Seungchan Kim, Ph.D.

Director
CRI Center for Computational Systems Biology

Chief Scientist & Executive Professor
Department of Electrical and Computer Engineering
Roy G. Perry College of Engineering
Prairie View A&M University
Prairie View, TX 77446

Summary

I am a Chief Scientist and Executive Professor at the Department of Electrical and Computer Engineering and Director of CRI Center for Computational Systems Biology at the Prairie View A&M University (PVAMU), initiated by a generous funding from Texas A&M University Systems Chancellor Research Initiative (CRI) and Prairie View A&M University. Prior to this appointment, I was the Head of Biocomputing Unit and an Associate Professor at Integrated Cancer Genomics Division of Translational Genomics Research Institute (TGen; http://www.tgen.org). I have led computational systems biology research at the institute since 2003. I was also an Assistant Professor in the School of Computing, Informatics, Decision Systems Engineering (CIDSE) at the Arizona State University from 2004 till 2011.

My research interests include: 1) mathematical modeling of molecular networks, 2) development of computational methods to analyze high throughput multi-omics data to identify disease biomarkers, and 3) computational models to diagnose patients or predict patient outcomes, for example, disease subtypes or drug response. My research objective is to understand underlying mechanisms for the development and the molecular mechanisms of complex diseases such as cancer and neurological disorders.

Current research projects include the discovery of exosome biomarkers for early detection of pancreatic cancer (NCI sponsored, in collaboration with City of Hope), the biomarker discovery of bladder cancer subtypes (DoD CDMRP sponsored, in collaboration with Johns Hopkins Medical School), the discovery of exosome biomarkers for Parkinson's diseases (Michael J. Fox Foundation, in collaboration with Translational Genomics Research Institute), and the repurposing of chemotherapies for cancer to pulmonary hypertension (in collaboration with University of Pittsburgh Medical Center).

Education/Training

1989 – 1993	Seoul National University, Seoul, Korea B.S. in Agricultural Engineering
1993 - 1995	Seoul National University, Seoul, Korea M.S. in Agricultural Engineering Thesis: *Neural Network Modeling and Simulation of Fuzzy Control for Bread-baking Process*
1996 – 2001	Texas A&M University, College Station, TX Ph.D. in Electrical Engineering Thesis Advisor: Prof. Edward R. Dougherty

	Thesis: *A General Nonlinear Framework for the Analysis of Gene Interaction via Multivariate Expression Arrays* (Final Defense on Feb. 26th, 2001)
2001 – 2003	National Human Genome Research Institute of NIH, Bethesda, MD Cancer Genetics and Computational Biology

Experience

1996 – 1997	Research Assistant, Blackland Research Center, Temple, TX
1997 – 1998	Research Assistant, CAMDI Lab/Texas Center for Applied Technology, TEES, College Station, TX
1999 – 2001	Research Assistant, CAMDI Lab, Electrical Engineering, Texas A&M University, College Station, TX
May 2 – 19, 2000	Visiting Scholar, TICSP/Tampere University of Technology, Finland
June – Aug, 2001	TEES Research Engineer, Electrical Engineering, Texas A&M University, College Station, TX
Sept. 2001 – March 2003	Visiting Fellow, NIH/NHGRI/CGB, Bethesda, MD
Apr. 2003 – April 2011	Investigator, Computational Biology Division, Translational Genomics Research Institute, Phoenix, AZ
Aug. 2004 – May 2011	Assistant Professor, Dept. of Computer Science and Engineering, Arizona State University, Tempe, AZ
Sept. 2006 – Dec 2009	Affiliate Faculty, Dept. Biomedical Informatics, Arizona State University, Tempe, AZ
July 2008 – Dec. 2016	Adjunct Faculty, Mayo Clinic Cancer Center, Scottsdale, AZ
May 2011 – Dec. 2016	Associate Professor, Integrated Cancer Genomics Division, Translational Genomics Research Institute, Phoenix, AZ
May 2011 – Dec. 2016	Key faculty, Center for Evolutionary Medicine and Informatics, The Biodesign Institute at Arizona State University, Tempe, AZ
Dec 2016 – Dec 2020	Adjunct Faculty, Translational Genomics Research Institute, Phoenix, AZ
Dec 2016 – current	Chief Scientist and Executive Professor, Department of Electrical and Computer Engineering Director, Center for Computational Systems Biology, Prairie View A&M University, Prairie View, TX

Contribution to Science

I am well recognized in the field of Bioinformatics and Computational Systems Biology research both nationally and internationally, and I have published **more than 100 peer-reviewed articles with more than 5,000 citations**. My research interests include: 1) mathematical modeling of genetic regulatory networks, 2) computational methods to analyze multitude of high throughput genomic and proteomic data, annotated with other relevant clinical information to identify biomarkers, and 3) computational models to diagnose patients or predict patient outcomes, for example, disease subtypes or drug response. My studies have had a large influence on the development of computational tools to help biologists study underlying mechanisms for cancer development, which in fact have led to better understanding of the molecular mechanisms

behind cancer biology and biological systems. Some of my research have produced **two US patents (granted) with five additional US patent applications pending**.

Specifically, my research interest includes (See full bibliography at the end):

1. **Mathematical modeling of genetic regulatory networks** – This has been one of my main research areas since my PhD program. Starting with Boolean network modeling of gene regulations (Kim et al., Genomics 2000), I worked with my collaborator to extend it to Probabilistic Boolean networks (PBNs) (Shmulevich et al., Bioinformatics 2002), which introduces stochastic behavior to Boolean networks, a critical property in faithfully approximating gene regulations, and later also studied the relationships between PBNs and Markov chains. More recently, I have extended the network modeling and inference to context-specific genomic regulations, which lead to the development of computational algorithms to identify molecular contexts, infer context-specific gene set interactions. Most recently, I have developed a novel computational method, EDDY: Evaluation of Differential DependencY, which is capable of sensitive and specific identification of pathways with phenotype-specific dysregulation, i.e., rewiring of dependencies between genes in different conditions. In addition, I have published in more traditional network modeling approach (Goutsias and Kim, Biophys J. 2004) and network intervention (Verdicchio and Kim, EURASIP Bioinformatics and Systems Biology 2014).
    a. **Kim S**, Dougherty ER, Chen Y, Sivakumar K, Meltzer P, Trent JM, Bittner M. Multivariate measurement of gene expression relationships. Genomics. 2000 Jul 15;67(2):201-9. PubMed PMID: 10903845.
    b. Shmulevich I, Dougherty ER, **Kim S**, Zhang W. Probabilistic Boolean Networks: a rule-based uncertainty model for gene regulatory networks. Bioinformatics. 2002 Feb;18(2):261-74. PubMed PMID: 11847074.
    c. Goutsias J, **Kim S**. A nonlinear discrete dynamical model for transcriptional regulation: construction and properties. Biophys J. 2004 Apr;86(4):1922-45. PubMed PMID: 15041638; PubMed Central PMCID: PMC1304049.
    d. Verdicchio M, **Kim S**. Template-Based Intervention in Boolean Network Models of Biological Systems. EURASIP Bioinformatics and Systems Biology. 2014; 11.
    e. Ramesh A, Trevino R, VON Hoff DD, **Kim S**. Clustering context-specific gene regulatory networks. Pac Symp Biocomput. 2010;PubMed PMID: 19908396.
    f. Nasser S, Cunliffe HE, Black MA, **Kim S**. Context-specific gene regulatory networks subdivide intrinsic subtypes of breast cancer. BMC Bioinformatics. 2011 Mar 29;12 Suppl 2:S3. PubMed PMID: 21489222; PubMed Central PMCID: PMC3073183.
    g. Jung S, Verdicchio M, Kiefer J, Von Hoff D, Berens M, Bittner M, **Kim S**. Learning contextual gene set interaction networks of cancer with condition specificity. BMC Genomics. 2013 Feb 19;14:110. PubMed PMID: 23418942; PubMed Central PMCID: PMC3644282.
    h. Jung S, **Kim S**. EDDY: a novel statistical gene set test method to detect differential genetic dependencies. Nucleic Acids Res. 2014 Apr;42(7):e60. PubMed PMID: 24500204; PubMed Central PMCID: PMC3985670.
    i. Speyer G, Kiefer J, Dhruv H, Berens M, **Kim S.** (2016) Knowledge-Assisted Approach to Identify Pathways with Differential Dependencies. *Pacific Symposium on Biocomputing*, Jan. 2016, 21:33-44.
    j. Speyer G, Mahendra D, Tran HJ, Kiefer J, Schreiber SL, Clemons PA, Dhruv H, Berens M, **Kim S.** (2017) Differential Pathway Dependency Discovery Associated with Drug

Response across Cancer Cell Lines. *Pacific Symposium on Biocomputing*, Jan. 2017, 22:497-508.

k. Negi V, Yang J, Speyer G, Pulgarin A, Handen A, Zhao J, Tai YY, Tang Y, Culley MK, Yu Q, Forsythe P, Gorelova A, Watson AM, Al Aaraj Y, Satoh T, Sharifi-Sanjani M, Rajaratnam A, Sembrat J, Provencher S, Yin X, Vargas SO, Rojas M, Bonnet S, Torrino S, Wagner BK, Schreiber SL, Dai M, Bertero T, Al Ghouleh I, **Kim S**, Chan SY. Computational repurposing of therapeutic small molecules from cancer to pulmonary hypertension. *Sci Adv*. 2021 Oct 22;7(43):eabh3794. doi: 10.1126/sciadv.abh3794.

2. **Molecular classification of cancers** – Classification has emerged as a major area of investigation in bioinformatics due to the desire to discriminate phenotypes, in particular, disease conditions, using high-throughput genomic data. My initial research into classification was to develop a robust estimate of classification error for a small sample size data (Kim et al., 2002) by proposing a model-based error-estimation approach to identify strong feature sets. This approach inspired many other model-based approaches and rigorous studies of classification error estimation. Molecular classification studies called for various collaborations as the experimental validation of findings is critical, including lung cancer, lymphoma (Kobayashi et al. 2003), GBM (Joy et. al., 2014), and bladder cancer (Choi et. al., 2014).

   a. **Kim S**, Dougherty ER, Shmulevich I, Hess KR, Hamilton SR, Trent JM, Fuller GN, Zhang W. Identification of combination gene sets for glioma classification. Mol Cancer Ther. 2002 Nov;1(13):1229-36. PubMed PMID: 12479704.

   b. Kobayashi T, Yamaguchi M, **Kim S**, Morikawa J, Ogawa S, Ueno S, Suh E, Dougherty E, Shmulevich I, Shiku H, Zhang W. Microarray reveals differences in both tumors and vascular specific gene expression in de novo CD5+ and CD5- diffuse large B-cell lymphomas. Cancer Res. 2003 Jan 1;63(1):60-6. PubMed PMID: 12517778.

   c. Joy A, Ramesh A, Smirnov I, Reiser M, Misra A, Shapiro WR, Mills GB, **Kim S**, Feuerstein BG. AKT pathway genes define 5 prognostic subgroups in glioblastoma. PLoS One. 2014;9(7):e100827. PubMed PMID: 24984002; PubMed Central PMCID: PMC4077731.

   d. Choi W, Porten S, **Kim S**, Willis D, Plimack ER, Hoffman-Censits J, Roth B, Cheng T, Tran M, Lee IL, Melquist J, Bondaruk J, Majewski T, Zhang S, Pretzsch S, Baggerly K, Siefker-Radtke A, Czerniak B, Dinney CP, McConkey DJ. Identification of distinct basal and luminal subtypes of muscle-invasive bladder cancer with different sensitivities to frontline chemotherapy. Cancer Cell. 2014 Feb 10;25(2):152-65. PubMed PMID: 24525232; PubMed Central PMCID: PMC4011497.

   e. Zheng S, Cherniack AD, Dewal N, Moffitt RA, Danilova L, Murray BA, Lerario AM, Else T, Knijnenburg TA, Ciriello G, **Kim S**, Assie G, Morozova O, Akbani R, Shih J, Hoadley KA, Choueiri TK, Waldmann J, Mete O, Robertson AG, Wu HT, Raphael BJ, Shao L, Meyerson M, Demeure MJ, Beuschlein F, Gill AJ, Sidhu SB, Almeida MQ, Fragoso MC, Cope LM, Kebebew E, Habra MA, Whitsett TG, Bussey KJ, Rainey WE, Asa SL, Bertherat J, Fassnacht M, Wheeler DA; Cancer Genome Atlas Research Network, Hammer GD, Giordano TJ, Verhaak RG. Comprehensive Pan-Genomic Characterization of Adrenocortical Carcinoma. Cancer Cell. 2016 May 9;29(5):723-36. doi: 10.1016/j.ccell.2016.04.002. PubMed PMID: 27165744; PubMed Central PMCID: PMC4864952

3. **Identification of biomarkers and/or therapeutic targets for cancers** – High-throughput biological technologies offer the promise of finding biomarkers and therapeutic targets for cancers, a problem known as feature selection in machine learning; however, the number of

potential features in high-throughput biological data is far greater than that envisioned in the classical machine learning literature. So, a critical question is: how does the classification accuracy achieved with a selected feature set compare to the accuracy when the best feature set is. My research on a robust estimation of classification (described above) has played a significant role in this research area, hence, I have been involved in many collaborative researches to identify mRNA and miRNAs markers, many of which are now being followed up by other biological and clinical scientists.

a. Arora S, Ranade AR, Tran NL, Nasser S, Sridhar S, Korn RL, Ross JT, Dhruv H, Foss KM, Sibenaller Z, Ryken T, Gotway MB, **Kim S**, Weiss GJ. MicroRNA-328 is associated with (non-small) cell lung cancer (NSCLC) brain metastasis and mediates NSCLC migration. Int J Cancer. 2011 Dec 1;129(11):2621-31. PubMed PMID: 21448905; PubMed Central PMCID: PMC3154499.
b. Loftus JC, Ross JT, Paquette KM, Paulino VM, Nasser S, Yang Z, Kloss J, **Kim S**, Berens ME, Tran NL. miRNA expression profiling in migrating glioblastoma cells: regulation of cell migration and invasion by miR-23b via targeting of Pyk2. PLoS One. 2012;7(6):e39818. PubMed PMID: 22745829; PubMed Central PMCID: PMC3382150.
c. Baker A, Braggio E, Jacobus S, Jung S, Larson D, Therneau T, Dispenzieri A, Van Wier SA, Ahmann G, Levy J, Perkins L, **Kim S**, Henderson K, Vesole D, Rajkumar SV, Jelinek DF, Carpten J, Fonseca R. Uncovering the biology of multiple myeloma among African Americans: a comprehensive genomics approach. Blood. 2013 Apr 18;121(16):3147-52. PubMed PMID: 23422747; PubMed Central PMCID: PMC3630830.
d. Burgos KL, Javaherian A, Bomprezzi R, Ghaffari L, Rhodes S, Courtright A, Tembe W, **Kim S**, Metpally R, Van Keuren-Jensen K. Identification of extracellular miRNA in human cerebrospinal fluid by next-generation sequencing. RNA. 2013 May;19(5):712-22. PubMed PMID: 23525801; PubMed Central PMCID: PMC3677285.

4. **Statistical Pattern Recognition** – This research falls into more traditional statistical pattern recognition and machine learning research. In 2002, I have co-developed coefficient of determination for non-linear model which in the context of image processing, but later this was extended to network modeling and classification error estimation (Dougherty et al., 2000, Dougherty et. al., 2001). My initial research on model-based, robust error estimation (see Molecular Classification section) was later more formalized into Bayes error estimation (Brun et. al., 2003). Finally, integration of prior-knowledge into data analysis has been also my research area (Tari et. al., 2009), as proposed in the current application.

a. Dougherty E, **Kim S**, Chen Y. Coefficient of determination in nonlinear signal processing. Signal Processing. 2000; 80:2219-2235.
b. Kim S, Dougherty ER, Barrera J, Chen Y, Bittner ML, Trent JM. Strong feature sets from small samples. J Comput Biol. 2002;9(1):127-46. PubMed PMID: 11911798.
c. Brun M, Sabbagh DL, **Kim S**, Dougherty ER. Corrected small-sample estimation of the Bayes error. Bioinformatics. 2003 May 22;19(8):944-51. PubMed PMID: 12761056.
d. Tari L, Baral C, **Kim S**. Fuzzy c-means clustering with prior biological knowledge. J Biomed Inform. 2009 Feb;42(1):74-81. PubMed PMID: 18595779; PubMed Central PMCID: PMC2673503.

Teaching Experience

1. Undergraduate courses

a. ECE 300 (Fall 2004 – 42 students, Fall 2005 – 40 students) – Intermediate Engineering Design
b. CSE 463/598 (Spring 2007 – 21/1 students) – Introduction to Human Computer Interactions
c. CSE 310 (Spring 2008 – 34 students) – Data Structure
d. CSE 110 (Fall 2008 – 71 students) – Programming in Java
e. CSE 485/486/461/462 (Fall 2009, Spring 2010 – ~40 students) – Capstone Project

2. Graduate courses
   a. CSE 591 (Spring 2005, Spring 2006, Fall 2006, Fall 2007, Spring 2009) – Modeling and Analysis of Biological Interactions; Modeling and Inference Gene Regulatory Networks
   b. ELEG 6913-P24 ST: Computational Biology and Bioinformatics (Fall 2018, Spring 2021)
   c. ELEG 6380 Introduction to Bioinformatics (Spring 2023, Spring 2024)
   d. ELEG 6381 Advanced Bioinformatics (Fall 2023)

Honors & Awards

1. Sept. 1998 ASAE Transactions Honorable Mention Paper Award (M.S. Thesis paper)
2. Jan. 2000 Student Travel Award for SPIE Conference 2000, San Jose, CA
3. May 2002 AACR-AstraZeneca Scholarship-in-Training Award, Dublin, Ireland
4. Dec 2009 The Best Paper Award, 2009 IEEE-BIBM, Washington, DC

Mentoring

Graduate Advisors and Postdoctoral Sponsors	
Graduate Advisor	Edward Dougherty, PhD (Robert M. Kennedy '26 Chair, and Distinguished Professor of Electrical Engineering at Texas A&M University)
Post-doctoral advisor	Jeffery Trent, PhD (President and Research Director, Translational Genomics Research Institute)

Thesis Advisor and Postgraduate-Scholar Sponsor.	
Post-doctoral advisor	
Xishuang Dong, Ph.D.	Assistant Professor, Prairie View A&M University
Gil Speyer, Ph.D.	Research Assistant Professor, Translational Genomics Research Institute
Sungwon Jung, Ph.D.	Assistant Professor, Gwacheon Medical School, Korea
Sara Nasser, Ph.D.	Staff Scientist, Translational Genomics Research Institute
Taehoon Chung, Ph.D.	Research Associate, National University of Singapore
Ph.D. advisor	
Ina Sen, Ph.D.	Paypal, Inc.
Archana Ramesh, Ph.D.	Microsoft Research

Michael Verdicchio, Ph.D.	Associate Professor, The Citadel University

MS advisor

Siddharth Raghavan	
Zachary Henkel	Microsoft
Younghee Tak	
Neha Somani	
Siddarth G. Selvaraj, Ph.D.	CEO, Arima Genomics, Inc,
Sidharth Gupta	
Robert Trevino	US Air Force Research Laboratory (AFRL)

Undergraduate Research Mentor via Fulton Undergraduate Research Initiative	
James Long	Bioengineering
Christine Parsons	Bioengineering
Milad Behbahaninia	Bioengineering
Randall Noriega	Computer Science
Robert Fruchtman	Computer Science
Michael Verdicchio	Computer Systems Engineering
Robert Trevino	Computer Science

Professional Activities

Professional Societies

1. IEEE (formerly, the Institute of Electrical and Electronics Engineers, Inc)

   – Computer Society, Signal Processing

2. ISCB - International Society for Computational Biology

Journal Editor

- ***Associate Editor***
  1. *Frontiers in Plant Science; Computational Biology*
  2. *J. Biological Systems* (Oct 2013 – current)
  3. *EURASIP J. Bioinformatics and Systems Biology* (June 2007 – Dec. 2015)
  4. *Molecular Cancer Therapeutics* (Spring 2008 – Dec 2012)

- ***Guest Editor***
  1. *Current Genomics Special Issue on Genomic Signal Processing* (Summer 2008 – Fall 2009)

Journal Review

- ***Engineering/computer science/informatics journals***
  1. *IEEE Transactions on Signal Processing*
  2. *IEEE Transactions on Information Theory*
  3. *IEEE Transactions of Systems, Man and Cybernetics, Part A: Systems and Human (SMCA)*
  4. *Briefing in Bioinformatics*

5. *Bioinformatics*
6. *Journal of Computational Biology*
7. *Journal of Biological Systems*
8. *Journal of Biomedical Informatics*
9. *Journal of Signal Processing Systems*
10. *BMC Bioinformatics*
11. *PLoS Computational Biology*
12. *EURASIP Journal of Systems Biology and Bioinformatics*

- ***Biomedical journals***
  1. *Cancer Research*
  2. *Scientific Reports*
  3. *Molecular Cancer Therapeutics*
  4. *Genomics*
  5. *BMC Genomics*
  6. *Cancer Research*
  7. *PLoS ONE*

Conference Program Committee and Chair

1. GENSIPS (2001 – 2013) – Special Session Chair (2006), Publicity Chair (2008)
2. RECOMB-SB/RG/DREAM (2007-2015)
3. BIBM (2009-2015)
4. ACM BCB (2011)
5. ICMLA (2006-2010)
6. MLBB (2008)
7. BioKDD (2008)
8. RECOMB (2008)
9. BIBE (2008)
10. CSB (2007-2008)
11. PSB (2009)

Scientific Advisory Group/Board

1. Ontario Genomics Institute, Toronto, ON (Canada) (July 2009 – current) – serve as reviewer for scientific proposals submitted to the program coordinated by OGI and Ontario Ministry of Research and Innovation (MRI).

NIH Grant Review

1. ZRG1 BST-D 10 B (July, 2007; Nov., 2007) – SBIR/STTR Bioinformatics Software study section
2. ZRG1 BST-F (Oct. 2008) – Assays and Detectors study section
3. ZRG1 BST-D (50) (Feb. 2009) – TCNP bioinformatics core study section
4. ZRG1 BST-Q (01) (Mar. 2009, Jun. 2009) – R01 Software Update and Maintenance study section
5. ZRG1 BST-M (58) (CG) (Jun. 2009) – ARRA Challenge Grant special study section
6. ZRG1 IMST (Jun. 2009 – July 2021) – Various SBIR/STTR Bioinformatics Software study sections
7. BDMA (Oct. 2009) – Biological Data Management and Analysis study section
8. NLM-R01-K99 (Jan 2022)
9. NIDDK-B-K99 (Mar 2023, Oct 2023)

10. NLM-ZLM1 AS-C (July 2023)

NSF Grant Review

1. Bioinformatics and other informatics (2019)
2. Systems and Molecular Biology (2023)

Other Grant Review

1. PCORI (Aug. 2012, Oct. 2012)
2. OGI-BCB (Sept. 2012, Feb. 2016)
3. Phoenix Children Hospital (Feb 2016)
4. Academy of Finland (July 2016)
5. AIBS/INBRE Nevada (Feb. 2020, April/August/October 2021)
6. MJFF (June 2021)
7. INSERM-MIC (Mar 2022)

University Services (at Prairie View A&M University)

1. University
    a. Participated in The Quality Education in Minorities (QEM) ALC HBCU Research Action & Practice (RAP) Symposium on behalf of PVAMU (September 11-12, 2018 in Washington, DC)
    b. Search Committee for Director of Office of Sponsored Program (Jan 2018)
    c. Search Committee for Director of CRI International Food Security (Fall 2020 – Spring 2022)
    d. Limited Submission Review Committee (July 2018)
    e. Information Technology Governance Council (ITGC): Spring 2022 – current
    f. Review for PRISE grants (2021, 2022)
2. College
    a. Faculty Search Committee for Biomedical Informatics Program (BMI): Fall 2005 – Fall 2006
    b. Curriculum Development Committee for BMI: Fall 2005 – Fall 2008
    c. Graduate Admission Committee: Fall 2007 – current
    d. Computer Science Department Promotion Committee for Associate Professor to Full Professor (2022)
    e. Computer Science Post-tenure review committee (Spring 2024)
3. Department
    a. Graduate Program Committee: Fall 2019 - current
    b. Curriculum Committee for Computer Engineering: Fall 2021 – current
    c. PhD Preliminary Exam Appeal Committee (Spring 2021)
    d. Post-tenure review committee (Spring 2024)

University Services (at Arizona State University)

4. University
    a. Faculty search/recruiting committee (Evolutionary Bioinformatics), School of Life Science, Committee Chair: Dr. Jeff Touchman (SoLS, Arizona Biodesign Institute): Fall 2004 – Spring 2005
5. College

   a. Faculty Search Committee for Biomedical Informatics Program (BMI): Fall 2005 – Fall 2006
   b. Curriculum Development Committee for BMI: Fall 2005 – Fall 2008
   c. Graduate Admission Committee: Fall 2007 – current
6. Department
   a. Grad Admissions Committee (GAC): 2004 – 2006
   b. TAC (Artificial Intelligence): 2004 – 2006
   c. TAC (Algorithms): 2006

Publications and Presentations

Refereed Archived Journal Articles

1. Tai YY, Yu Q, Tang Y, Sun W, Kelly NJ, Okawa S, Zhao J, Schwantes-An TH, Lacoux C, Torrino S, Al Aaraj Y, El Khoury W, Negi V, Liu M, Corey CG, Belmonte F, Vargas SO, Schwartz B, Bhat B, Chau BN, Karnes JH, Satoh T, Barndt RJ, Wu H, Parikh VN, Wang J, Zhang Y, McNamara D, Li G, Speyer G, Wang B, Shiva S, Kaufman B, Kim S, Gomez D, Mari B, Cho MH, Boueiz A, Pauciulo MW, Southgate L, Trembath RC, Sitbon O, Humbert M, Graf S, Morrell NW, Rhodes CJ, Wilkins MR, Nouraie M, Nichols WC, Desai AA, Bertero T, Chan SY. Allele-specific control of rodent and human lncRNA KMT2E-AS1 promotes hypoxic endothelial pathology in pulmonary hypertension. *Sci Transl Med*. 2024 Jan 10;16(729):eadd2029. PubMed ID: 38198571.
2. Feng M, Matoso A, Epstein G, Fong M, Park YH, Gabrielson A, Patel S, Czerniak B, Compérat E, Hoffman-Censits J, Kates M, Kim S, McConkey D, Choi W. Reply to Kentaro Inamura's Letter to the Editor re: Mingxiao Feng, Andres Matoso, Gabriel Epstein, et al. Identification of Lineage-specific Transcriptional Factor-defined Molecular Subtypes in Small Cell Bladder Cancer. Eur Urol. In press. https://doi.org/10.1016/j.eururo.2023.05.023. *Eur Urol.* 2023 Sep 27; PubMed ID: 37775361.
3. Feng M, Matoso A, Epstein G, Fong M, Park YH, Gabrielson A, Patel S, Czerniak B, Comperat E, Hoffman-Censits J, Kates M, Kim S, McConkey D, Choi W (2023) Identification of Lineage-specific Transcriptional Factor-defined Molecular Subtypes in Small Cell Bladder Cancer. *European Urology.* 2023. https://doi.org/10.1016/j.eururo.2023.05.023.
4. Nwosu L, Li X, Qian L, Kim S, Dong X (2022). Calibrated bagging deep learning for image semantic segmentation: A case study on COVID-19 chest X-ray image. PLoS ONE. 2022. http://dx.doi.org/10.1371/journal.pone.0276250.
5. Nakamura K, Zhu Z, Roy S, Jun E, Han H, Munoz RM, Nishiwada S, Sharma G, Cridebring D, Zenhausern F, Kim S, Roe DJ, Darabi S, Han I, Evans D, Yamada S, Demeure MJ , Becerra C, Celinski S, Borazanci E, Tsai S, Kodera Y, Park JO, Bolton J, Wang X, Kim SC, Von Hoff D, Goel A. An exosome-based transcriptomic signature for noninvasive, early detection of patients with pancreatic ductal adenocarcinoma: a multicenter cohort study. *Gastroenterology*. 2022; https://doi.org/10.1053/j.gastro.2022.06.090.
6. Negi V, Yang J, Speyer G, Pulgarin A, Handen A, Zhao J, Tai YY, Tang Y, Culley MK, Yu Q, Forsythe P, Gorelova A, Watson AM, Al Aaraj Y, Satoh T, Sharifi-Sanjani M, Rajaratnam A, Sembrat J, Provencher S, Yin X, Vargas SO, Rojas M, Bonnet S, Torrino S, Wagner BK, Schreiber SL, Dai M, Bertero T, Al Ghouleh I, Kim S, Chan SY. Computational repurposing of therapeutic small molecules from cancer to pulmonary hypertension. *Sci Adv*. 2021 Oct 22;7(43):eabh3794. doi: 10.1126/sciadv.abh3794. Epub 2021 Oct 20. PMID: 34669463.

7. Craig DW, Hutchins E, Violich I, Alsop E, Gibbs JR, Levy S, Robison M, Prasad N, Foroud T, Crawford KL, Toga AW, Whitsett TG, Kim S, Casey B, Reimer A, Hutten SJ, Fraiser M, Kern F, Fehlman T, Keller A, Cookson MR, Van Keuren-Jensen K, PPMI. 2021, RNA sequencing of whole blood reveals early alterations in immune cells and gene expression in Parkinson's disease. *Nature Aging* **1**, 734-747 (2021)

8. Culley MK, Zhao J, Tai YY, Tang Y, Perk D, Negi V, Yu Q, Woodcock CC, Handen A, Speyer G, Kim S, Lai YC, Satoh T, Watson AM, Al Aaraj Y, Sembrat J, Rojas M, Goncharov D, Goncharova EA, Khan OF, Anderson DG, Dahlman JE, Gurkar AU, Lafyatis R, Fayyaz AU, Redfield MM, Gladwin MT, Rabinovitch M, Gu M, Bertero T, Chan SY. 2021. Frataxin deficiency promotes endothelial senescence in pulmonary hypertension. *J Clin Invest.* 2021 Apr 27;136459. doi: 10.1172/JCI136459.

9. Woodcock C, Hafeez N, Handen A, Tang Y, Harvey LD, Estephan LE, Speyer G, Kim S, Bertero T, Chan SY (2021). Matrix Stiffening Induces a Pathogenic QKI-miR-7-SRSF1 Signaling Axis in Pulmonary Arterial Endothelial Cells. *Am J Physiol Lung Cell Mol Physiol*. 2021 May 1;320(5):L726-L738. doi: 10.1152/ajplung.00407.2020.

10. Sun W, Tang Y, Tai Y-Y, Handen A, Zhao J, Speyer G, Aaraj YA, Watson A, Romanelli ME, Sembrat J, Rojas M, Simon MA, Zhang Y, Lee J, Xiong Z, Dutta P, Vasamsetti S, McNamara D, McVerry B, McTiernan C, Sciurba F, Kim S, Smith A, Mazurek JA, Han Y, Vaidya A, Nouraie M, Kelly NJ, and Chan SY (2020). SCUBE1 Controls BMPR2-Relevant Pulmonary Endothelial Function: Implications for Diagnostic Marker Development in Pulmonary Arterial Hypertension. *JACC Basic to Translational Science* 2020 Nov; 5(11): 1073–1092. doi: 10.1016/j.jacbts.2020.08.010.

11. Kalani MYS, Alsop E, Meechoovet B, Beecroft T, Agrawal K, Whitsett TG, Huentelman M, Spetzler RF, Nakaji P, Kim S, Keuren-Jensen KV. (2020) Extracellular microRNAs in blood differentiate between ischaemic and haemorrhagic stroke subtypes, *Journal of Extracelluar Vescicles* 9(1): https://doi.org/10.1080/20013078.2020.1713540.

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Refereed Conference Articles

1. Peng S, Rath S, Vuong C, Bollam S, Eschbacher J, Dong X, Mehta S, Sanai N, Berens M, **Kim S**, Dhruv H. (2019) Probing glioblastoma and its microenvironment using single-nucleus and single-cell sequencing, IEEE Bioinformatics and Biomedicine (IEEE BIBM 2019), Nov. 18-21, 2019, San Diego, USA.
2. Speyer G, Rodriguez JJ, Bencomo T, Kim S. (2018) GPU-accelerated differential dependency network analysis. *26th Euromicro International Conference on Parallel,*

Distributed and Network-based Processing (*PDP 2018*), Mar 21-23, 2018. DOI: 10.1109/PDP2018.2018.00072.

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6. Ramesh, A. Nasser, S. Kim, S. (2011) Systematic Validation of Computationally Predicted Interaction Networks with a Literature-Derived Interaction Database, 8th International Workshop on Computational Systems Biology (WCSB 2011), June 6-8, 2011, Zurich, Switzerland
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10. Ramesh, A., Trevino, R., von Hoff, D., Kim, S. (2010) Clustering Context-Specific Gene Regulatory Networks, in the *Pacific Symposium on Biocomputing*. Jan 5-9, 2010, Big Island, Hawaii, US.
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12. Nasser, S., Weiss, G. J., Ranade, A. R., and Kim, S. (2009) In-silico conditioning of microRNA to identify potential biomarkers from serum for pancreatic cancer, *IEEE GENSIPS 2009,* May 17-19, 2009, Minneapolis, MN, USA.
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Conference Papers, Presentation, Abstracts and Invited Talks

1. S. Kim. Context-specific genomic regulation in cancer, ASU PSOC Seminar (invited talk).
2. S. Kim. Simplist's approach to modelling human aging, *Systems Biology of Human Aging*, Baltimore, MD. Dec 8-9, 2009 (invited talk)

3. Michael Verdicchio and S. Kim. Boolean Network Models of Human Aging, *The 7th Annual Rocky Mountain Bioinformatics Conference* (*Rocky 09*), Aspen/Snowmass, CO. Dec. 10-12, 2009 (both oral and poster presentation, given by MV)
4. S. Kim. Contextual genomic regulation in cancer, *Translational Research Lunch Discussion*, Scottsdale Healthcare, Scottsdale, AZ, Aug. 3, 2009. (invited talk)
5. S. Kim. Context-specific biological interactions in cancer, *Systems Biology: Applications of Pathway Analysis Seminar*, The Scripps Research Institute, San Diego, CA, July 7, 2009. (invited talk)
6. D. Bidaye, J. Dzifcak, D. Stracuzzi, R. Chimera, M. P. Verdicchio, J. Furber, S. Kim, and P. Langley. An interactive environment for visualizing, developing, and evaluating biological process models of aging. *The 38th Annual Meeting of the American Aging Association*. Scottsdale, AZ, May 29 – June 1, 2009.
7. D. Bidaye, J. Dzifcak, D. Stracuzzi, R. Chimera, M. P. Verdicchio, S. Kim, P. Langley, An Interactive Environment for Visualizing, Interpreting, and Revising Biological Process Models, *RECOMB* 2009, Tucson, AZ, May 18 – 21, 2009.
8. S. Kim. Systems Biology: an Engineer's View. *Symposium on Systems Biology of Aging*, Arizona State University, Tempe, AZ, Dec. 6 – 7, 2008 (invited talk)
9. M. Verdicchio, X. Zhang, C. Baral, and S. Kim. Learning Causal Relationships between Genes from Steady State Data: Algorithms, Simulation and Application, *Sixth Annual Rocky Mountain Bioinformatics Conference* (*Rocky* 2008), Colorado, Dec. 4 – 7, 2008.
10. T. Gowda, S. Vrudhula, and S. Kim. A Novel Gene Regulatory Model for Embryonic Cell Differentiation in Drosophila Melanogaster, *Sixth Annual Rocky Mountain Bioinformatics Conference* (*Rocky* 2008), Colorado, Dec. 4 – 7, 2008.
11. L. Tari, C. Baral and S. Kim. Gene Function Prediction Using Prior Knowledge and Expression Data, *Sixth Annual Rocky Mountain Bioinformatics Conference* (*Rocky* 2008), Colorado, Dec. 4 – 7, 2008.
12. T. Gowda, S. Vrudhula and S. Kim. Modeling of Gene Regulatory Networks Using Threshold Logic, *DREAM 2*, New York, NY, Dec. 3-4, 2007 (invited as one of the best performers in the challenge).
13. S. Kim, I. Sen, M.L. Bittner. Mining Molecular Contexts of Cancer via In-Silico Conditioning. *The 2007 IEEE Workshop on Statistical Signal Processing*, Madison, WI, Aug. 26-29, 2007 (invited presentation).
14. S. Kim, A Model for Contextual Regulatory Controls and Identifying Molecular Contexts in Cancers, at KRIBB/NGIC, Yusong, Korea, Sept. 12, 2005 (invited talk)
15. S. Kim, Integrated Computational Approach for Translational Biomedical Research, at *National Center for Standardization for Herbal Medicine Workshop*. Seoul, Korea. Sept. 7, 2005 (invited talk)
16. S. Kim, A Model for Contextual Regulatory Controls and Identifying Molecular Contexts in Cancers, at *Korea Genome Organization (KoGO) Annual Meeting*, Seoul, Korea, Sept. 8-9, 2005 (invited talk)
17. S. Kim, Mathematical Modeling and Computational Simulation of Gene Regulatory Networks, at *Biomedical Engineering Seminar at University of Arizona*, Tucson, AZ, April 25, 2005 (invited talk)

18. T.-H. Chung, T. Price-Troska, R. Xu, I. Ghobrial, P. R. Greipp, V. Rajkumar, M. A. Gertz, S. A. van Wier, G. J. Ahmann, A. Baker, J. Carpten, R. Fonseca, S. Kim. Waldenstrom Macroglobulinemia Gene Expression Profiles and Chromosome 6 Aberration. *In 2nd Annual Rocky Mountain Regional Bioinformatics Conference*, Aspen, CO, Dec. 10-12, 2004.
19. S. Kim, Context-Sensitive Boolean Network to Model Biological Systems, In *Discrete Models for Genetic Regulatory Networks*, College Station, TX, Nov. 5-6, 2003 (invited talk)
20. S. Kim, Biological System: not random but contextual, In *Recent Progress in Genomics, Proteomics and Bioinformatics*, Daejun, Korea, Sept. 4-5, 2003 (invited talk)
21. Y. Balagurunathan, R.F. Hashimoto, *S.* Kim, J. Barrera, and E.R. Dougherty. Granulometric Classifiers from Small Samples. In Proc. SPIE – PHOTONICS WEST 2002, San Jose, CA. pp. 100-7.
22. S. Kim, Design and error estimation of classifiers based on small samples. In *Bioinformatics Seminar, Training Program in Bioinformatics*, Texas A&M University, Dec. 5, 2002 (invited talk).
23. S. Kim, Microarrays and Bioinformatics: Biological Story Makings. In *Annual Conference for Korean Society of Agricultural Chemistry and Biotechnology*, Suwon, Korea, Oct. 2002 (invited plenary talk).
24. S. Kim, E.R. Dougherty, Y. Chen, M.L. Bittner, K. Carr, and J.M. Trent. Using quality metric in pattern classification and its application to gene expression data. In *Oncogenomics: Dissecting Cancer Through Genome Research*, AACR, Dublin, Ireland, May, 2002.
25. S. Kim. Finding Genes for Cancer Classification based on Microarrays with small samples and many computers, In The Second Houston Forum on Cancer Genomics and Informatics, M.D. Anderson Cancer Center, Houston, TX, July 27-28, 2001 (invited).
26. A. D. Baxevanis, I. Makalowska, K. Trout, Q. Zhou, Z. Z. Zhou, J. Stein, E. R. Dougherty, S. Kim, P. S. Meltzer, Y. Chen, M. L. Bittner, and J. M. Trent. An Integrated Approach for the Storage, Exploration, and Analysis of Microarray Gene Expression Data, In RECOMB 2001, Montreal, Canada, April, 2001.
27. E. R. Dougherty, J. Barrera, M. Brun, S. Kim, R. M. Cesar, Y. Chen, M. L. Bittner, and J. M. Trent. Clustering Algorithms: Can Anything Be Concluded? In *Oncogenomics: Dissecting Cancer Through Genome Research*, Nature Genetics, Tucson, AZ, USA, January, 2001.
28. E. B. Suh, E. R. Dougherty, S. Kim, D. Russ, and R. L. Martino. Parallel Computing Methods for Analyzing Gene Expression Relationships, In *Microarrays: Optical Technologies and Informatics*, Photonics West 2001, SPIE, San Jose, CA, USA, January, 2001.
29. S. Kim, E. R. Dougherty, and J. Barrera, Y. Chen, M. L. Bittner, and J. M. Trent. Finding Robust Linear Expression-Based Classifier, In *Microarrays: Optical Technologies and Informatics*, Photonics West 2001, SPIE, San Jose, CA, USA, January, 2001.
30. E. R. Dougherty, J. Barrera, M. Brun, S. Kim, Y. Chen, M. L. Bittner, and J. M. Trent. Time Series Inference from Clustering, In *Microarrays: Optical Technologies and Informatics*, Photonics West 2001, SPIE, San Jose, CA, USA, January, 2001.
31. Y. Chen, Y. Jiang, E. R. Dougherty, S. Kim, Z. Yakhini, A. Ben-Dor, N. Sampas, M. Radamacher, R. Simon, M. Brun, M. D. Gubitoso, J. Barrera, C. Gooden, A. Glatfelter, P. Meltzer, J. M. Trent, M. L. Bittner. Estimating the Reliability of Inferences Based on cDNA Microarray Ratio Data, In *Beyond the Identification of Transcribed Sequences: Functional and Expression Analysis*, BIST, Heidelburg, Germany, October, 2000.

32. E. R. Dougherty, S. Kim, Y. Chen, M. L. Bittner, P. S. Meltzer, and J. M. Trent. Image Analysis and Signal Processing for cDNA Microarrays, In *CERH/NIEHS's Second Annual Scientific Symposium - GENOMICS & PROTEOMICS: Innovations in Environmental Health Research* sponsored by Center for Environmental and Rural Health of The National Institute of Environmental Health Sciences, Veterinary Multidisciplinary Building, College Station, TX, USA, May, 2000.
33. E. R. Dougherty, J. Barrera, G. Mozelle, S. Kim, and M. Brun. Multiresolution Filter Design, In *Nonlinear Image Processing XI*, Photonics West 2000, SPIE, San Jose, CA. January, 2000. Paper No. EI3961-02.
34. S. Kim, E. R. Dougherty, M. L. Bittner, Y. Chen, K. Sivakumar, P. S. Meltzer, and J. M. Trent. Automated analysis of multivariate nonlinear gene relations based on cDNA microarray expression data, In *Advances in Nucleic Acid and Protein Analyses, Manipulation, and Sequencing*, Photonics West 2000, SPIE, San Jose, CA. January, 2000. Paper No. PW 3926-27
35. E. R. Dougherty, S. Kim, M. L. Bittner, Y. Chen, K. Sivakumar, P. S. Meltzer, and J. M. Trent. Nonlinear stochastic determination for gene expressions via cDNA microarrays. In *The Microarray Meeting: Technology, Applications & Analysis*, Nature Genetics, Scottsdale, Arizona, September, 2000.
36. E. R. Dougherty, M. L. Bittner, Y. Chen, S. Kim, K. Sivakumar, J. Barrera, P. S. Meltzer, and J. M. Trent. Nonlinear Filters in Genomic Control, *Proceedings of IEEE-EURASIP Workshop on Nonlinear Signal and Image Processing (NSIP'99)*, Antalya, Turkey, June, 1999.
37. S. Kim, S. Batman, and E. R. Dougherty. A Fast Run-Length-Based Algorithm for One-Dimensional Flat Opening, in *Proceedings of Parallel and Distributed Methods for Image Processing*, SPIE 43rd Annual Conference, San Diego, CA, USA, July, 1998, Paper No. 3452-18.

Patents

1. Methods of Assessing A Risk Of Cancer Progression (**Published on Dec 16, 2014, US 8911940 B2**)
2. Quantifying Gene Relatedness Nonlinear Prediction of Gene Expression Levels (**Published on Feb, 21, 2006, US 7003403 B1**)
3. THERAPEUTIC SMALL MOLECULES FOR TREATMENT OF PULMONARY HYPERTENSION (June, 2021, Pending, US Provisional Application)
4. SYSTEMS AND METHODS FOR IDENTIFYING THE RELATIONSHIPS BETWEEN A PLURALITY OF GENES (Nov 14, 2012, Pending, US Patent Application)
5. DISCOVERY OF GBM MOLECULAR CONTEXTS ASSOCIATED WITH PATIENT SURVIVAL (Mar 12, 2012, Pending, US Patent Application)
6. Evaluating Data Clustering Procedures / Inferential Performance of Clustering Algorithms (Pending, US Provisional Patent Application)
7. Generating Feature Sets from Samples / Discovering Strong Classification Features from Small Samples (Pending, US Provisional Application)

Book and Book Chapters

1. D. Bryce and S. Kim. Planning Interventions for Gene Regulatory Networks as Partially Observable Markov Decision Process. In *Computational Methodologies in Gene Regulatory Networks*. IGI Global, 2010. Eds S. Das, D. Caragea, W. H. Hsu, S. M. Welch.
2. S. Kim, P. Stafford, M. L. Bittner, E. Suh. Integrated Approach for Computational Systems Biology. In *EURASIP Book Series on Signal Processing and Communications: Genomic Signal Processing and Statistics*. IEEE Press, 2005. Eds E. R. Dougherty, I. Shmulevich, J. Chen, Z. J. Wang.
3. E.B. Suh, E.R. Dougherty, S. Kim, M.L. Bittner, Y. Chen, S. Muju, D.E. Russ, R.L. Martino. Parallel Computation and Visualization Tools for Codetermination Analysis of Multivariate Gene-Expression Relations. In *Computational and Statistical Approaches To Genomics*, Kluwer Academic Publishers, Boston, 2002, edited by W. Zhang and Il Shmulevich.

Research Support

Ongoing Research Support

05/01/2022-04/30/2025 **USDA/NIFA**

PI: Tesfamichael Kebrom **Role: co-PI**

Molecular and Genetic Analysis of Axillary Bud Dormancy and Outgrowth in Sorghum and Maize to Identify Shoot Branching Genes

The overall goal of this study is to identify genes that control shoot branching in sorghum and maize using molecular (RNA-seq) and genetic (QTL mapping) approaches

Specific Aims: 1. Identify genes controlling pre-flowering axillary bud transition from growth to dormancy. 2. Identify genes controlling post-flowering axillary bud transition from dormancy to growth. 3. Characterize the genetic basis of variation in shoot branching.

01-14-2022 – 09-30-2024 **2338270, Sandia National Lab**

PI: Seungchan Kim **Role: PI**

Engineering Methanotrophy for Carbon Capture and Utilization

The goals of this research are to evaluate the potential to arrest methane production and promote methane utilization from dilute natural and human activities-associated emissions sources using engineered microbial consortia and biological control agents. The expected outcomes of the effort include a new experimental testbed for generating data required to predicting microbial population dynamics, prototype anti-methanogenic inocula arising from various environmental conditions, and computational analysis from our Prairie View A&M University collaborator for identifying microbiological and metabolic networks for biosystem optimization. Success in this endeavor will support cost-effective methane emissions reduction technology, thereby mitigating the most severe near-term impacts of climate change.

01-01-2021 – 12/31/2022 **USDA/NIFA**

PI: Tesfamichael Kebrom **Role: co-PI**

Physiological and Molecular Characterization of Tillering, Internode Elongation, and Stunting in the Tiller Inhibition (tin) Mutant Wheat

Most of the yield of wheat is contributed by the main shoot and a few tillers. We hypothesize that a wheat plant with two to three tillers and restricted growth of unproductive tillers will maximize grain yield. The tin mutant wheat is ideal for modulating tillering and identifying the optimal tiller number. Tiller inhibition in tin is associated with precocious stem internode elongation. Internodes in tin start to elongate immediately after the transition of the shoot apex from vegetative to flowering phase. Internode elongation indirectly reduces tillering by limiting supply of sugars to tiller buds. By modulating flowering time, thus the timing of internode elongation in tin, the number of productive tillers could be specified and the yield per shoot and per plant could be analyzed. Besides precocious internode elongation, the tin tends to stunt in long days and lower temperatures. Identifying the molecular basis of precocious internode elongation and stunting will be useful for improving tillering and yield of wheat. Therefore, this project has the following two objectives: a) modulating timing of internode elongation in tin indirectly by inducing flowering at different times and investigating its effect on tiller number and yield. b) Transcriptome analysis to identify molecular mechanisms controlling precocious internode elongation and stunting in tin.

09/21/2021 – 09/20/2025 **90PH0003, ONC via UTHSC**

PI: Eric Boerwinkle **Role: co-I**

The PHIT Workforce Development Program: Creating a diverse and inclusive health information technology (IT) workforce in Texas

PVAMU team will be closely working with UTHSC team and other consortium members to recruit and mentor students from PVAMU site. PVAMU team will also collaborate with the consortium members to develop and customize course materials and workshop program for the proposed consortium and to deliver those materials to PVAMU students. We plan to recruit 25-40 students (per year) for course curriculum, 15-30 students (per year) to the proposed boot camps, and 5-15 students for the proposed certificate program.

2019/07/01 – 2023/06/30 **W81XWH-19-1-0149, DOD/CDMRP**

MPI: Woonyoung Choi & Seungchan Kim **Role: PI (MPI)**

Development of Classifiers for Novel Bladder Cancer Subtypes

To characterize our novel immune subtypes (BIE and BIS), define signaling pathways that are differentially activated between subtypes and are candidate therapeutic targets, and identify subtype-specific therapeutic strategies including combined chemotherapy and immunotherapy and to discover subtype-specific biomarkers for clinical assay development.

2017/09/01-2023/07/31 **1U01CA214254-01, NIH/NCI**

MPI: Ajay Goel & Dan Von Hoff **Role: Co-Investigator**

Noncoding RNA Biomarkers for Noninvasive and Early Detection of Pancreatic Cancer

We will perform a comprehensive and genome-wide evaluation of cell-free and exosomal microRNA biomarkers in serum samples as potential noninvasive biomarkers for the early detection of pancreatic cancers and precancerous lesions. Successful identification of such biomarkers will exert a substantial diagnostic and prognostic impact on the management of this fatal disease.

Completed Research Support

2019/03/01 – 2021/02/29 **MJFF #16521**
PI: Kendall Van-Buren Jensen **Role: Co-PI**
Extracellular vesicles from urine are enriched in brain transcripts and have potential as noninvasive biomarkers
Our goal is to begin development of a noninvasive diagnostic that could be used early – before symptoms have occurred. To do this successfully, the test would have to be sensitive, selective, and inexpensive. These diagnostic attributes would be ideal, and would reach the greatest number of people, before their disease has progressed significantly, and when therapeutic interventions would be at their most effective. We propose to use exRNAs isolated from urine extracellular vesicles (EV), as carriers of useful information to monitor brain health and disease.

2017/09/01 – 2020/08/31 **NSF #173619**
PI: Qian, Lijun **Role: Co-PI**
HBCU-RISE: Bridging Quantitative Science with Biological Research
The research objective of this proposal is to study and analyze the dynamic evolution of drug/cell interaction using biomedical big data including both public domain data and dynamic time series data from systematic drug perturbations experiments. The educational goal is to enhance the PhD program in ECE department and broad participation in computational biology at PVAMU to improve students' retention and competence.

SU2C-CRUK Dan von Hoff (PI) 1/1/2016 – 6/30/2020
SU2C-Cancer Research UK-Lustgarten Foundation
Reprogramming of Transcriptional Circuitry to Control Pancreatic Cancer

The Dream Team believes that the biological machinery involved is controlled through hot spots in a cell's DNA called Super Enhancers (SE), which control not only the cancer cell, but also surrounding non-cancerous cells, upon which the cancer cells rely for support. The Dream Team aims to develop new approaches to reset malfunctioning SEs in pancreatic tumors thereby dialing-up the sensitivity to chemotherapy and to anti-cancer immune cells and pushing pancreatic tumors into lasting remission.
Role: Investigator

NVIDIA Compute Cure Seungchan Kim (PI) 1/1/2017 – 12/31/2018
NVIDIA Foundation

Discovery of individualized therapeutic vulnerability in cancer, enabled by single cell transcriptomic profiling

We propose to test and further optimize GPU-EDDY as a statistically robust and efficient application to address the rigorous computational requirements for a deployable single-cell RNAseq analysis platform. Specifically, scRNAseq profiles of gliomablastoma patients and patient-derived xenograft (PDX) will be analyzed to identify potential therapeutic mediators for each tumor. This approach further strengthens from ongoing Glioma Precision Medicine efforts at TGen, which primarily rely on molecular profiling of bulk tumor.
Role: Investigator

U23/34 Kendall Van Keuren-Jensen/Matt Huentelman (multi PIs) 6/1/2013 – 5/31/2018
NIH/NINDS
exRNA signatures Predict Outcomes after brain injury

The goal of this project is to identify extracellular RNA biomarkers in blood and cerebrovascular fluid (CSF) of outcome for individuals suffering aneurysmal subarachnoid hemorrhage (aSAH) and newborns with intraventricular hemorrhage (IVH).
Role: Investigator

U01 Michael Berens (PI) 5/01/2012 – 04/30/2017
NIH/NCI
Systematic development of novel, druggable cancer targets

The goal of this study is to use newly uncovered knowledge about the genomes of hundreds of glioblastoma specimens to discover new medicines that can precisely target tumors, shrinking or even eliminating them, with minimal harm to other cells and minimal side effects for patients.
Role: Investigator

Grant John Carpten (PI) 03/01/2011 - 12/31/2017
MMRF
Whole Transcriptome RNA Sequencing of Multiple Myeloma Tumors using Next Generation Sequencing Technologies

The goal is to utilize NGS technologies to perform a deeper analysis of the MM transcriptome, and to put the transcriptional consequences of genomic alterations discovered to date into the larger molecular context of the disease.
Role: investigator

KG111063PP Jeff Trent (PI) 4/11/2011-3/31/2016
Susan G. Komen for the Cure
Targeting Stem Cells in Triple-Negative Breast Cancer (TNBC) in Different Racial Populations

We propose to test two main hypotheses: 1) an increase in the cancer stem cell (CSC) populations in Black African (BA) and African-American (AA), as compared to Caucasian American (CA) women, contributes to their more aggressive biological character, increased incidence of triple-negative (TNBC), and poorer outcome; 2) agents which inhibit CSC regulatory pathways will specifically target and reduce the CSC population in women with locally advanced and metastatic TNBC.
Role: Co-Investigator

Contract Jeff Kiefer (PI) 09/01/2009 – 05/31/2012
NIH/SAIC
In-silico Research Center of Excellence (ISRCE) technical proposal.
Role: co-Investigator

R21LM009706S Seungchan Kim (PI) 10/01/2009 – 09/30/2010
NIH/NLM
Supplement to R21LM009706,
Role: Principal Investigator

R21LM009706 Seungchan Kim (PI) 07/01/2008 – 12/31/2010
NIH/NLM
Integrating Genomic Data and Biological Knowledge to Learn Context-Specific Gene Regulatory Networks
This application proposes to develop computational methods that can search through heterogeneous sample sets to identify subsets of samples in which sets of genes that collaborate to carry out particular pathologic functions are homogeneously regulated.
Role: Principal Investigator

CAA 0243-08 Seungchan Kim (PI) 06/02/2008 - 12/31/2009
Science Foundation Arizona
Integrating Genomic Data and Biological Knowledge to Learn Context-Specific Gene Networks
The major goal is to develop novel computational methods to support the integration of multiple types of genomic and expression measurements, clinical information and existing biological knowledge to stratify molecular subtypes of cancer and to learn its underlying regulatory mechanisms.
Role: Principal Investigator

W81XWH-06-1-090 V. Craig Jordan (PI) 09/01/2006 - 08/31/2009
Department of Defense/CDMRP
A New Therapeutic Paradigm for Breast Cancer Exploiting Low-Dose Estrogen-Induced Apoptosis
The goal of the project is 1) to conduct exploratory clinical trials to determine the efficacy and dose response of pro-apoptotic effects of estrogen [diethylstilbestrol (DES)] in patients following the failure of two successive antihormonal therapies 2) to elucidate the molecular mechanism of E2-induced survival and apoptosis in breast cancer cells resistant to either selective ER modulators (SERMs) or long-term estrogen deprivation and 3) to decipher cellular signaling pathways using proteomics.
Role: Investigator

P01 CA109552 Daniel Von Hoff (PI) 07/01/2005 - 06/30/2010
NIH/National Cancer Institute
Targets to Therapeutics in Pancreatic Cancer
The goal of this P01 is to speed delivery into the clinic of new therapeutics against new targets in pancreatic cancer. In each year of this P01, we will deliver a new agent into clinical trials in patients with pancreatic cancer, which hits a target discovered and validated in one of the

projects of this P01.
Role: Investigator

U19 AI067773 David Brenner (PI) 08/31/2005 - 07/31/2010
NIH/NIAID
Center for High-Throughput Minimally-Invasive Radiation Biodosimetry (Core C)
The project is to study the evolution of cells' response to DNA damage, and to examine issues such as how certain portions of the response remain active for many days after the initial damaging event and DNA repair.
Role: Co-Investigator

Grant Seungchan Kim (PI) 09/01/2005 – 08/31/2007
ASU/Mayo
A Software Environment to Integrate Multiple Data Type for the Analysis of Genomic Data for Multiple Myeloma (ASU-Mayo Seed Grant)
The major goal is to jumpstart the development of the algorithms to integrate such heterogeneous genomic data from various high throughput measurements such as gene expression microarrays, single nucleotide polymorphism (SNP), and genome copy number changes based on comparative genomic hybridization (CGH), and the implementation of those algorithms into user-friendly software tools with intuitive graphical user interface and data management.
Role: Principal Investigator

P01 CA27502 David Alberts (PI) 07/01/2004 - 06/30/2009
NIH/NCI
Chemoprevention of Skin Cancer - Project III
The overall goal of the Chemoprevention of Skin Cancer Program Project is to develop new strategies to eradicate intraepithelial neoplasias in the skin and dramatically reduce the risk of melanoma and non-melanoma skin cancer.
Role: Co-Investigator (TGen)