SSBH 2023

The 11ᵗʰ Seoul Symposium on Bone Health
& the 35ᵗʰ Spring Scientific Congress of the Korean Society for Bone and Mineral Research

Meet the Expert 4

Dong-Guk Shin

Curriculum Vitae

Professor and Director, Bioinformatics and Bio-Computing Institute
University of Connecticut

● Educational Background & Professional Experience

2015-2016	JAX-GM, Senior Visiting Scientist
2004-	NIH Bioinformatics Study Section Reviewer
2000-	UConn, Professor, Computer Science Engineering
2000	Invited Speaker, National Academy of Sci., NRC Bioinformatics Workshop
1993-1994	Johns Hopkins, Visiting Faculty, Genome Data Base
1992-1999	UConn, Associate Professor, Computer Science Engineering
1986-1992	UConn, Assistant Professor, Computer Science Engineering

● Research Interests

Biomedical data mining has been my research passion for the past 25 years which started with my sabbatical leave at Genome Data Base (GDB), Johns Hopkins University (1993) with my first NIH R01 funding as a computer scientist. In 2003, I established the Bioinformatics and Bio-Computing Institute (BIBCI) at UCONN with the NIGMS planning grant. Since then, I have been working with numerous biomedical scientists to help their biomedical data get analyzed. My bioinformatics data analysis utilizes molecular interaction relationships captured in the topology-based pathways. I began incorporating, namely, "route-based" analysis idea into the topological pathway diagrams and I developed a user-friendly pathway scoring and visualization system, called TOPAS. Lately, my research focuses on mining of high-throughput multi-omics data sets at single cell level.

● Publications

1. Wang H, Joshi P, Hong SH, Maye PF, Rowe DW, Shin DG. Predicting the targets of IRF8 and NFATc1 during osteoclast differentiation using the machine learning method framework cTAP. BMC Genomics. 2022 Jan 7;23(1):14. doi: 10.1186/s12864-021-08159-z. PMID: 34991467; PMCID: PMC8740472.

2. Rowe DW, Adams DJ, Hong SH, Zhang C, Shin DG, Renata Rydzik C, Chen L, Wu Z, Garland G, Godfrey DA, Sundberg JP, Ackert-Bicknell C. Screening Gene Knockout Mice for Variation in Bone Mass: Analysis by mCT and Histomorphometry. Curr Osteoporos Rep. 2018 Apr;16(2):77-94.

3. Becker T, Lee WP, Leone J, Zhu Q, Zhang C, Liu S, Sargent J, Shanker K, Mil-Homens A, Cerveira E, Ryan M, Cha J, Navarro FCP, Galeev T, Gerstein M, Mills RE, Shin DG, Lee C, Malhotra A. FusorSV: an algorithm for optimally combining data from multiple structural variation detection methods. Genome Biol. 2018 Mar 20; 19(1):38. doi: 10.1186/s13059-018-1404-6. PMID: 29559002.

4. Hong SH, Jiang X, Chen L, Josh P, Shin DG, Rowe D. Computer-Automated Static, Dynamic and Cellular Bone Histomorphometry. J Tissue Sci Eng. 2012 Dec 24;Suppl 1:004.

5. Shin, D-G., Kazmi, S., Baikang, P. Kim, Y-A., Maddox, J., Nori. R. Wong, A., Krueger, W., and Rowe, D. (2009). "Computing Consistencies between Microarray Data and Known Gene Regulation Relationships", IEEE Transactions on Information Technology in Biomedicine, 13(6):1075-82, 2009. PMID: 19783507.