FindMyCells Handbook

LINUX

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Requirements:

Linux >17.04 is **highly** recommended. The reason is that *caffe* must be built on your machine otherwise, which is a complicated task. In case if You have <17.04 Linux, please visit https://github.com/BVLC/caffe for further instructions.

The following software components are required to run the software:

- *sudo apt-get install caffe-gpu,* if You want to use the GPU version, or
- *sudo apt-get install caffe-cpu* otherwise

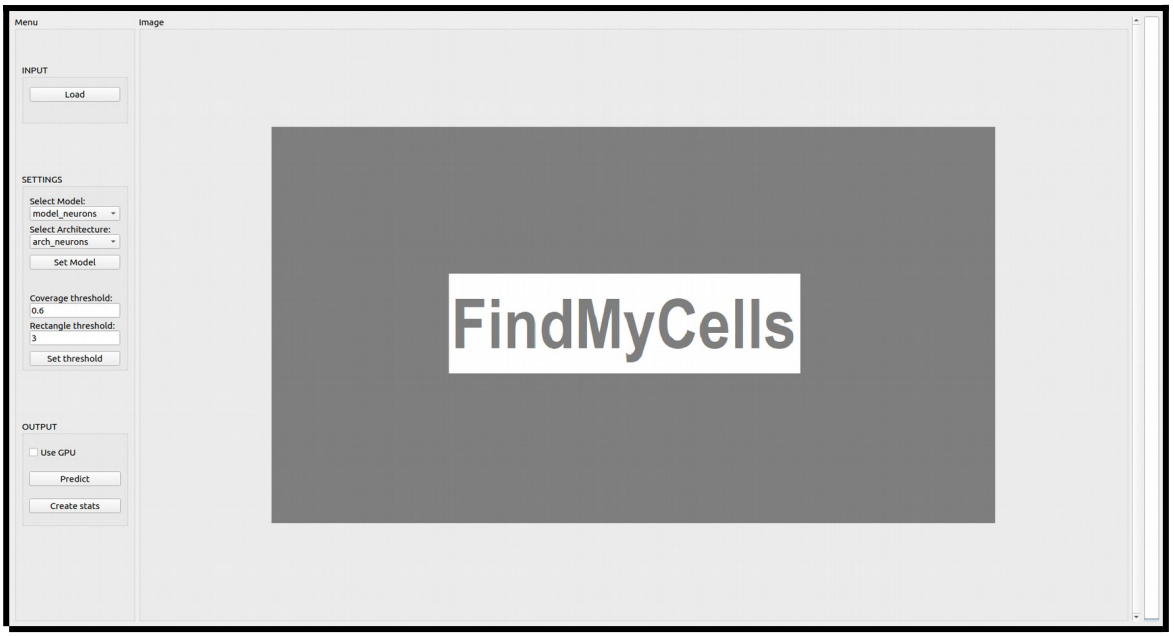
- Required Python packages (*pip install*):
    - PyQt5
    - PIL

Running the software:

To run the software from terminal:

- Go to the root directory
- Run the software with the simple *./run.sh* command (You might need to give permission to this file: *chmod a+x run.sh*)

User Interface:



Load button:
FindMyCells (FMC) loads in the selected images. The currently supported file formats are: jpg, jpeg, png, tif and tiff. By mouse scrolling the previous/next image will be shown.

Network scrollbars:
FMC uses *caffe*[1] based network model. In case of a new detection task, a trained *caffe* network architecture file (*prototxt*) and model/weights file (*caffemodel*) should be copied into **`AI/models/`**. These files can then be selected in the dropdown menus.

Coverage threshold:
A real number (between 0 and 1). It defines the threshold for recognizing an object. Larger number results more conservative detection.
Note: A negative threshold value will automatically be set back to the default value (0.6).

Rectangle threshold:
An integer number defining the threshold for the overlapping bounding boxes. Clustering grouped rectangles.
Note: If the number is lower than zero, then it will be set back to the default value (3).

Use GPU checkbox:
Check this box if You are using GPU (*caffe-gpu*), otherwise leave it unchecked. This will handle if the predictions are calculated on cpu or on gpu.

Predict button:
With the predict button the user can predict objects on the current image. Using the middle (scroll) button will reset the bounding boxes.

Output stat:
Creates a statistical report file results.csv in **`graphics/`** folder.

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1 Caffe is a deep learning framework, made by BAIR - http://caffe.berkeleyvision.org/

The fields in this report file contain six values, which are the following:

- Image Name: this filed will contain the full path to the predicted image
- Cell ID: each identified cell has a unique number as ID (it resets at each image)
- X1 & Y1: starting X and Y coordinates of the predicted bounding box
- X2 & Y2: ending X and Y coordinates of the predicted bounding box