**SimPlatform – Simulation Codes**

These simulation codes are adapted from the simulation used in the "Corona" paper: O. Solomon et al., "Deep Unfolded Robust PCA with Application to Clutter Suppression in Ultrasound," IEEE TMI, vol. 39, no. 4, pp. 1051–1063, 2020.

The code can be found at https://github.com/KrakenLeaf/CORONA/tree/master

There are three changes compared to the Corona code:

* The generated data are real-valued instead of complex.
* The tissue amplitude is higher (x2).
* Convolution uses circular boundary conditions.

**DataGen.py** contains a simple example to generate a simulation of 50 frames (T = 50), where the image size is defined by params['shape']=(128,128). In particular, the command sim.generate(T) will generate a different set each time it is executed.

The generated data follow the observation model: where corresponds to Sum, is the simulated Point Spread Function (PSF), is the ground truth (GT) for the bubbles and corresponds to Bubbles, T is the GT for the tissue (i.e., high-resolution tissue) and corresponds to Tissue, is the convolution operator with circular boundary conditions, and is Gaussian white noise.

X is generated to be sparse and T is generated to be low-rank (though not static). H is Gaussian. An example of data, normalized in amplitude, can be found in the file `\DRPCA\_Net\Data\_325Norm.mat` with the following correspondences:

- Y : Sum,

- HX : Bubbles,

- HT : Tissue,

- X : Bubbles2,

- T : Tissue2.

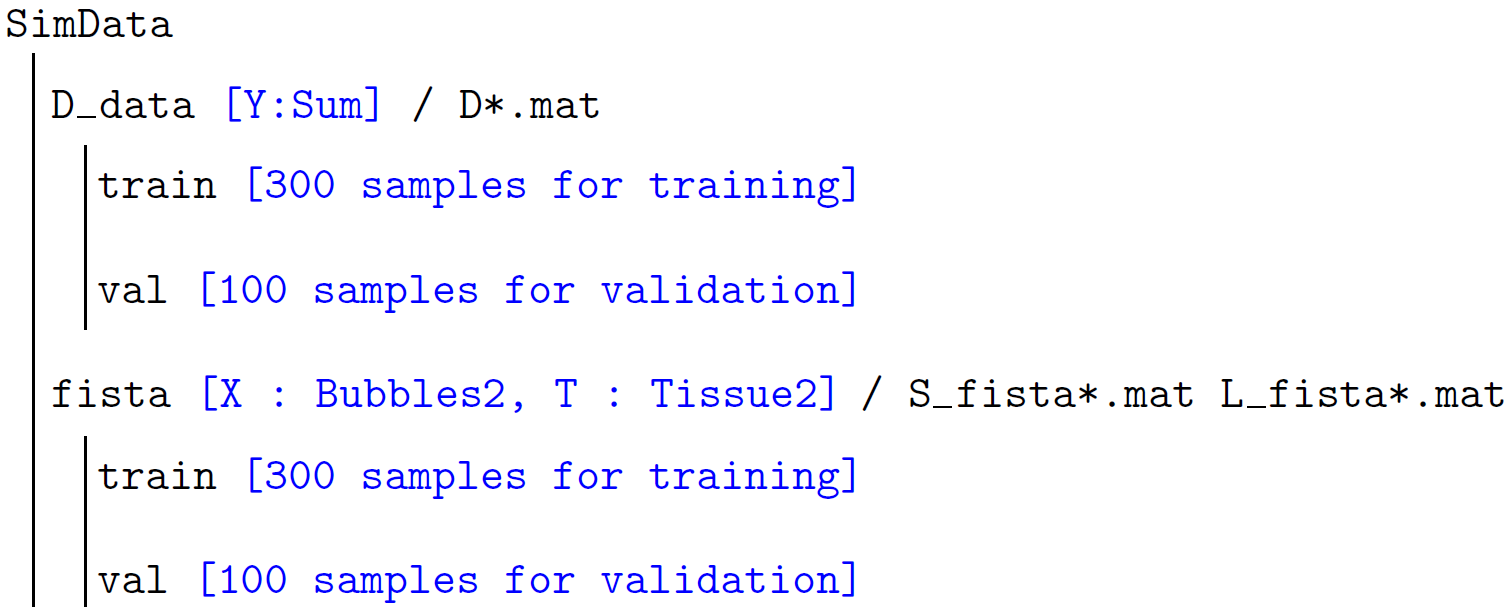
The noise can be obtained with N = Y – HX – HT.

The PSF H used for this data is found in the file `psf\_corona.mat` under the variable `[psf]`. Specifically, in Matab:

(Bubbles2, psf, 'conv', 'circ') = Bubbles and (Tissue2, psf, 'conv', 'circ') = Tissue.

The other Python (.py) files in the folder control the simulation parameters. Information about these parameters can be found in the Supplementary Materials associated with the Corona paper.

**SimData – SimulatedTrain/Test Datset**



The SimData folder contains 400 samples of data with dimensions 128x128x50, simulated using the SimPlatform code with the PSF found in the file psf\_corona.mat[psf]. There are 300 samples for training and 100 for validation. The observation data Y are located in the D\_data folder, and the corresponding ground truths are in the fista folder. The filenames used are the same as those in the Corona code to avoid having to rewrite the data loading functions.

**DRPCA\_Net**

This folder contains the codes associated with our "Deep Unfolding RPCA for High Resolution Flow Estimation", 2022 IEEE IUS paper. Specifically, it includes the network code, training and testing scripts, as well as the code for the metrics.

The network was trained and tested on the data contained in the SimData folder.