# Tutorial of using our trained model as a detector

## Preparation

1. In *Eclipse*, run the Java script named *“copy\_rename\_mld\_batch”* (maybe need modification).

The object is to copy the original *LayerData* to another mld file and to rename it, automatically for every slide.

## Workflow\_1 (not used, to see Workflow\_2)

For this workflow, we need to set a threshold (hard to be decided) in the step 8. No use of ROIs from Visiopharm. No evaluation, nor calculation for the optimal threshold for each slide.

1. Select and open a slide in *Visiopharm*.
2. Record this slide in table *“E:\deeplearning\data\5x\contenu.xlsx*”. Edit the column E “*Detector”* to *train* or *test*.
3. Create a folder for the slide in “*E:\deeplearning\data\5x\detector”* and its sub-folder.

For example,

* HMNT0001
  + 512\_image
  + results
    - label
  + split64\_image

1. In *RStudio*, open the script “*D:\deeplearning\Hepatocarcinomes\codes\5x\data\split\_to\_tile\* *write\_img\_512\_detector”*.

Comment out the line 13, 26, 27, 28 and save it.

Modify the slide name in line 18 and save it.

1. In *Visiopharm*, open the APP *“dl/split/split\_5x/split\_detector\_512”* and run it.
2. In *RStudio*,open the script *“D:\deeplearning\Hepatocarcinomes\codes\5x\data\split\_to\_subtile\\_split64\_detector”*.

Modify the slide name in line 11 and save it.

1. In *RStudio*,open the script *“D:\deeplearning\Hepatocarcinomes\codes\5x\test\\_test\_detector\_tum\_slide”*.

Modify the slide name in line 14 and save it.

1. In *RStudio*,open the script *“D:\deeplearning\Hepatocarcinomes\codes\5x\result\_vis\as\_label\return\_label\_64\_detector”*.

Modify the slide name in line 11 and save it.

Modify the threshold to an appropriate one in line 30 and save it.

1. In *Visiopharm*, open the APP *“dl/change\_roi”* and run it.

Then open another APP *“dl/test/test\_5x/return\_label\_512\_detector”* and run it.

## Workflow\_2 (used now)

We add the evaluation and the calculation for the optimal threshold for each slide. One whole script in RStudio. Save ROIs (ground-truth) from Visiopharm not as a tiff image but a table which contains the number of tumoral pixels.

1. Select and open a slide in *Visiopharm*.
2. Record this slide in table *“E:\deeplearning\data\5x\contenu.xlsx*”. Edit the column E “*Detector”* to *train* or *test*.
3. Create a folder for the slide in “*E:\deeplearning\data\5x\detector”* and its sub-folder.

For example,

* HMNT0001
  + 512\_image\_label
  + results
    - label
  + split64\_image\_label

1. In *RStudio*, open the script “*D:\deeplearning\Hepatocarcinomes\codes\5x\data\split\_to\_tile\* *write\_img\_512\_detector”*.

Modify the slide name in line 18 and save it.

1. In *Visiopharm*, open the APP *“dl/split/split\_5x/split\_detector\_512”* and run it.
2. In *RStudio*,open the script *“D:\deeplearning\Hepatocarcinomes\codes\5x\detector\_rstudio\_workflow\split64\_test\_evaluate\_detector”*.

Modify the slide name in line 16 and save it.

1. In *RStudio*,open the script *“D:\deeplearning\Hepatocarcinomes\codes\5x\result\_vis\as\_label\return\_label\_64\_detector”*.

Modify the slide name in line 11 and save it.

Modify the threshold to the optimal one in line 14 and save it.

1. In *Visiopharm*,

For the slide, if the whole image is ROI “default”:

* Open the APP *“dl/change\_roi”* and run it.
* Then open another APP *“dl/test/test\_5x/return\_label\_512\_detector”* (**sampling regions** should be *“Entire image”*) and run it.

For the slide, if some parts are ROI “clear”:

* Open the APP *“dl/test/test\_5x/return\_label\_512\_detector”*. Set the **sampling regions** from *“Entire image”* to *“All”* and run it.
* Then open another APP *“dl/change\_roi”* and run it.