

# User Manual

## 1 Computer requirements

**System:** Win10

**GPU:** Nvidia 1080Ti or better (at least 10G memory), with Nvidia corresponding driver

**CUDA:** cuda 10

**CPU:** Intel i7 or better

**System Memory:** 16G or better

## 2 Supported WSI formats

The software supports the WSI formats supported by the opensource *OpenSlide* library, including *x.svs*, *x.mrxs*, *x.tif*, etc.

WSI resolution: 20× or 40× (0.1 – 0.6 μm/pixel, 0.1 – 0.4 μm/pixel is better)

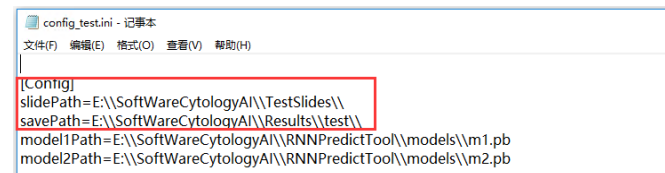
## 3 Functions of the software

Recommend the top 10 lesion cells and predict the positive probability of WSIs.

## 4 Steps of using the software

**Step1:** Edit the *slidePath* and *savepath* of the *config.ini* file according to your paths as the format of the example

Note: please use absolute path



```
config_test.ini - 记事本
文件(F) 编辑(E) 格式(O) 查看(V) 帮助(H)

[Config]
slidePath=E:\\SoftWareCytologyAI\\TestSlides\\
savePath=E:\\SoftWareCytologyAI\\Results\\test\\
model1Path=E:\\SoftWareCytologyAI\\RNNPredictTool\\models\\m1.pb
model2Path=E:\\SoftWareCytologyAI\\RNNPredictTool\\models\\m2.pb
```

**Step2:** Edit the paths of TfModel1, TfModel2 and TfRnn1-TfRnn6 as the format of the example

Note: please use absolute path



```
config_test.ini - 记事本
文件(F) 编辑(E) 格式(O) 查看(V) 帮助(H)

[Config]
slidePath=E:\\SoftWareCytologyAI\\TestSlides\\
savePath=E:\\SoftWareCytologyAI\\Results\\test\\
model1Path=E:\\SoftWareCytologyAI\\RNNPredictTool\\models\\m1.pb
model2Path=E:\\SoftWareCytologyAI\\RNNPredictTool\\models\\m2.pb

[TfModel2]
input=input_1:0
output=dense_2/Sigmoid:0,global_max_pooling2d_1/Max:0
path=E:\\SoftWareCytologyAI\\RNNPredictTool\\models\\m2.pb

[TfRnn1]
input=feature_input:0
output=output/Sigmoid:0
path=E:\\SoftWareCytologyAI\\RNNPredictTool\\models\\rnn\\10_1.pb

[TfRnn2]
input=feature_input:0
output=output/Sigmoid:0
path=E:\\SoftWareCytologyAI\\RNNPredictTool\\models\\rnn\\10_2.pb
```

```
[TfRnn3]
input=feature_input:0
output=output/Sigmoid:0
path=E:\\SoftWareCytologyAI\\RNNPredictTool\\models\\rnn\\20_1.pb

[TfRnn4]
input=feature_input:0
output=output/Sigmoid:0
path=E:\\SoftWareCytologyAI\\RNNPredictTool\\models\\rnn\\20_2.pb

[TfRnn5]
input=feature_input:0
output=output/Sigmoid:0
path=E:\\SoftWareCytologyAI\\RNNPredictTool\\models\\rnn\\30_1.pb

[TfRnn6]
input=feature_input:0
output=output/Sigmoid:0
path=E:\\SoftWareCytologyAI\\RNNPredictTool\\models\\rnn\\30_2.pb
```

**Step3:** Edit the paths of the *rnnPredict.exe* and the *config.int* in the *test.bat* file

```
test.bat - 记事本
文件(F) 编辑(E) 格式(O) 查看(V) 帮助(H)

set CUDA_VISIBLE_DEVICES=1
E:\\SoftWareCytologyAI\\RNNPredictTool\\rnnPredict.exe E:\\SoftWareCytologyAI\\config_test.ini
E:\\SoftWareCytologyAI\\RNNPredictTool\\rnnPredict_after.exe E:\\SoftWareCytologyAI\\config_test.ini
pause
```

**Step4:** Run the *test.bat* file

```
C:\Windows\system32>set CUDA_VISIBLE_DEVICES=1
C:\Windows\system32>E:\\SoftWareCytologyAI\\RNNPredictTool\\rnnPredict.exe E:\\SoftWareCytologyAI\\config_test.ini
2021-04-09 11:57:58.324721: I E:\\tensorflow\\tensorflow-1.10.0\\tensorflow\\core\\platform\\cpu_feature_guard.cc:141] Your CPU supports instructions that this TensorFlow binary was not compiled to use: AVX AVX2
2021-04-09 11:58:02.663217: I E:\\tensorflow\\tensorflow-1.10.0\\tensorflow\\core\\common_runtime\\gpu_device.cc:1405] Found device 0 with properties:
name: TITAN V major: 7 minor: 0 memoryClockRate(GHz): 1.455
pciBusID: 0000:1d:00.0
totalMemory: 11.87GiB freeMemory: 10.49GiB
2021-04-09 11:58:02.663217: I E:\\tensorflow\\tensorflow-1.10.0\\tensorflow\\core\\common_runtime\\gpu_device.cc:1405] Found device 1 with properties:
```

**Step5:** View the results

For each slide, the results include the cropped image patches of recommended top 10 lesion cells and the predicted positive probability of the slide in *xx.rmnscore*.

In *xx.txt* below, the positive probability, (x, y) position of recommended cells are provided. Notably, the (x, y) position is relative to the rectangle bounding the non-empty region of the slide, if available by querying slide properties by *OpenSlide*.

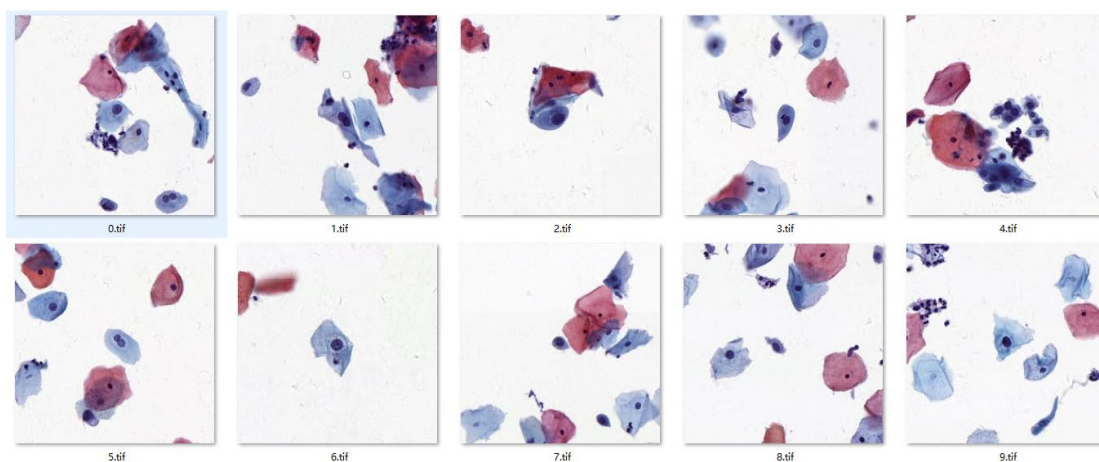
```
1110441 0893050.txt - 记事本
文件(F) 编辑(E) 格式(O) 查看(V) 帮助(H)
1.000000,44767,67231
1.000000,47327,69983
1.000000,32671,70431
1.000000,32607,91039
1.000000,30047,70175
1.000000,28895,70559
1.000000,11679,70815
1.000000,79391,69727
1.000000,51231,14815
1.000000,15519,38751
1.000000,15839,45151
```

## 5 Example

Slide 1: 1110441 0893050.mrxs

Predicted score of slide: 1.00

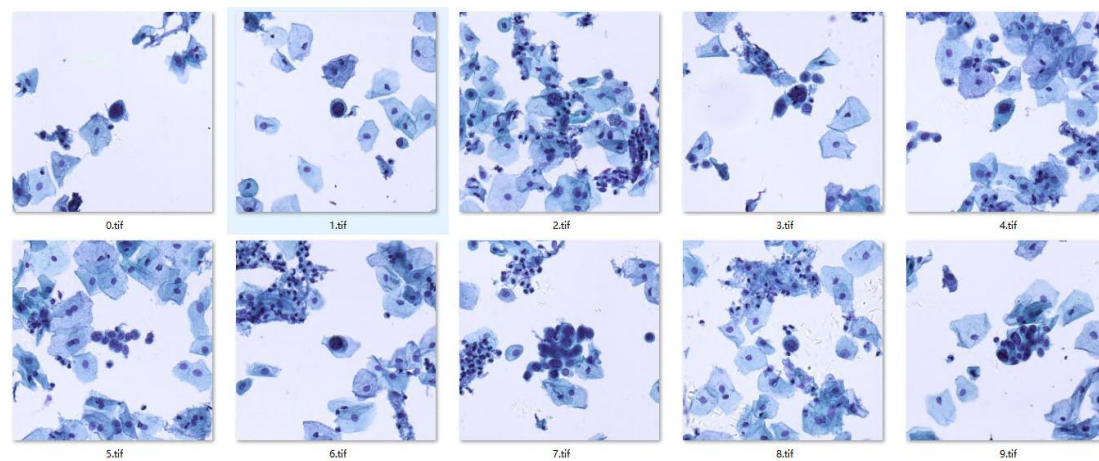
Recommended lesion cells: the recommended lesion cells refer to the cells in center region of the patch (about 243  $\mu\text{m}^2$ )



Slide2: 1179536.svs

Predicted score of slide: 1.00

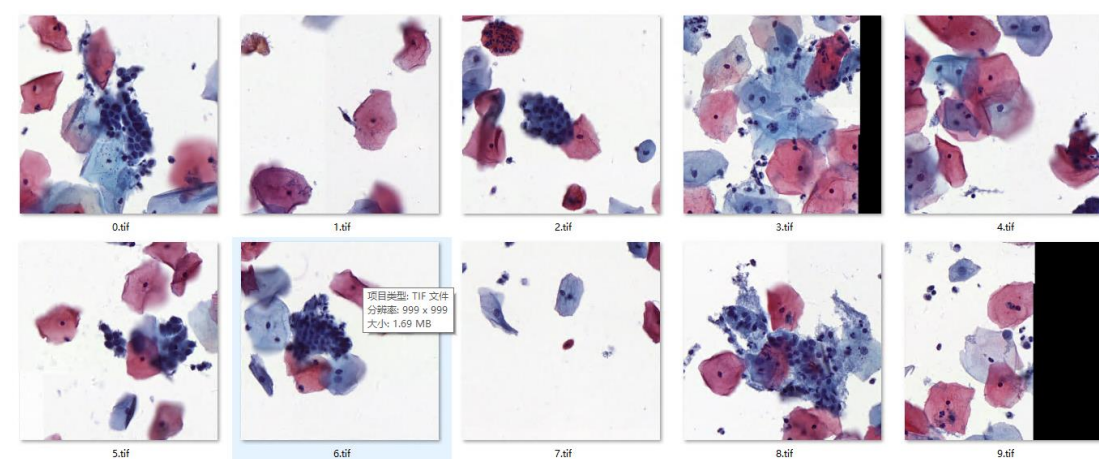
Recommended lesion cells:



Slide3: 0067309 1009017.mrxs

Predicted score of slide: 0.00

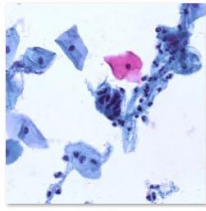
Recommended lesion cells:



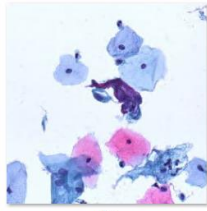
Slide4: 1159929.svs

Predicted score of slide: 0.009

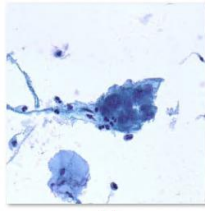
Recommended lesion cells:



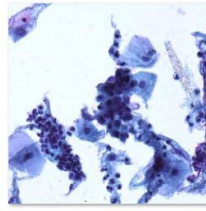
0.tif



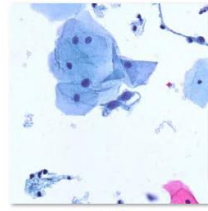
1.tif



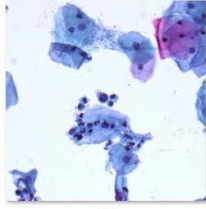
2.tif



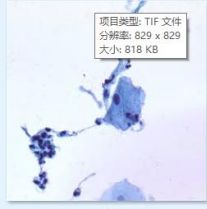
3.tif



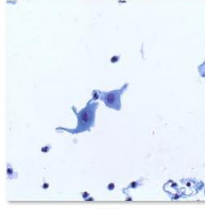
4.tif



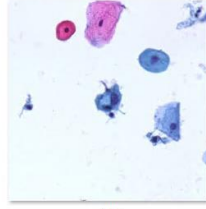
5.tif



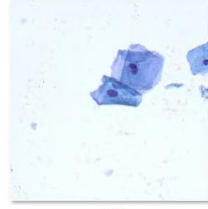
6.tif



7.tif



8.tif



9.tif