I just built a new computer and am unfamiliar with windows commands but am attempting to run HiCNN one more time! It sounds like people had success with using HiCARN as a vessel to use other models.

I first has to install [git](#) Then [docker](#).

1. Clone repository

```
git clone https://github.com/OluwadareLab/HiCARN.git && cd HiCARN
```

2. Pull docker image

```
docker pull oluwadarelab/hicarn:latest
```

3. Run the HiCARN container and mount the present working directory to the container

```
docker run --rm --gpus all -it --name hicarn -v ${PWD}:/workdir oluwadarelab/hicarn
```

This is mine: `root@f4adb5424896:/workspace#`

`cd` to your home directory.

Dependencies

- [Python 3.8](#)
- Pytorch 1.10.0, CUDA 11.3
- Numpy 1.21.1
- Scipy 1.7.0
- Pandas 1.3.1
- Scikit-learn 0.15.2
- Matplotlib 3.4.2
- tqdm 4.61.2

Preprocessing

I once again used the GM12878 primary chromosome.

In `Arg_Parser.py` set our root directory and then create a raw file to store raw data sets.

I placed my GM12878_primary into the raw directory. To read the raw data:

```
python Read_Data.py -c GM12878_primary
```

Then read the 50kb data:

```
python Read_data.py -c GM12878_primary -hr 50kb
```

Downsample:

```
python Downsample.py -hr 10kb -lr 50kb -r 16 -c GM12878_primary
```

Generate, train, validation, and test datasets

(Couldn't get this to work)