**COVID-19 Outcome Prediction Guideline**

## Environment Building

### Python Environment

Install a python **3.6** environment using **conda**

### Packages

1. Install gdcm using command conda install -c conda-forge gdcm
2. Install majority of packages using command pip install -r requirements.txt
3. Install pytorch using command conda install pytorch-cpu==1.1.0 torchvision-cpu==0.3.0 cpuonly -c pytorch

Or follow this [link](https://pytorch.org/get-started/previous-versions/#conda-4) to install pytorch 1.1.0

1. Install pyradiomics from source using command git clone git://github.com/Radiomics/pyradiomics

For unix like systems (MacOSX, linux):

cd pyradiomics

python -m pip install -r requirements.txt

python setup.py install

python setup.py build\_ext --inplace

For Windows:

cd pyradiomics

python -m pip install -r requirements.txt

python setup.py install

1. (HELPER) If you run into problem described by this [link](https://github.com/Radiomics/pyradiomics/issues/592) when extracting features, you can replace the files in

“anaconda\envs\<env\_name>\lib\site-packages\radioimcs\”

with the corresponding files we provided in folder radiomics\_patch.

## Feature extraction pipeline usage

### Input

1. Place unsegmented dicom image series in a folder (e.g. <dcm>), and arrange the dicom series in the following way:

<dcm>

---<patient\_id>

------<study\_uid>

---------<series\_uid>

-------------000001.dcm

-------------000002.dcm

-------------..........

-------------000333.dcm

1. Convert segmentation mask images into PNG format, named them in a sequence of numbers (e.g. 000.png, 001.png, …, 332.png), and place them in another folder (e.g. <seg>) for segmentation, and arrange them in the following way:

<seg>

---<patient\_id>

------<study\_uid>

---------<series\_uid>

-------------000.png

-------------001.png

-------------.......

-------------332.png

### Execution

1. Open terminal in root directory (COVID-19\_predictor) of the prediction pipeline.
2. Activate the conda environment in the terminal.
3. Extract radiomics features using the following command:

python proc\_radiomic\_feature.py --dicom\_root <dcm> --lesion\_mask\_root <seg> --save\_root <save\_root>

### Output

1. Extracted features will be saved in the <save\_root> directory with file name: “final\_merge\_feature.csv”.

## Prediction Pipeline Usage

### Input

1. For radiomics-only models (Radiom), use command

python COVID-19\_prediction.py --radiomics\_data <save\_root\final\_merge\_feature.csv>

1. For models that include clinical symptoms, demographics and lab test results (RadioClinLab), you can prepare an additional CSV input, according to “example\_lab\_input.csv” (refer to the “units.txt” for units and meanings of the entries). This file should also be placed into the root directory of the prediction pipeline (COVID-19\_predictor\<lab\_input.csv>).
2. To use the “RadioClinLab” model, use the command line code

python COVID-19\_prediction --radiomics\_data <save\_root\final\_merge\_feature.csv> --lab\_data <lab\_input.csv>