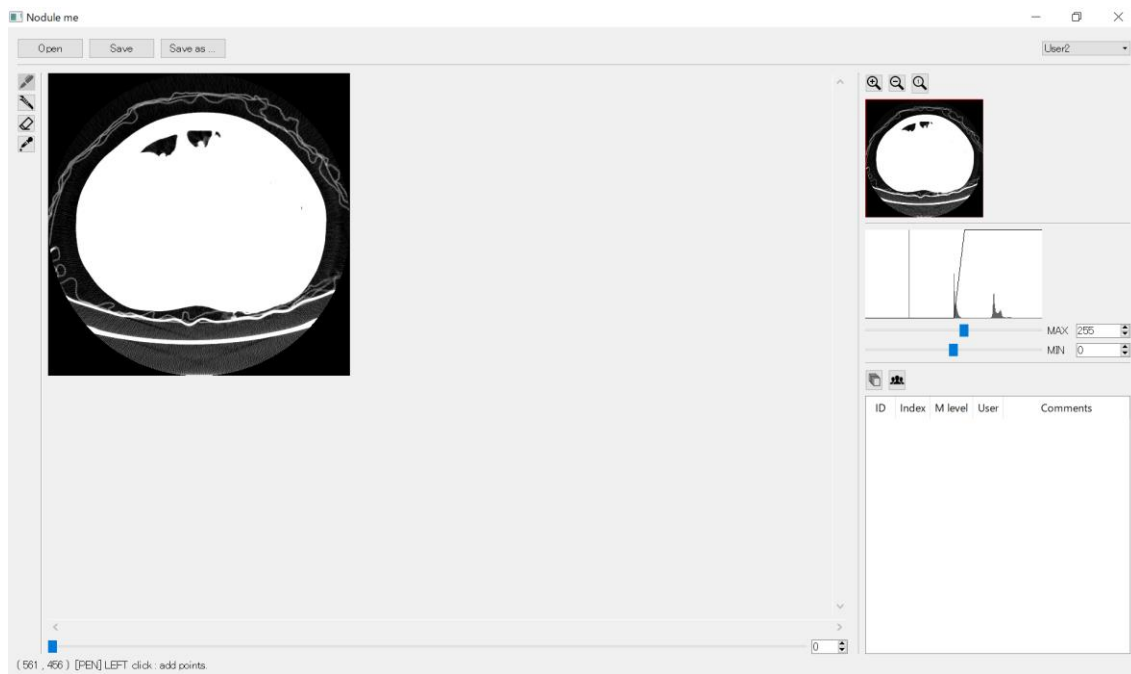
Please try if you don't have any .dcm data.

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

Nodule01(3000566-03192)	2019/10/24 10:22	ファイル フォルダー
Nodule02(3000611-03264)	2020/01/07 20:56	ファイル フォルダー
Nodule03(3000522-04919)	2020/01/07 20:56	ファイル フォルダー



3.3 open DICOM data.

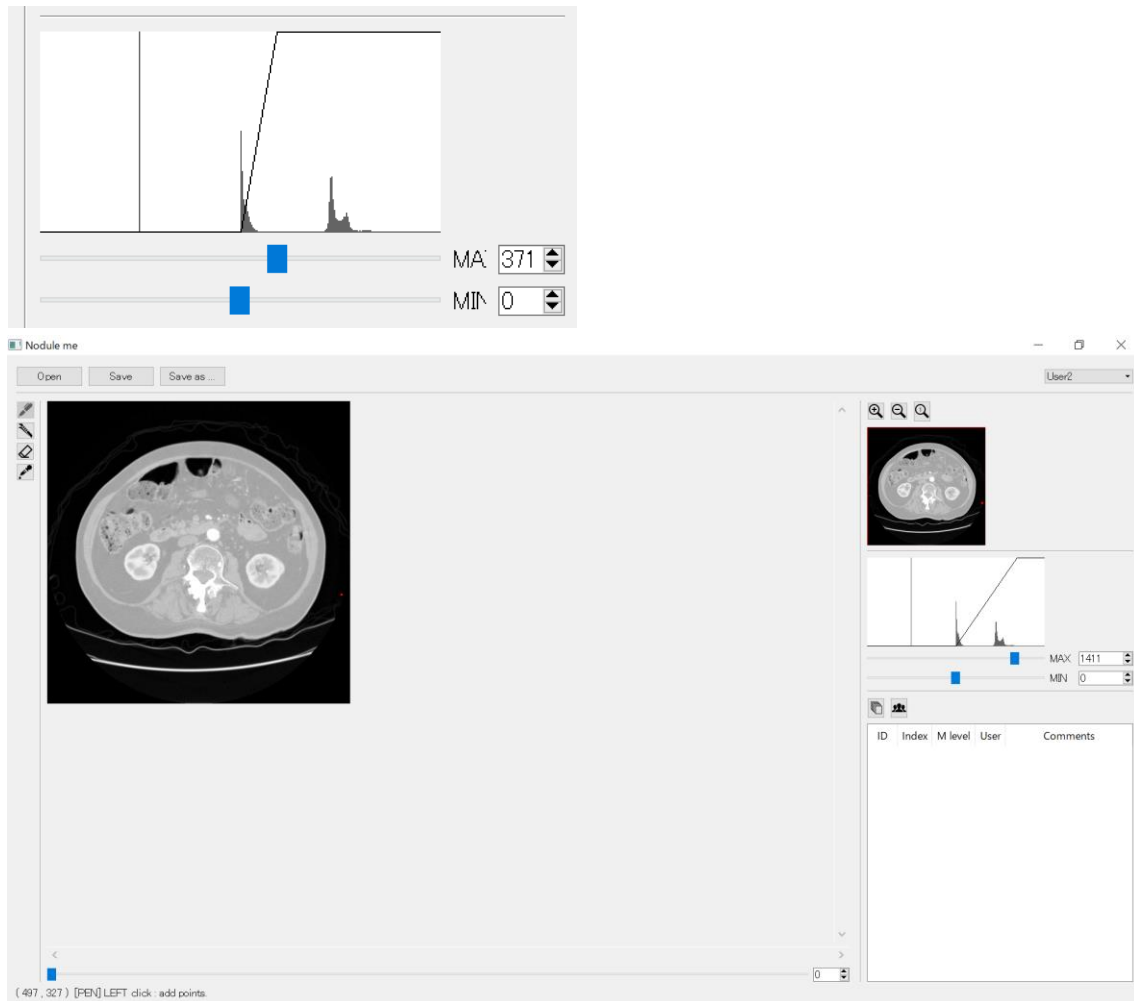


4. Find lung nodule by yourself.

4.1 change contrast

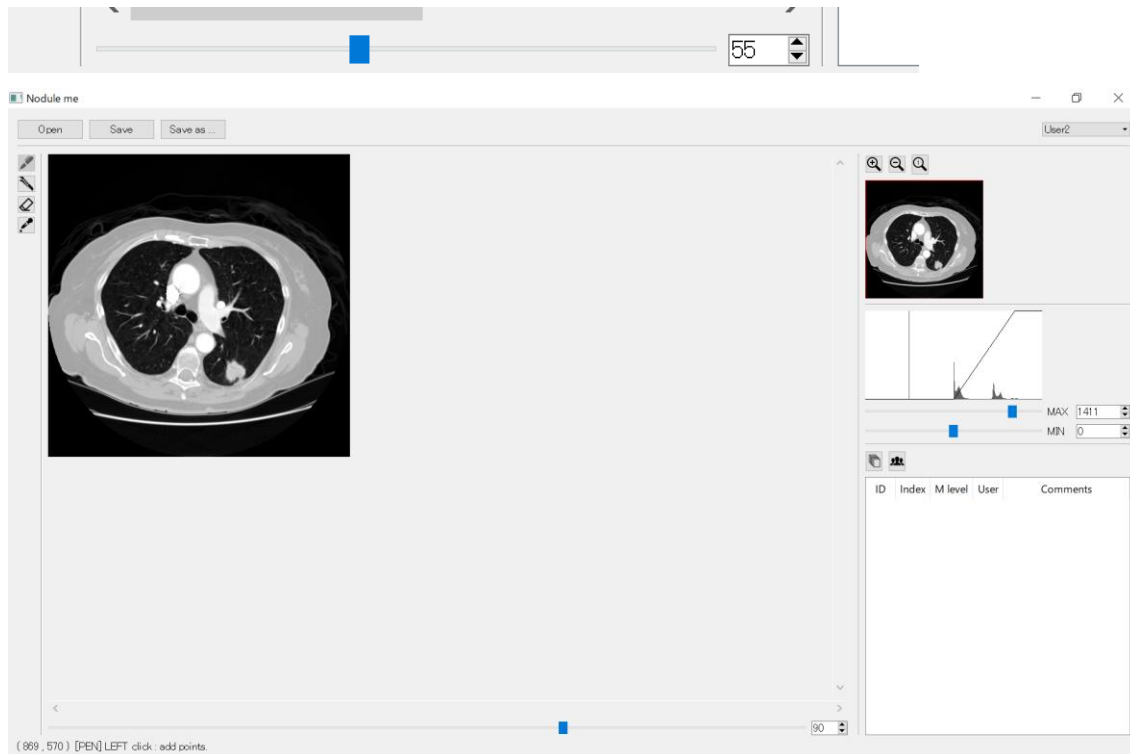
You change contrast to make CT image more easy to look up for you.

Detail about contrast is [8 section](#).




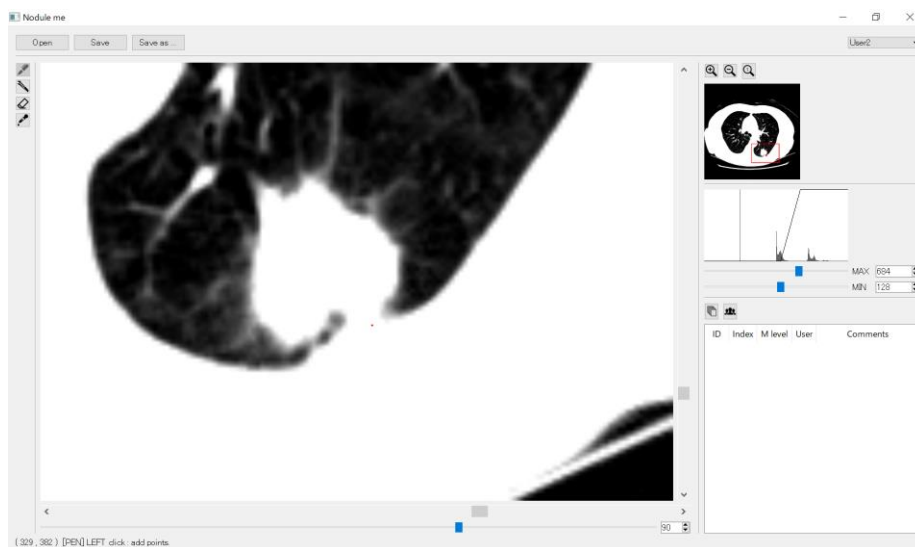
4.2 change z-index and find lung nodule.

You can change z-index by scroll below bar.



4.3 zoom in the nodule.

You can zoom in by mouse wheel or push  button.



5. Labeling

5.1 set [PEN] tool

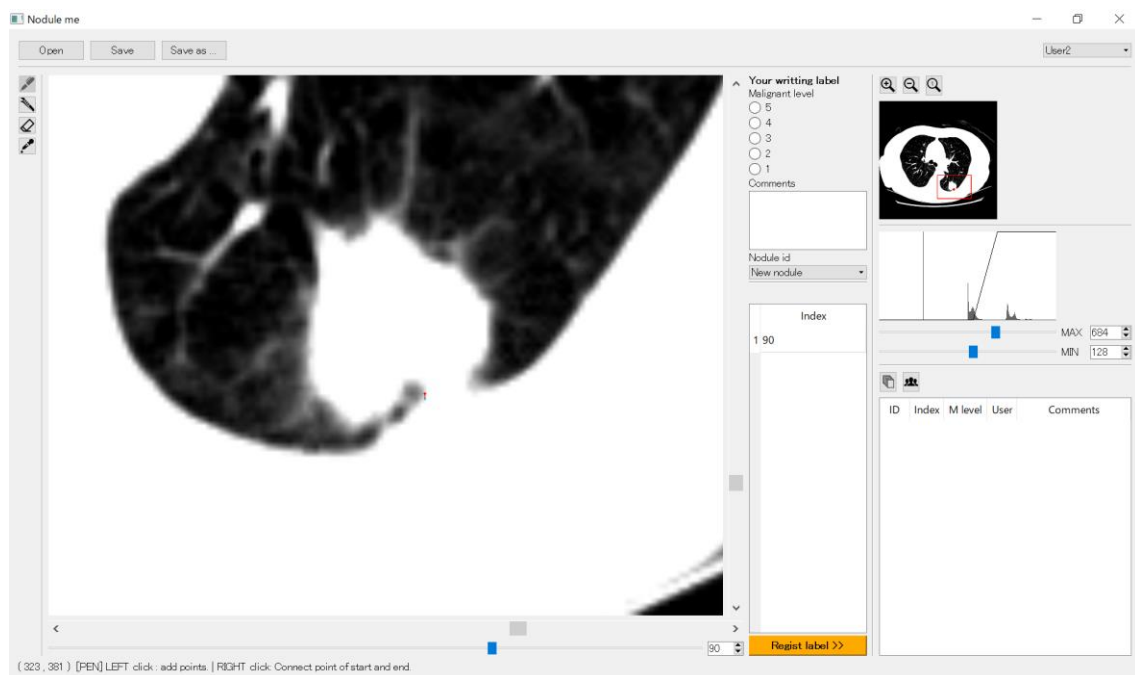
If you don't close PEN, please select PEN tool.



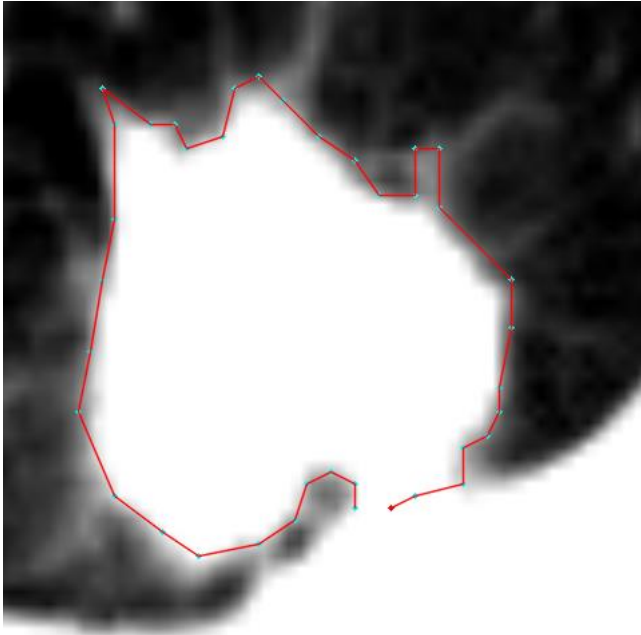
5.2 click canvas and add points of label.

When you find nodule, please start to label by click in canvas.

(New area will be appeared at center, it is for annotation nodules. Please ignore now.)



Please label nodule in one like this.

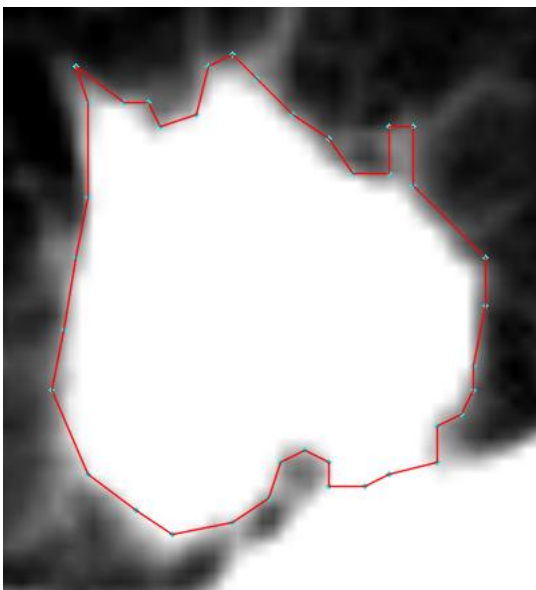


5.2 connect points of label in the slices.

When you finish labeling in one slide, please **RIGHT CLICK**.

The start and end of your points will be connected automatically

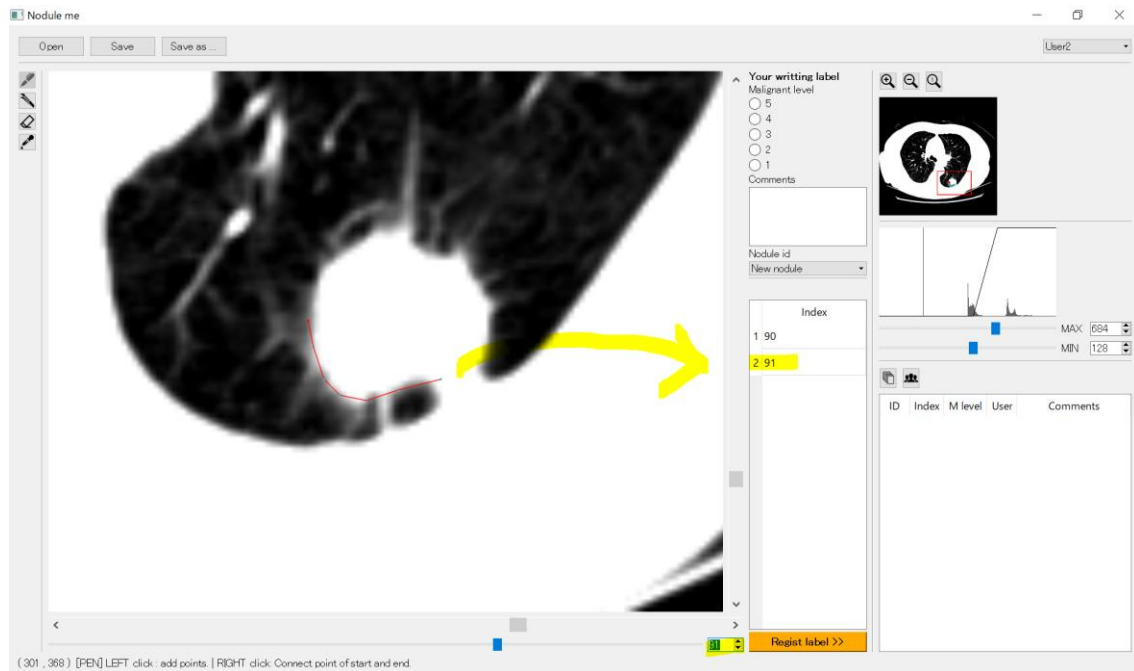
Temporarily, the label is saved but labeling has NOT completed yet.



5.3 move other slices (z-index) to annotate one nodule.

Usually, one nodule spans many slices so you should label all slices which the nodule has. After label one in slice, please move next or prev slice.

Your writing labels are stacked at center table.



5.4 annotate label

After you finish labeling one nodule, please annotate malignant_level.

5 means you think the nodule is high malignant level.

1 means you think the nodule is low malignant level (benign).

You can also write comments if you want.

After you complete annotate, please push

Register label >>

button.

Your writing label

Malignant level

☐ 5

☐ 4

☐ 3

☐ 2

☐ 1

Comments

Nodule id

New nodule ▾

	Index
1	90
2	91
3	92
4	93
5	94
6	94
7	95
8	96
9	89
10	88
11	87
12	86

Regist label >>

Your writing label

Malignant level

☐ 5

☐ 4

☒ 3

☐ 2

☐ 1

Comments

I don't know if this nodule is benign or malignant.

Nodule id

New nodule ▾

	Index
1	90
2	91
3	92
4	93
5	94
6	94
7	95
8	96
9	89
10	88
11	87
12	86

Regist label >>

5.5 complete labeling

Your labels will be added in right label table.

The screenshot displays a software interface with a table of data. The table has the following columns: ID, Index, M level, User, and Comments. There are 9 rows of data, all for 'User2'. The 'Index' values are 90, 91, 92, 93, 94, 94, 95, 96, and 89. The 'Comments' for all rows are 'I dnot't know if t...'. The interface also features a sidebar with a histogram, a control bar with 'MAX 684' and 'MIN 128' values, and a bottom status bar showing '85'.

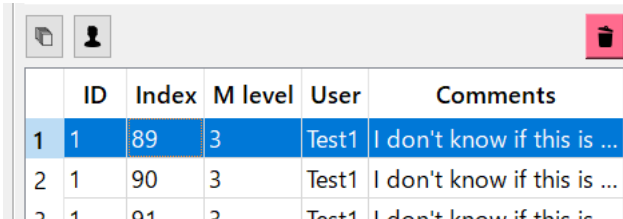
	ID	Index	M level	User	Comments
1	1	90	3	User2	I dnot't know if t...
2	1	91	3	User2	I dnot't know if t...
3	1	92	3	User2	I dnot't know if t...
4	1	93	3	User2	I dnot't know if t...
5	1	94	3	User2	I dnot't know if t...
6	1	94	3	User2	I dnot't know if t...
7	1	95	3	User2	I dnot't know if t...
8	1	96	3	User2	I dnot't know if t...
9	1	89	3	User2	I dnot't know if t...

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.



	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	2	Test1	I don't know if this is ...

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. Contrast, Zoom and z-index.

● Contrast Adjustment function

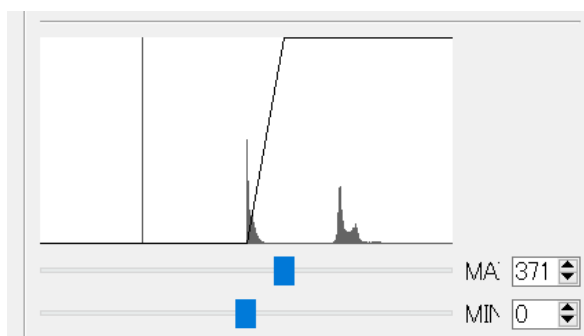
Usually, DICOM data is 16bit but most display can only show 8bit.

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.

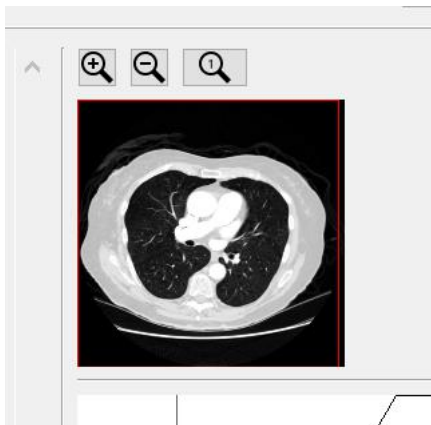
Please adjust contrast to your liking by moving below MAX/MIN slide bar.



● Zoom and Map function

You can zoom up/down by pushing button or mouse rotate mouse wheel.

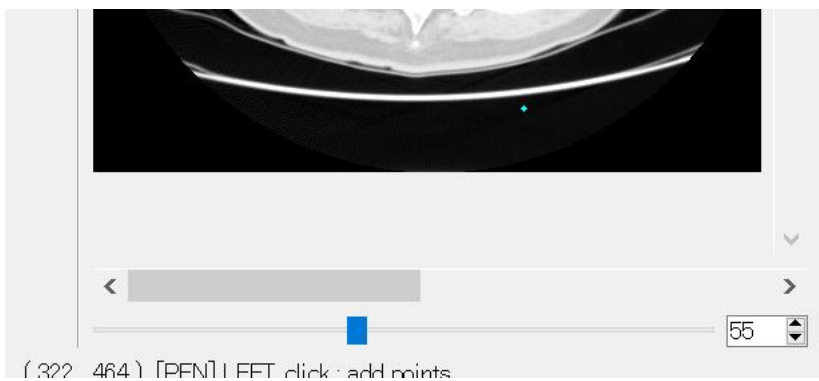
Also you can change area by dragging red square or scroll bar around canvas.



- **Z-index function**

Usually, CTimages is 3D volume data.

You can change z-index by index slide bar or spin box.

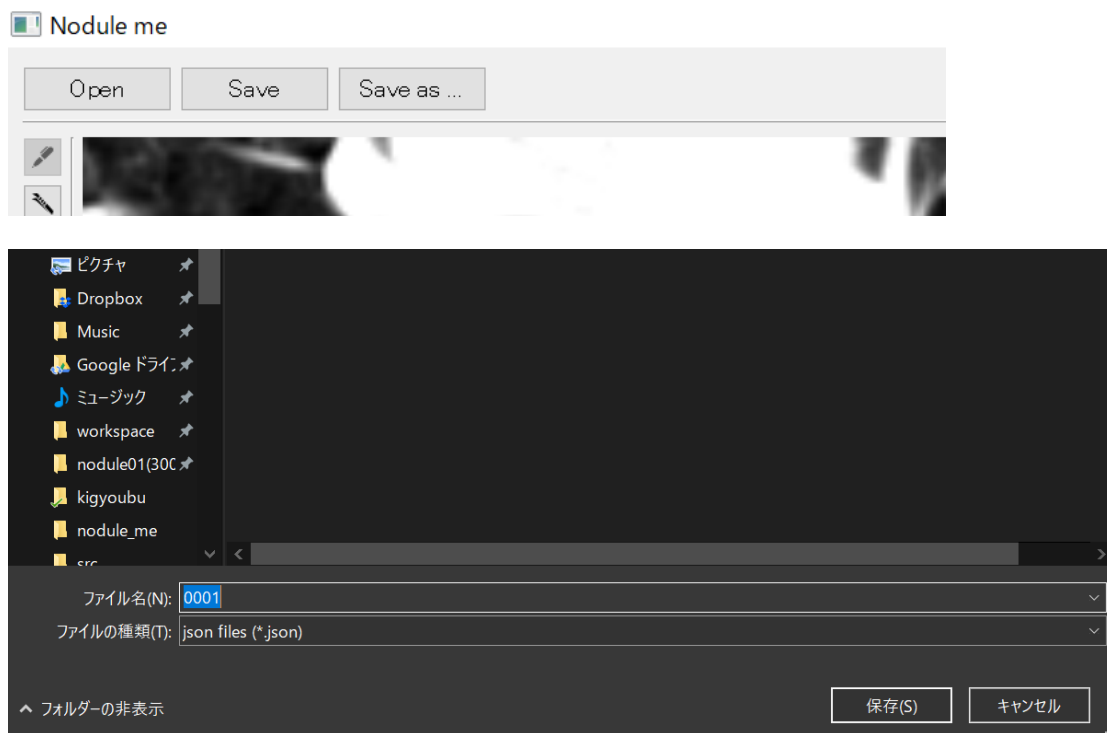


9. Save data

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

0001.json	2020/01/06 3:49	JSON File	24 KB
0001.npy	2020/01/06 3:49	NPY ファイル	68,097 KB

.npy file is meta data for nodule_me.

.npy file includes pixel arrays of DICOM data.