CURRICULUM VITAE
Sael Lee

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1 Gwanak-ro, Gwanak-gu,
Seoul, Republic of Korea 08826

Pen name: **Lee Sael**
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RESEARCH INTERESTS

Bioinformatics, Data Mining, and **Machine Learning:** focusing on development of methods and algorithms for mining and inferring biological data of various types (**variety**), both small and large sizes (**volume**), with the emphasis on improved explainability (**interpretability**) to solve various problems for realizing **precision medicine**.

EDUCATION HISTORY

Purdue University, West Lafayette, IN
    Ph. D., Computer Science   Aug. 2005 – Aug. 2010
Korea University, Seoul, Republic of Korea
    Bachelor of Science, Computer Science   Mar. 2000 – Feb. 2005

AWARDS & FELLOWSHIPS

Best Paper Award (runner up) 6th International Conference on Emerging Databases (EDB)   2016
Best Poster Award International Conference on Structure Genomics 2011   May 14, 2011
Best Paper Award The 21th International Conference on Genome Information (GIW)   Dec. 18, 2010
Grace Hopper Scholarship sponsored by the National Science Foundation   2008

RESEARCH EXPERIENCE

BK Associate Professor
    Department of Computer Science and Engineering, Seoul National University   Mar. 2018 – Present
    1 Gwanak-ro, Gwanak-gu, Seoul, Republic of Korea 08826
Assistant Professor   Sept. 2012 – Feb. 2018
    BioData Mining Lab
    Department of Computer Science, **State University of New York Korea**
    119 Songdo Moonwha-ro, Yeonsu-Gu, Incheon, Korea 21985
Research Staff Member   Sept. 2011 – Aug. 2012
    Future IT Research Center, **Samsung Advanced Institute of Technology**
    Giheung-gu, Yougin-si, Gyeonggi-do, Korea
Postdoctoral Research Associate   Sept. 2010 – Aug. 2011
    Bioinformatics Laboratory (P.I. Dr. Daisuke. Kihara)
    Purdue University, West Lafayette, IN
    Funding sources: National Science Foundation (DMS800568, IIS0915801, EF0850009)
Research Assistant   Aug. 2006 – Aug. 2010
    Bioinformatics Laboratory (P.I. Dr. Daisuke. Kihara)
    Purdue University, West Lafayette, IN
    Funding source: National Institute of General Medical Sciences of the NIH (R01 GM075004)

PUBLICATIONS

<u>PH. D. THESIS</u>

    Title: "High throughput screening of global and local protein surfaces"
    Acceptance date: Aug. 7, 2010
    Advisor Committee: Daisuke Kihara (Chair), Michael Gribskov, Robert Skeel, Mikhail Atallah, and Lou Si

PEER REVIEWED JOURNAL PUBLICATIONS (using name Lee Sael)

[26] J. Lee, S. Oh, and **L. Sael**, "GIFT: Guided and Interpretable Factorization for Tensors with an Application to Large-Scale Multi-platform Cancer Analysis," **Bioinformatics**, vol. bty490, Jun. 2018. (SCI Q1; top 2.6%; IF=7.307)

[25] Thomas, J., and **Sael, L.** (2017). Multi-Kernel LS-SVM based integration bio-clinical data analysis and application to ovarian cancer. International Journal of Data Mining and Bioinformatics (IJDMB), 19(2) 150-166. (SCIE Q4; IF=0.624)

[24] Shin, K., **Sael, L.,** & Kang, U. (2017). Fully Scalable Methods for Distributed Tensor Factorization. IEEE Transactions on Knowledge and Data Engineering (**TKDE**) 29(1), 100–113. (SCI Q1; top 14.0%; IF=3.438)

[23] Thomas, J., Seo, D., & **Sael, L**. (2016). Review on graph clustering and subgraph similarity based analysis of neurological disorders. International Journal of Molecular Sciences (IJMS), 17(6), 862. (SCIE Q2; top 32.2%; IF=3.226)

[22] Jung, J., Shin, K., **Sael, L**., & Kang, U. (2016). Random walk with restart on large graphs using block elimination. ACM Transactions on Database Systems (**TODS**) 41(2): 1–43. (SCI Q2; top 47.6%; IF=1.517)

[21] Jeon, I., Papalexakis, E. E., Faloutsos, C., **Sael, L**, Kang, U. (2016). Mining billion-scale tensors: algorithms and discoveries. The **VLDB Journal**, 1-26. (SCI Q1; top 5.1%; IF=4.269)

[20] Kim, S., **Sael, L**., & Yu, H. (2015). A mutation profile for top-k patient search exploiting Gene-Ontology and orthogonal non-negative matrix factorization. **Bioinformatics**, 31(22), 3653-3659. (SCI Q1; top 2.6%; IF=7.307)

[19] Kim, S., **Sael, L.,** & Yu, H. (2015). LMDS-based approach for efficient top-k local ligand-binding site search. International Journal of Data Mining and Bioinformatics (IJDMB), 12(4), 417–433. (SCIE Q4; IF= 0.624)

[18] **Sael, L**., Jeon, I., & Kang, U. (2015). Scalable tensor mining. Big Data Research, 2(2), 82–86.

[17] Pi, J., **Sael, L.** (2013) Mass spectrometry coupled experiments and protein structure modeling methods. International Journal of Molecular Sciences, 14:10, 20635-20657. (SCIE Q2; top 32.2%; IF=3.226)

[16] Kim, S., **Sael, L.,** Yu, H. (2013). Efficient protein structure search using indexing methods. BMC Medical Informatics and Decision Making, 13 (Suppl 1), S8   (SCIE Q2; IF=1.496).

[15] Mullins, E. A., Starks, C. M., Francois, J. A., **Sael, L.**, Kihara, D., & Kappock, T. J. (2012). Formyl-coenzyme A (CoA):oxalate CoA-transferase from the acidophile Acetobacter aceti has a distinctive electrostatic surface and inherent acid stability. **Protein Science**, 21:5, 686-696. (SCI Q3; IF=2.735)

[14] **Sael, L.**, Chitale, M., & Kihara, D. (2012). Structure and sequence-based function prediction for non-homologous proteins. Journal of Structural and Functional Genomics, 13:111-123.

[13] **Sael**, **L.,** & Kihara, D. (2012). Detecting local ligand-binding site similarity in non-homologous proteins by surface patch comparison. **Proteins**: Structure, Function, and Bioinformatics, 80:4, 1177-1195. (SCI Q2; IF=3.337)

[12] **Sael**, **L.,** & Kihara, D. (2012). Constructing patch-based ligand-binding pocket database for predicting function of proteins. **BMC Bioinformatics**, 13(Suppl 2):S7.

[11] Kihara, D., **Sael**, **L.,** Chikhi, R., & Esquivel-Rodriguez, J. (2011). Molecular surface representation using 3D Zernike descriptors for protein shape comparison and docking. Current Protein and Peptide Science, 12:6, 520-530.*(SCIE Q2; IF=2.886)*

[10] **Sael, L.** (2011). Structural bioinformatics and application to future drug design evolution. Communications of KIISE, 29:4, 26-32.

[9] Chikhi, R., **Sael**, **L.,** & Kihara, D. (2010). Real-time ligand binding pocket database search using local surface descriptors. **Proteins**: Structure, Function, and Bioinformatics, 78:9, 2007-2028. (SCI Q2; IF=3.337)

[8] **Sael**, **L.,** & Kihara, D. (2010). Binding ligand prediction for proteins using partial matching of local surface patches. International Journal of Molecular Sciences, 11:12, 5009-5026.

[7] **Sael**, **L.,** & Kihara*, D.* (2010). Improved protein surface comparison and application to low-resolution protein structure data. **BMC Bioinformatics**, 11 (Suppl 11): S2, 1-12. *GIW2010 - BEST PAPER AWARD*

[6] **Sael**, **L.,** & Kihara*, D.* (2010). Characterization and classification of local protein surfaces using self-organizing map. International Journal of Knowledge Discovery in Bioinformatics, 1:1, 32-47

[5] La, D., Esquivel, J., Venkatraman, V., Li, B., **Sael**, **L.,** Ueng, S., Ahrendt, S., & Kihara, D. (2009). 3D-SURFER: software for high-throughput protein surface comparison and analysis. **Bioinformatics***, 25:21, 2843-2844. (SCI Q1; IF=5.766)

[4] Venkatraman, V., **Sael, L.,** & Kihara, D. (2009). Potential for protein surface shape analysis using spherical harmonics and 3D Zernike descriptors. Cell Biochemistry and Biophysics, 54:1-3, 23-32. (SCIE Q2; IF=3.337)

[3] Venkatraman, V., Yang, Y., **Sael, L.,** & Kihara, D. (2009). Protein-protein docking using region-based 3D Zernike descriptors. **BMC Bioinformatics**, 10:407, 1-21. (SCIE Q1; IF=3.024)

[2] **Sael**, **L.,** La, D., Li, B., Rustamov, R., & Kihara, D. (2008). Rapid comparison of properties on protein surface. **Proteins**: Structure, Function, and Bioinformatics, 73:1, 1-10. (SCI Q2; IF=3.337)

[1] **Sael**, **L.,** Li, B., La, D., Fang, Y., Ramani, K., Rustamov, R., & Kihara, D. (2008). Fast protein tertiary structure retrieval based on global surface shape similarity. **Proteins**: Structure, Function, and Bioinformatics, 72:4, 1259-1273. (SCI Q2; IF=3.337)

CONFERENCE PROCEEDINGS (using name Lee Sael)

[14] Oh, S., Park, N., **Sael, L**., & Kang, U., (2017) Scalable Tucker Factorization for Sparse Tensors - Algorithms and Discoveries. In 34th IEEE International Conference on Data Engineering (**ICDE** 2018). **(BKCS0051 IF=2)**

[13] Thomas, J., Thomas, S., **Sael, L.** (2017) DP-miRNA: An Improved Prediction of precursor microRNA using Deep Learning Model. BIGCOMP 2017. Jeju, Korea.

[12] Jung, J., Park, N., **Sael, L** and Kang, U. (2017) BePI: Fast and Memory-Efficient Method for Billion-Scale Random Walk with Restart. In Proceedings of the 2017 ACM **SIGMOD** International Conference on Management of Data. Chicago, USA; ACM Press. **(BKCS0017 IF=4)**

[11] Thomas, J., & **Sael, L**. (2016). Maximizing information through multiple kernel-based heterogeneous data integration and applications to ovarian cancer. In 6th International Conference on Emerging Databases. ***BEST PAPER*** (Runner-Up)

[10] Jung, J., Jin, W., **Sael, L.,** & Kang, U. (2016) Personalized ranking in signed networks using signed random walk with restart. In IEEE International Conference on Data Mining (**ICDM 2016**). **(BKCS0043 IF=2)**

[9] Jeon, B., Jeon I., **Sael, L.**, & Kang, U. (2016) SCouT: Scalable coupled matrix-tensor factorization - Algorithm and Discoveries. In 32nd IEEE International Conference on Data Engineering (**ICDE** 2016). **(BKCS0051 IF=2)**

[8] Thomas, J., & **Sael, L.** (2015). Overview of integrative analysis methods for heterogeneous data. In 2015 International Conference on Big Data and Smart Computing (BIGCOMP) (pp. 266–270).

[7] Shin, K., Jung, J., **Sael, L**., & Kang, U. (2015). BEAR: Block elimination approach for random walk with restart on large graphs. In Proceedings of the 2015 ACM **SIGMOD** International Conference on Management of Data. Melbourne, Victoria, Australia: ACM. (pp. 1571-1585) **(BKCS0017 IF=4)**

[6] Kang, D., Lim, W., Shin, K., **Sael, L**., & Kang, U. (2014). Data/Feature Distributed Stochastic Coordinate Descent for Logistic Regression. In Proceedings of the 23rd International Conference on Information and Knowledge Management (**CIKM** 2014). Shanghai, China: ACM. **(BKCS0027 IF=2)**

[5] Kim, S., **Sael, L**., & Yu, H. (2014). Identifying cancer subtypes based on somatic mutation profile. In Proceedings of the 8th International Workshop on Data and Text Mining in Biomedical Informatics - DTMBIO'14. Shanghai, China: ACM.

[4] Coelho, D., & **Sael, L** (2013). Breast and prostate cancer expression similarity analysis by iterative SVM based ensemble gene selection. In Proceedings of the 7th International Workshop on Data and Text Mining in Biomedical Informatics - DTMBIO '13 (pp. 23–26). San Francisco, USA: ACM.

[3] Kim, S., **Sael, L.,** & Yu, H. (2013) Efficient local ligand-binding site search using landmark MDS. Proceedings of the 7th International Workshop on Data and Text Mining in Biomedical Informatics – DTMBIO'13. San Francisco, USA: ACM.

[2] Kim, S., **Sael, L.,** & Yu, H. (2013) Fast protein 3D surface search. Proceedings of the 7th International Conference on Ubiquitous Information Management and Communication - ICUIMC'13 (pp. 1–8). Kota Kinabalu, Malaysia: ACM.

[1] Kim, S., **Sael, L.**, & Yu, H. (2012). Indexing methods for efficient protein 3D surface search. In Proceedings of the ACM 6th International Workshop on Data and Text Mining in Biomedical informatics - DTMBIO '12 (p. 41). New York, New York, USA: ACM.

ARCHIVED/ IN REVIEW / IN DRAFT

[7] Lim, Y., Yu, I., Seo, D. Kang, U, & **Sael, L.** (2018) PS-MCL: Parallel Shotgun Coarsened Markov Clustering of Protein Interaction Networks. (in submission)

[6] Dehiya, V., & **Sael, L.** (2017). Impact of structural prior knowledge in mutation prioritization: Towards causal variant finding in rare disease. (PLOS ONE - in review)

[5] Lee, J., Choi, D., & **Sael, L.** (2017). CTD: Fast, Accurate, and Interpretable Method for Static and Dynamic Tensor Decompositions. arXiv:1710.03608. (PLOS ONE – in review)

[4] Choi, D. & **Sael, L.** (2017). SNeCT: Integrative cancer data analysis via large scale network constrained tensor decomposition. arXiv:1711.08095 (in submission)

[3] Thomas, J., Thomas, S. & **Sael, L.** (2017). Feature versus Raw Sequence: Deep Learning Comparative Study on Prediction of Precursor microRNA. arXiv:1710.06798. (in submission)

[2] Thomas, J., & **Sael, L.** (2017). Deep Neural Network Based Precursor microRNA Prediction on Eleven Species. arXiv:1704.03834.

[1] Vo, Q. D., Thomas, J., Cho, S., De, P., Choi, B. J., & **Sael, L.** (2017). Next Generation Business Intelligence and Analytics: A Survey. arXiv:1704.03402

BOOK CHAPTERS (using name Lee Sael)

[4] Xiong, Y., Esquivel-Rodriguez, J., **Sael, L.,** & Kihara, D. (2014). 3D-SURFER 2.0: Web platform for real-time search and characterization of protein surfaces. Methods in Molecular Biology, 1137, 105–117.

[3] Tang, M., Tan, K. M., Tan, X. L., **Sael, L**., Chitale, M., Esquivel-Rodríguez, J., & Kihara, D. (2013). Graphical models for protein function and structure prediction. In M. Elloumi & A. Y. Zomaya (Eds.), Biological Knowledge Discovery Handbook: Preprocessing, Mining, and Postprocessing of Biological Data (pp. 191-222).. Hoboken, New Jersey: John Wiley & Sons, Inc.

[2] Chikhi, R., **Sael, L.,** & Kihara, D. (2011). Protein binding ligand prediction using moment-based methods. In D. Kihara (Ed.), Protein Function Prediction for Omics Era (pp. 145–163). Dordrecht: Springer Netherlands.

[1] **Sael, L.**, & Kihara, D. (2009). Protein surface representation and comparison: New approaches in structural proteomics. In J. Y. Chen & S. Lonardi (Eds.), Biological Data Mining (pp. 89–109). USA: Chapman & Hall/CRC Press

CONFERENCE PRESENTATIONS (**selected** posters or orals at conferences that do not have proceedings)

[6] (poster) **Sael Lee**, J. Thomas, Y. Shin, H. Yoon, Y. Park. "Data Mining Bio-clinical Data." at World IT Show, May 17-20, 2016, Seoul, Korea.

[5] (*poster*) **Sael, L.,** & Kihara, D. "Binding ligand prediction by comparing local surface patches of potential pocket regions." at International Conference on Structural Genomics, May 10-14, 2011, Toronto, Canada. ***BEST POSTER***

[4] *(poster)* **Sael, L.,** & Kihara, D. (2011). Local Protein Surface Patch Method for Protein-Ligand Binding Prediction. BIOPHYSICAL JOURNAL 100, 3, 1: 394. (Mar. 5-6, 2011, 55th Annual Meeting of the Biophysical-Society Location: Baltimore, MD)

[3] *(poster)* **Sael. L.**, Esquivel-Rodriguez, J., & Kihara, D. (2011). Novel Methods for Rapid Comparison and Multimeric Protein Complex Fitting for Low-Resolution Electron Microscopy Data. BIOPHYSICAL JOURNAL 100, 3, 1: 323. (Mar. 5-6, 2011, 55th Annual Meeting of the Biophysical-Society Location: Baltimore, MD)

[2] (*oral*) **Sael, L.,** & Kihara, D. "Patch-Surfer: Alignment free surface patch-based ligand binding pocket comparison." at Great Lakes Bioinformatics Conference 2011, May 2-4, 2011, Ohio University, Athens, Ohio

[1] *(oral)* **Sael, L.,** & Kihara, D. "Improved protein surface comparison and application to low-resolution protein structure data." The 21st International Conference on Genome Informatics, Hangzhou, China, December 16-18, 2010

PATENTS

[1] Dong-Min Seo, Seok-Jong Yu, Min-Ho Lee, U kang, Yong-Sub Lim, In-Jae Yoo, **Sael Lee**. "Method and Apparatus for Network Clustering" Korean patent number: 10-2016-0101611, filed 10 Aug 2016.

CURRENT/PAST RESEARCH GRANTS

[6] PI: [2015.11-2018.10] *Basic Science Research Program*, "Development of Multi-layer Network Analysis Methods for Integrative Analysis Algorithms of Bio-Clinical Data" funded through the National Research Foundation of Korea (NRF) funded by the Ministry of Science, ICT and Future Planning (NRF-2015R1C1A2A01055739).

[5] PI: [2015.06- 2018.02] *Global ATC Program* "Development of business intelligence platform service which enables a non-expert to realize 'Data Processing and User Interface' within 3 seconds in Petabyte level based on 0.5 billion data (10053204) " funded by Korea Evaluation Institute of Industrial Technology, Republic of Korea.

[4] Co-PI: [2015.03-2015.08] "Development of biomedical data network analysis technology based on high performance computing for dementia researches (K-15-L03-C02-S01)" funded by Korea Institute of Science and Technology Information.

[3] PI: [2012.06-2015.05] *Basic Science Research Program,* funded through the National Research Foundation of Korea (NRF) funded by the Ministry of Science, ICT and Future Planning (2013005259)

[2] Co-PI: [2012.09-2018.02] *IT Consilience Creative Program* (NIPA-2013-H0203-13-1001), supported by the MSIP (Ministry of Science, ICT and Future Planning), Korea, supervised by the NIPA (National IT Industry Promotion Agency)

[1] Co-PI: [2012.09-2014.08] *Global Research Network Program* funded through Ministry of Education and Science Technology, Republic of Korea: "Development of RAVAT: the tool that uncovers the roles of rare variants and their functions on common diseases with next generation sequencing data." (20120910)

TALKS

<u>TUTORIALS</u>

[5] Sael Lee, "Tutorial on AI/ML/DL." *The Korean Institute of Broadcast and Media Engineers (KIBME) Spring Workshop* May 31, 2018. Seoul Korea.

[4] Sael Lee, "AI/Machine Learning/Deep Learning Tutorial and Current Research Trends." *Open Standards and Internet Associations (OSIA) Workshop* Nov. 30, 2017. Seoul, Korea .

[3] Sael Lee, "Interpretable Deep Learning and Applications to Bio-healthcare." *Open Standards and Internet Associations (OSIA) Workshop* June 30, 2017. Konkuk University.

[2] Sael Lee. "Deep Learning in BioHealth: Detailing Interpretability." Korean Computer Congress 2017, Jeju Island, Korea. June 18-20, 2017.

[1] Sael Lee. "Mining and Learning Bio-Big Data." Bioinformatics & Machine Learning for Life Scientists Workshop, Seoul National University, Korea, Feb. 16, 2017.

<u>INVITED CONFERENCE/WORKSHOP SPEAKER</u>

[9] Sael Lee, "Scalable Network Constrained Tensor Mining." Korea AI Society Workshop jointly held with ACML 2017. Seoul, Korea.

[8] Sael Lee, "Scalable Tensor Factorization and Applications in Bioinformatics." GIW/BIOINFO 2017. Seoul, Korea.

[7] Sael Lee, "Deep learning applications published in my favorite journals." Annual Korean Society for Bioinformatics Conference, Aug. 18, 2016. Incheon Global Campus.

[6] Sael Lee, "Orthogonal NMF-based Top-K Patient Mutation Profile Searching." Current Trends in AI Workshop, June 29, 2016. Jeju, Korea.

[5] Sael Lee, "Using functional information to prioritize single nucleotide polymorphisms." Conference on BioMedical Informatics. Nov. 12, 2013. Busan, Korea.

[4] Sael Lee, "Towards Computational Screening of Global and Local Protein Surface for Drug Discovery." jCB Symposium on Frontier in Structural Biology of Cells and Molecules. Dec. 7, 2012. Incheon, Korea.

[3] Sael Lee, "AI in the Clinics: Clinical Decision Support System." Annual Conference of BioMedical Society. Nov. 23, 2012. Ohsong, Korea.

[2] Sael Lee, "Drug development in the perspective of structural bioinformatics." Korea Information Processing Society Biomedical and Information Technology Workshop, Dec. 13, 2011. Korea University, Seoul, Korea

[1] Sael Lee, "Structural Bioinformatics." NewDB Workshop, Sept. 24, 2011, National Information Society Agency (NIA).

<u>INVITED SEMINARS</u> (selected)

[10] Sael Lee, "Tensor Based Multiplatform Biodata Analysis." SNU Bioinformatics Seminar, May 24, 2018. Seoul National University, Seoul Korea.

[9] Sael Lee, "Machine Learning for Bio-medical Data Analysis - Towards Precision Medicine." ETRI, Daejeon, Korea

[8] Sael Lee, "Machine Learning for Bio-medical Data Analysis towards Healthcare and Precision Medicine." Computer Science Graduate Seminar, June 22, 2017. Hanyang University, Seoul, Korea.

[7] Sael Lee, "Discovering the Challenges and Solving the Problems in Bio-medical Data Analysis." Computer Science Graduate Seminar, March 28, 2017. Korea University, Seoul, Korea.

[6] Sael Lee, "Studies in protein binding site conservation for identifying recognition patterns of molecules." Open BioHealth Data Pseudonymization and Analytics Seminar Jan. 6, 2014. Kyungpook National University, Daegu, Korea.

[5] Sael Lee, "Computational Biology Applications to Drug Development." CiTE Seminar. Nov. 5, 2013. POSTECH, Pohang, Korea.

[4] Sael Lee, "Genomic difference between you and me: single nucleotide polymorphisms." Nov. 6, 2013. POSTECH, Pohang, Korea.

[3] Sael Lee, "Computational Biology Applications to Drug Development." Computer Science Graduate Seminar. April 4, 2013. Seoul National University, Seoul, Korea.

[2] Sael Lee, "Exploring Data Driven Science: Computational Pharmacology & Translational Bioinformatics." Computer Science Graduate Seminar. Feb, 22, 2013. Stony Brook University, NY, USA.

[1] Sael Lee, "Predicting Protein Function by Surface Comparison." Statistical Bioinformatics Seminar Series, February 15, 2011. Purdue University, Indiana, USA.

TEACHING EXPERIENCE

Undergraduate/ Graduate Core Courses

CSE 214 Computer Science II (Data Structure),	SUNY Korea
CSE 305 Principles of Database Systems,	SUNY Korea
CSE 373 Analysis of Algorithms,	SUNY Korea
CSE 532 Theory of Database Systems,	SUNY Korea
CSE 537 Artificial Intelligence,	SUNY Korea
CSE 548 Analysis of Algorithms,	SUNY Korea
CSE 549 Computational Biology,	SUNY Korea

Project/Seminar Courses

CSE 600: Topics in Modern Computer Science,	SUNY Korea
CSE 646: Seminar on Artificial Intelligence,	SUNY Korea
CSE 523 Advanced Project in Computer Science I,	SUNY Korea
CSE 524 Advanced Project in Computer Science II,	SUNY Korea

Special Courses

Basic Math for Big Data	SNU 4th Industrial Revolution Academy (SNU FIRA)

PROFESSIONAL SERVICES

Member of board of directors:

KIISE Artificial Intelligence Society	2013 – present
Korean Society for Bioinformatics (KSBI)	2015 – present
KIISE Database Society of Korea	2016 – present

Guest editor:

Journal of Bioinformatics and Computational Biology (JBCB)	2017

Local chair:

Annual Korean Society for Bioinformatics Conference (BIOINFO2016)	2016

Organizing committee:

2017 Korean AI Research Council Workshop **"AI for Everyone"**	2017

Program committee:

World Wide Web Conference (**WWW**)	2018
Pacific-Asia Conference on Knowledge Discovery and Data Mining (**PAKDD**)	2018
ACM International Conference on Information and Knowledge Management (**CIKM**)	2017
International Conference on Genome Informatics (**GIW**) / BIOINFO	2017
Translational Bioinformatics Conference (**TBC**)	2015 – 2017
International Conference on Emerging Databases (EDB)	2016
Workshop on Current Trends in AI	2016
WWW 2014 Workshop on Big Graph Mining (BGM 2014)	2014
ACM International Workshop on Data and Text Mining in Biomedical Informatics (DTMBIO)	2012 – 2018

Session chair for many conferences and workshops	2012 – present

Reviewer for many journal and conferences, including the following:
Bioinformatics, BMC Bioinformatics, CIKM, RECOMB, IJMS, TBC, and DTMBIO.

ACADEMIC MEMBERSHIP

Member of Korean Institute of Information Scientists and Engineers (KIISE)	2012 – present
Member of International Society for Computational Biology (ISCB)	2011 – present
Member of Biophysical Society	2011 – 2015
Member of The Protein Society	2008 – 2015
Member of Association for Computing Machinery (ACM)	2004 – present