Good Afternoon Dr. ....,

I am a masters student at Auburn University. I am supervised by Dr. Bhattacharya. I am conducting research on HiC datasets. Specifically, I am looking at local differences between normal and leukemic cells. In my research I am using your datasets from the link below:

`http://sysbio.rnet.missouri.edu/T0510/tmp_download/link_to_download_genome_data/`

I am emailing you since I have a question that I haven't been able to resolve. I have been trying different normalization methods on HiC contact matrices that I have extracted from datasets in link above ; however, I haven't be able to reproduces contact files that are here:

`http://sysbio.rnet.missouri.edu/bdm_download/chromosome3d/unzipped/Input/HiC/`

I have tried sequential component normalization (SCN) and pearson correlation but the results are not as smooth and clean as the ones in the link above. For the sake of reproductibility, could you let me know how such normalizations were made on the original HiC contact maps? I would greatly appreciate your response since it will be a great help in my research.

Regards,

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`test.py`

I have been playing with HiC data some more. I have tried setting the values on and around the main diagonal to 0 and calc¡F9¿