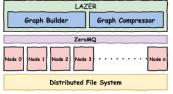
DEPARTMENT OF Computer Science

Computational Sciences based on AI and Supercomputers

- Whole & Meta genome sequence assembly and error correction software tools
 - LAZER (@SC16, Bigdata16), LaSAGNA (@IPDPS2018), ParLECH (@BIBM18)





 High throughput virtual screening AlphaFold, Docking.

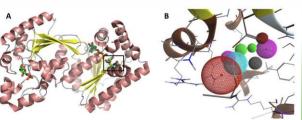
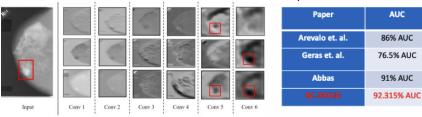
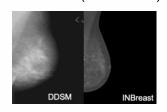


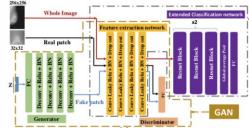
Fig. 4. Pharmacophore map used in PFKFB3 virtual screening

- Biomedical data analysis
 - ▶ Breast Cancer Diagnosis Using Deep Learning and Region of Interest Detection: BC-DROID (ACM BCB17)



➤ Deep Generative Breast Cancer Diagnosis with DDSM & INbreast datasets (MICCAI 18)





AUC

86% AUC

91% AUC

PoC

- Seung-Jong Jay Park, Professor & Chair
- E-Mail: seung-jong.park@mst.edu
- Website: https://sites.mst.edu/sjpark/
- Phone: 1-573-341-4531

Funding

- Funding agencies:
- NSF, NIH, DoD, NASA



Keywords:

Large-scale data analysis (for whole genome and meta genome sequence data), extreme-scale computation using supercomputers, Al-based biomedical data analysis (e.g., mammogram, ECG, fMRI, etc.).

Publications and Recognitions:

- Link to my publications
- · IBM faculty research award
- Kummer Endowed Professor

