PREDICT tool User Manual

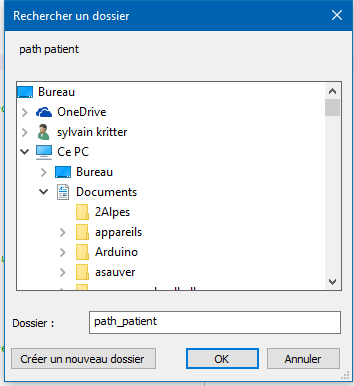
Version 1.0

Author : Sylvain Kritter Date : 28 April 2017

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# Start

After launch a menu appears:



## Select the path to directory where patients Dicom databases are stored

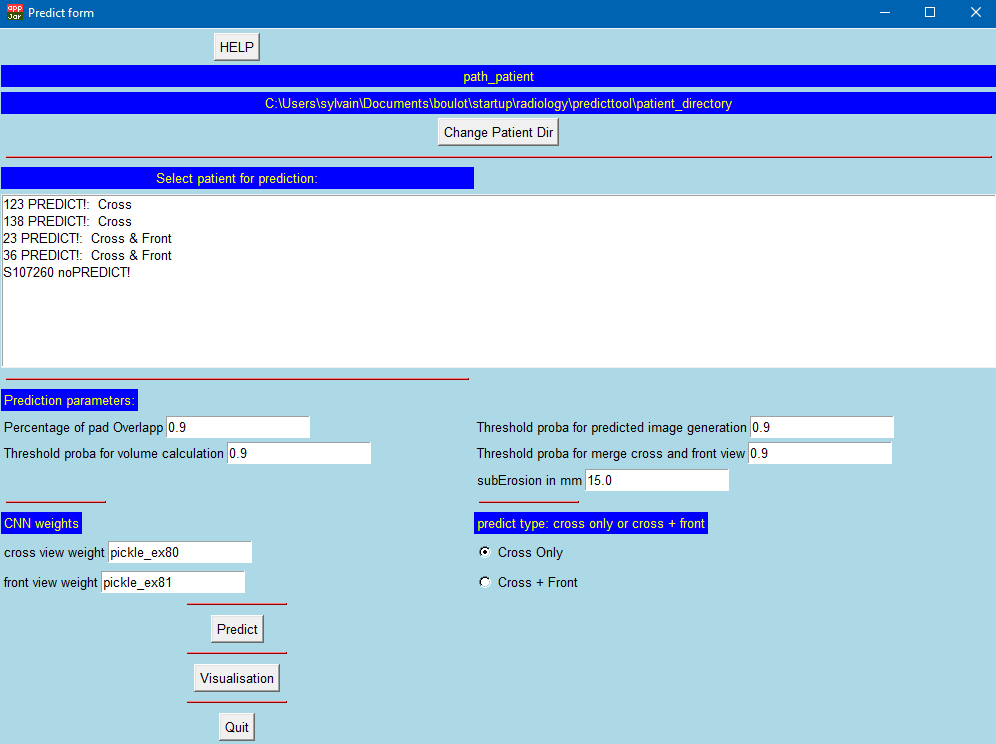
## When done click on *OK*

## You can exit here

# Select patient data set

## To visualize this Help File

## To Change the directory where DICOM for patient are stored



## Here you have the list of patients, with indication if predict has been already done

Cross: predict only on cross slices

Cross &Front predict both on cross and front slices

## Patient selection:

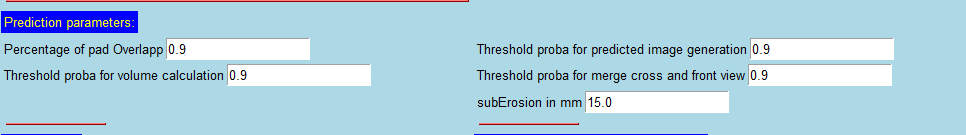
You select the list of patients for predictions, can be one or multiple at same time, by clicking on them

On click LEFT: one patient

On click LEFT with shift key: all the patients between 2 click position

One click LFT with CTRL key: only the selected, not the list in between 2 clicks

# Prediction screen and associated parameters



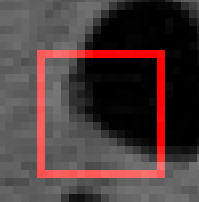
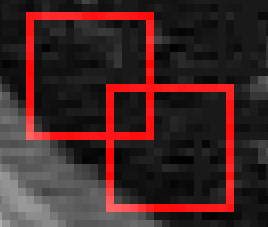
## Percentage of pad overlap:

Numeric value between 0 and 1

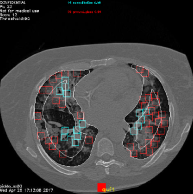
Minimum percentage of patch area overlap between patch and lung area,

Or

100%- Value between 2 patches : ex 0.9🡺 10 % maximum patches overlap between 2 patches

## Threshold Proba for predicted image generation



Numeric value between 0 and 1

After prediction, image of results, slice per slice, are stored as Jpeg files in a sub-directory:

‘Patient name’/predicted\_results

This parameters indicated the minimum threshold for prediction confidence, as calculated by prediction engine, to be kept for image generation.

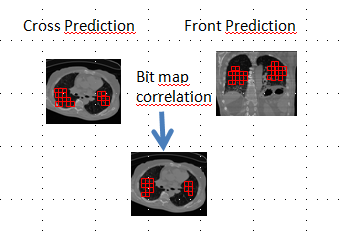
## Threshold Proba for volume calculation

## 

Same as above, but for 3d reconstruction of lung, stored in

‘Patient name’/html as html files

## Threshold Proba for merge cross and front view



Same as above, but for view reconstructed from cross and fron t prediction, projected in cross.

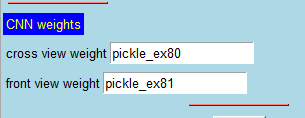
Stored in: ‘Patient name’/predicted\_results\_merge as jpeg file

## SuErosion in mm

Indicates in mm the distance from external border of lung to consider as sub-pleural area



## CNN weights

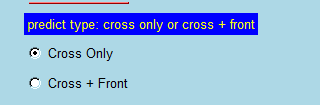


To choose between Cross only or Cross and Front prediction

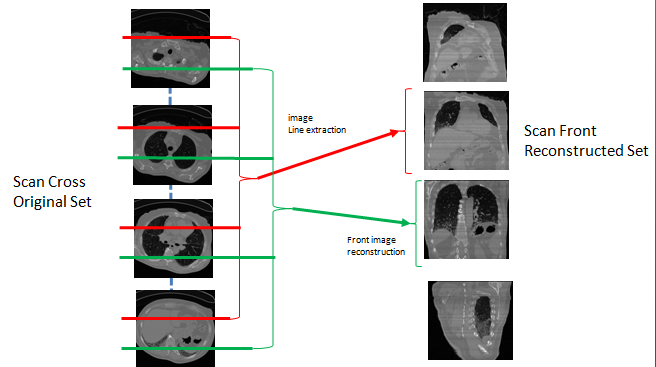
Front prediction can be very long (3 to 5 times longer than cross only

Name of Convolutional Neural Network parameters for cross and front prediction. They correspond to different training sets and parameters used for CNN training

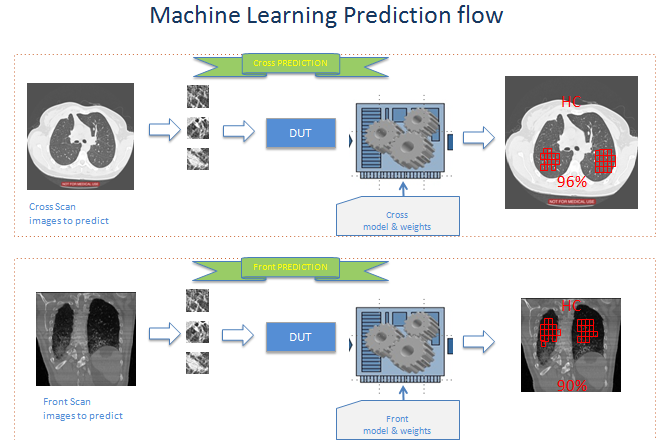
## Type of prediction to be run



For front prediction, front slices are re-constructed from cross slices:



Prediction is run on the reconstructed set, with a dedicated CNN parameter file

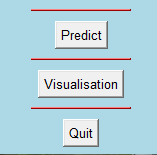


## Commands

Run prediction engine (on one or several patients)

Run directly visualization tool (only one patient must be selected)

Quit



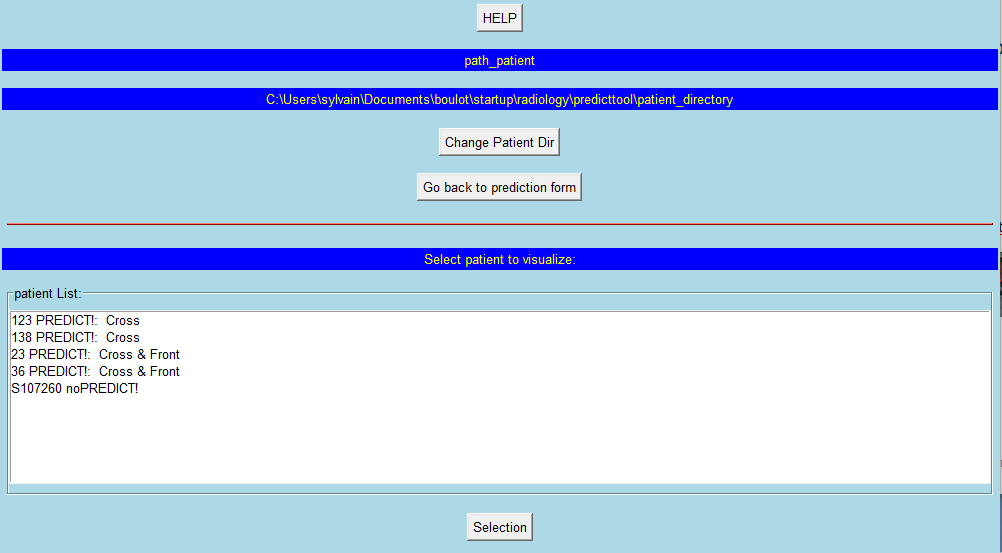
# Vizualization screen

## Selection screen

If no patient was selected on prediction screen, before calling Visualisation, this form allows to select one. Only one can be selected, then press on select button.

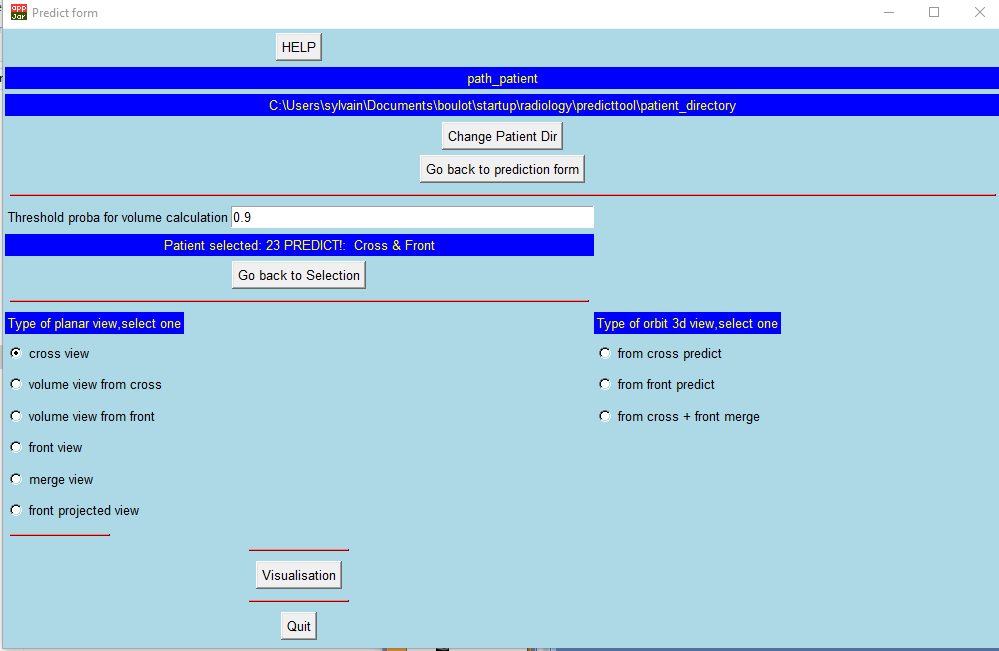
Indication is given if Cross only or both Cross and Front prediction have been run.

Patients without prediction are not listed.



## Visualisation parameter screen

## This part allows to go back previous screens



## Visualisation parameter for online calculation

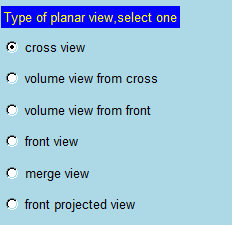
Visualization of predict results is interactive (selection of patterns to visualize, selection of slice, etc., except for merge view, which is very much resource consuming, and done one for once during prediction process

## Threshold Proba



This parameters is used for starting Threshold (probability of prediction as defined by engine) for visualization

## Visualization 2D view



Selection of which view to select from Cross prediction result

## Cross view

Prediction result visualize as overlay on the original slices

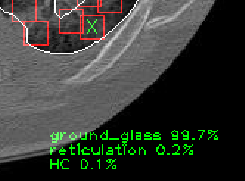
Two windows appear:

Information on view (patient name, slice number, threshold for probability

List of visualized patterns, with average probabilities

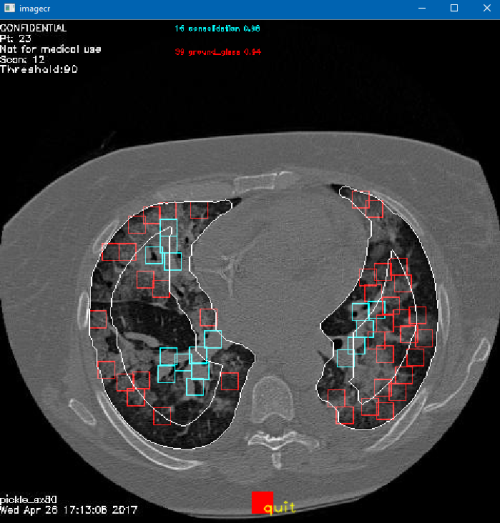
Interaction on this view :

Click LEFT on a patch, gives the top pattern probabilities



To Quit this view ( ONLY WAY ! DO NOT TRY TO CLOSE IT ANOTHER WAY)

1. Actual view



1. Parameters select on this view:

To change brighness

To change contrast

To change threshold for probability

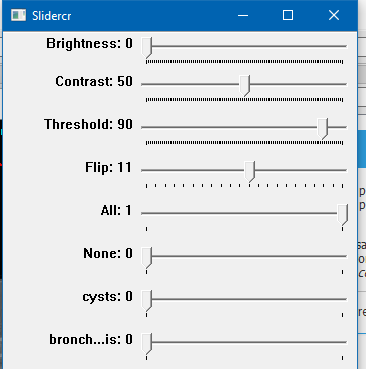
To change visualized slice

To show ALL patterns

To show NO pattern

To select the patterns to visualize

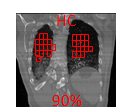
(ALL and NONE must be Zero)



Important Note: this window will be closed when actual visualization will be closed by clicking on red rectangle “Quit” on it, no other way to close it.

## Front view and Merge View

Work the same than Cross view, but on Front slices



## Front projected view.

For this view, no interactivity, except slice selection , in term of threshold, patterns to visualize. Parameters used are the one defined during prediction.

## Volume view from Cross ( and from front)

Two windows appear:

Information on view (patient name, slice number, threshold for probability.

List of visualized patterns, with total volume, as per threshold, for all the scans.

Volume percentage for different lung sections

-When ALL is selected (see parameter select )

The dominant patterns are visualized

-When one pattern is selected (see parameter select )

Volume and percentage corresponds to this pattern only

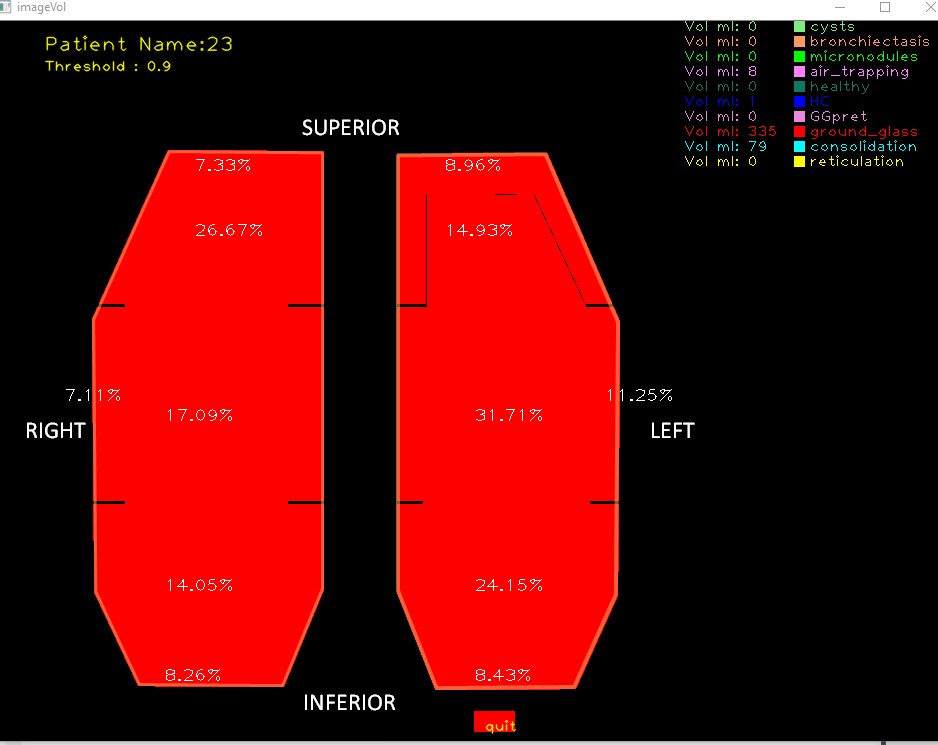
Example: Ground glass

31.71% of LEFT MIDDLE LUNG TOTAL AREA (including SubPleural

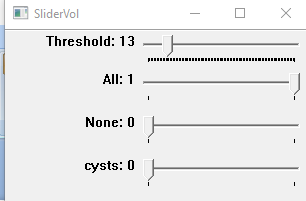
11.25% in Left MIDDLE Subpleural compared to LEFT MIDDLE LUNG TOTAL AREA

To Quit this view ( ONLY WAY ! DO NOT TRY TO CLOSE IT ANOTHER WAY)

1. For actual view



1. Parameters select on this view:



To change threshold for probability

To show ALL patterns

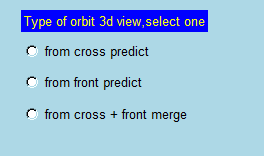
To show NO pattern

To select the patterns to visualize

(ALL and NONE must be Zero)

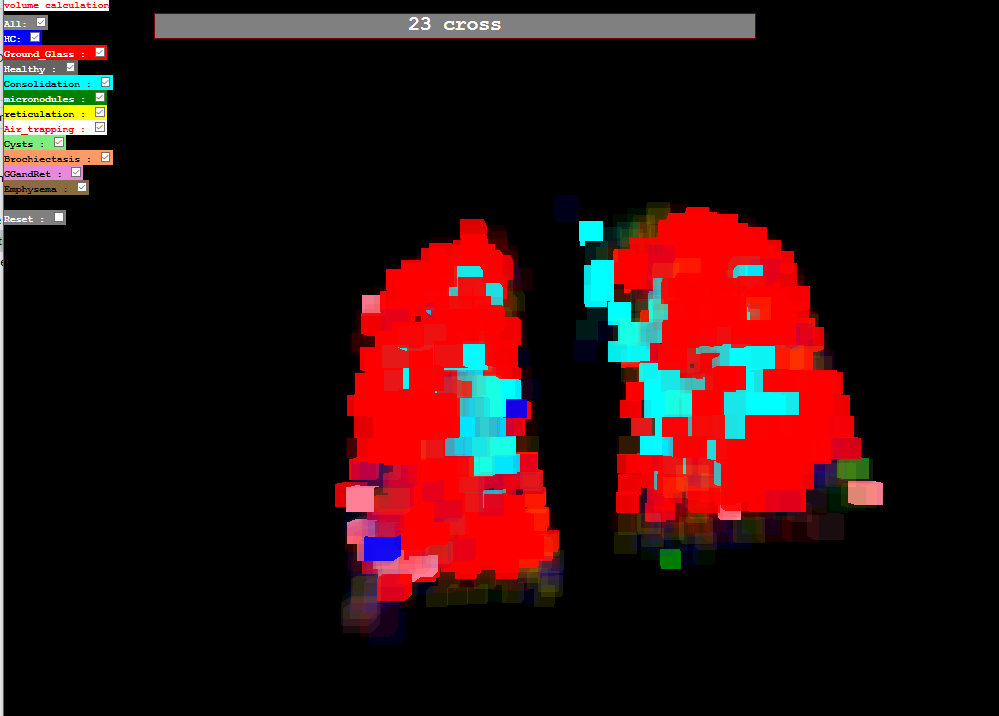
ONLY ONE to be selected

## Visualization 3D view



This allows to visualize prediction in 3D, with possibility to change perspective (view from different angles, zoom) interactively.

This opens a new window in the default Internet Browser tool (IE, Chrome, etc..), according to user windows preferences when an html file is opened.

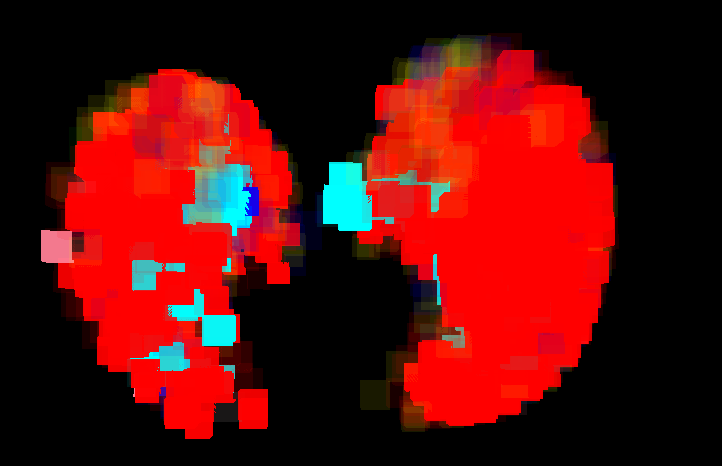


Patient Name

Pattern selection (all to view or specific select)

Reset: reset view to original perspective

Different perspective can be done by dragging the mouse, with left button maintain pressed



Zooming is done with scroll wheel of mouse

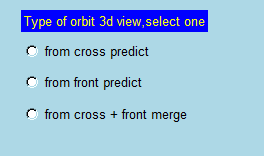
NOTE: calculation time can be few seconds for perspective change or zoom

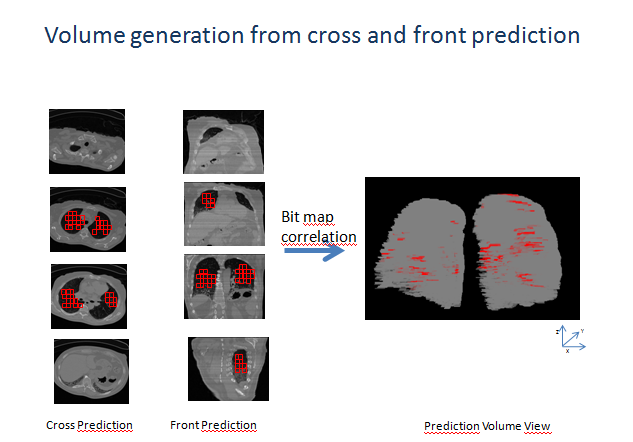
## Visualization 3D view options

From Cross prediction

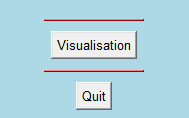
From Front Prediction

From Cross and front prediction, with bit map correlation





## Main command



Launch visualization when type has been selected (only one possible at a time)

Quit the tool