Kun Huang, PhD, FAIMBE

Professor and Chair of Biostatistics and Health Data Science
IUSM PHI Chair in Genomic Data Science
Director for Data Science and Informatics, IU Precision Health Initiative
Associate Director for Data Science, IU Simon Comprehensive Cancer Center
Indiana University School of Medicine
IUPUI Fairbanks School of Public Health
Investigator, Regenstrief Institute
E-mails: kunhuang@iu.edu
Phone: 317-278-7722 (Office), 614-596-2471 (Cell)

Research Interest:

- Translational informatics and integrative genomics tools for precision medicine

- Algorithms, software, and pipelines for computational pathology and bioimage informatics

- Data science theory and methods for mining and visualizing big and complex biomedical data

- Theory and algorithms for computer vision, machine learning, and AI

Education:

- University of Illinois at Urbana-Champaign, **Ph.D. in Electrical and Computer Engineering**, October 2004.
  Dissertation: *Geometric Principles of Visual Sensor Networks*
  Committee: Drs. P. R. Kumar (chair), Yi Ma (advisor), Thomas S. Huang, Robert Fossum, and Yizhou Yu.

- University of Illinois at Urbana-Champaign, **M.S. in Mathematics**, December 2002.

- University of Illinois at Urbana-Champaign, **M.S. in Electrical Engineering**, October 2000.

- University of Illinois at Urbana-Champaign, **M.S. in Molecular and Systems Physiology**, May 1998.

- Tsinghua University, Beijing, China, **B.S. in Biology**, July 1996.

- Tsinghua University, Beijing, China, **B.Engr. in Computer Science**, July 1996.

Academic Positions:

- Professor with Tenure, *Department of Biostatistics and Health Data Science*, Indiana University School of Medicine, 2021 - present

- Professor with Tenure, *Department of Medicine*, Indiana University School of Medicine, 2017 - 2021

- IUSM PHI Endowed Chair in Genomic Data Science, Indiana University School of Medicine, 2017 – present

- Investigator, Regenstrief Institute, 2017 – present

- Professor with Tenure, *Department of Biomedical Informatics*, The Ohio State University, 2016 – 2017

- Associate Professor with Tenure, *Department of Biomedical Informatics*, The Ohio State University, 2010 – 2016

- Assistant Professor, *Department of Biomedical Informatics*, The Ohio State University, 2004 – 2010

- Joint and adjunct faculty appointment:

  - *Department of Epidemiology, IUPUI (2017 – present)*
  - *Department of Computer Science, Indiana University Bloomington (2017 – present)*
  - *Department of Computer Science, IUPUI (2017 – present)*
  - *Department of Electrical and Computer Engineering, IUPUI (2017 – present)*
  - *Department of BioHealth Informatics, IUPUI (2017 – present)*
  - *Department of Biomedical Informatics, OSU (2017 – present)*
  - *Department of Computer Science and Engineering, OSU (2005 – present)*
  - *Biophysics Graduate Program, OSU (2008 – 2017)*
  - *Department of Pathology, OSU (2008 – 2017)*
  - *Department of Electrical and Computer Engineering, OSU (2005 – 2017)*
  - *Biomedical Science Graduate Program* (BSGP)*, OSU (2004 – 2017)*
  - *College of Public Health, Division of Biostatistics, OSU (2015 – 2017)*

- Guest professorship:

  - *Soochow University (2014 – 2017)*
  - *Harbin Engineering University (2015 – 2018)*
  - *Shenzhen University (2017-2020)*

Leadership Positions and Services:

- Member, Indiana University Research Data Commons Working Group (report to Vice President for Research), 2022 - present

- Chair, *Department of Biostatistics and Health Data Science*, Indiana University School of Medicine / Fairbanks School of Public Health, 2021 - present

- Vice Chair for Data Science, *Department of Biostatistics and Health Data Science*, Indiana University School of Medicine, 2021 - 2021

- Associate Director for Data Science, Indiana University Simon Comprehensive Cancer Center, 2020 – present

- Voting Member of IU Health/IUSM Strategic Research Initiative (SRI) Selection Committee, 2020 – present

- Executive Council Member, Regenstrief Institute, 2019 – present

- Founding Director of Data Science and Informatics Program in Precision Health Initiative, IUSM, 2017 – present

- Assistant Dean for Data Science, IUSM, 2017 – 2021

- Associate Dean for Genome Informatics, College of Medicine, OSU, 2015 – 2017

- Division Director for Bioinformatics and Computational Biology, Department of Biomedical Informatics, OSU, 2015 – 2017

- Founder of the *OSU-Soochow University Collaborative PhD Program in Biomedical Informatics*, the first international PhD program at OSU, 2015

- Bioinformatics and Computational Biology (BCB) Track Leader, *Biomedical Science Graduate Program* (BSGP), in charge of the curriculum for the BCB track, 2012 – 2017

- Senior Advisor, Comprehensive Cancer Center Biomedical Informatics Shared Resources, OSU, 2014 – 2017.

- Co-Director, Comprehensive Cancer Center Biomedical Informatics Shared Resources, OSU, 2007 – 2014.

- Member, Faculty Advisory Committee, OSU China Gateway, 2013 – 2017.

- Member, College Assembly, College of Medicine, OSU, 2013 – 2015.

- BMI representative to Faculty Council, College of Medicine, OSU, 2012 – 2015.

- BMI representative (alternate) to Faculty Council, College of Medicine, OSU, 2010 – 2012.

- Member, Graduate Study Committee, College of Medicine, OSU, 2007 – 2010.

- Member, Graduate Study Committee, The Biomedical Science Graduate Program, College of Medicine, OSU, 2011 – 2017.

- Member, Comprehensive Cancer Center Shared Resources Committee, OSU, 2010 – 2015.

- Chair, Translational Bioinformatics Faculty Search Committee, Department of Biomedical Informatics, OSU, 2012 – 2014.

- Member, Search Committee for the Data Analytics Initiative, Department of Biomedical Informatics, OSU, 2015 – 2017.

- Member, Graduate Study Coordination Committee, Department of Biomedical Informatics, OSU, 2014 – 2017.

- Member, Systems Committee, Department of Biomedical Informatics, OSU, 2012 – 2017.

- BMI representative in Graduate Interdisciplinary Specialization Comprehensive Engineering & Science of Biomedical Images (CESBMI), OSU, 2006 – 2009.

Awards and Scholarships:

- Multiple Myeloma Research Foundation Young Investigator Award (as mentor for awardee Dr. Travis Johnson), 2022.

- Elected to IEEE Senior Member, 2021.

- Young Scientist Award (mentor for awardee), MICCAI, 2019 (Five awards out of 1,800 submissions)

- ACM SIGBio Best Paper Award, 2019. (One paper was selected)

- Elected to Fellow of American Institute of Biological and Medical Engineering (AIMBE), 2018.

- Marco Ramoni Distinguished Paper Award, AMIA Summit of Translational Bioinformatics, 2016. (One paper was selected)

- Finalist for the Marco Ramoni Distinguished Paper Award, AMIA Summit of Translational Bioinformatics, 2015. (Four papers were selected)

- IEEE SciVis Contest Winning Team co-Leader, 2013.

- Distinguished Paper Award, AMIA Summit of Translational Bioinformatics, 2010.

- The National Institute of Drug Addiction Travel Award, 2010.

- The OSU Medical Center Teaching Excellence Award, 2010.

- Nominated for Packard Foundation Fellowship in Science and Engineering by OSU (two faculty members were nominated), 2007.

- IEEE Computer Society Student Travel Grant, 2004.

- Best Teaching Assistant Elected by Students, University of Illinois, 1998.

- Distinguished Graduate Medal, Tsinghua University, 1996.

- Outstanding Student Award in Science and Technology Areas, City of Beijing, 1995.

- Guanghua Scholarship, Tsinghua University, China, 1994.

- Excellent Student Scholarship, Tsinghua University, China, 1993.

- First Award in the 1st Chinese Mathematics Olympiad, 1991.

Grants:

- **Ongoing**: Bioinformatics Director - IUSM Alzheimer's Disease Drug Discovery Center, (NIH U54AG065181, PIs: Lamb, Palkowitz), 09/30/2019-08/31/2024

- **Ongoing**: MPI - QUBBD: Geometric time-frequency methods for multi-modal physiological monitoring, (NIH R01 EB025018, PIs: Chi, Lin, Huang, Wang), 05/12/2018 – 06/30/2020

- **Ongoing**: PI - BD4ISU: Big Data for Indiana State University (NIH R25, PIs: Bai, Huang, Coombes), 9/1/2017-4/30/2021.

- **Ongoing**: PI – Informatics links between histological features and genetics in cancer, (NCI ITCR U01, PI – Kun Huang), 5/18/2015-4/30/2019.

- **Ongoing**: MPI - MITF: Regulating osteoclast gene expression and function, (NIAAM R01, PIs: Ostrowski, Sharma, Huang, Weil), 2/1/2015-1/31/2020.

- **Ongoing**: co-Investigator – The Indiana University Center for Pediatric Pharmacology and Precision Medicine (NIH/NICHD U54, PI: Renbarger), 9/22/2016-06/30/2021

- **Ongoing**: Director for Data Science – Developmental and HyperActive Ras Tumor SPORE (NIH U54, PI: Clapp), 9/01/15-08/31/2021

- **Ongoing**: PI – High performance analytics and visualization of proteome and genomics data, (Leidos/Nvidia Foundation/NCI, PI – Kun Huang), 1/28/2015-1/27/2017.

- **Ongoing**: co-Investigator (OSU PI) – Quantitative structure-function analysis of cerebral cortex assembly at clonal level, (Human Frontier Science Program, Leading PI – Shi), 9/1/2014-8/31/2017.

- **NCE**: co-PI - BCSP: ABI Innovation: Collaborative Research: Predicting changes in protein activity from changes in sequence by identifying the underlying Biophysical Conditional Random Field, (NSF ABI Medium Grant, PIs – Ray, Machiraju, Magllery, Huang), 6/1/2014 – 5/31/2017.

- **NCE**: Partnering PI – Integrative lifecourse and genetic analysis of military working dogs, (Department of Defense, PIs – Alveraz, Huang, Couto), 9/1/2011-8/31/2015 (NCE to 8/31/2017).

- **Completed**: OSU PI – Web-Based Infrastructure for Comparison and Validation of Image Computing Methods (NIH STTR 9R42MH106302-02, PI: Aylward at Kitware, Inc), 03/01/2015 – 02/28/2017.

- **Completed**: co-Investigator - Functional genomics applied to innate immune determinants of human TB, (Bill and Melinda Gates Foundation, PIs: Schlesinger, Sadee), 2015-2018.

- **Completed**: co-Investigator – Enhancing NK Cell Activity by Dietary Diphyllin Lignans for Cancer Prevention (NCI R01 CA185301-01A1, PIs: Caligiuri, Yu), 12/18/2014-08/31/2019.

- **Completed**: co-Investigator - Chemoprevention of upper aerodigestive track cancer by dietary zinc (NCI R01 CA118560 07A1, PI: Fong), 04/01/2013-03/31/2017.

- **Completed**: senior personnel - STTR Phase I: Advanced Manufacturing Processes for Multiple Field Freeform Microlens Arrays for Ultra-Low Cost Medical Endoscopy, (NSF STTR Phase I #1448935, PIs – Shankar, Yi), 1/1/2015 – 12/31/2015.

- **Completed**: co-Investigator – Expression Genetics in Drug Therapy (NIDA 1U01GM092655-01, PI: Sadee), 7/1/2010-6/31/2015.

- **Completed**: co-Investigator – Center for Integrated Cancer Biology Program (NCI U54 CA113001-04 PPG Leader: Tim Huang), 9/30/2004 - 5/31/2015.

- **Completed**: co-Investigator - The Ohio State University Comprehensive Cancer Center (NCI CCSG P30 grant, PI: Michael Caligiruri).

- **Completed**: MPI - Informatics methods for identifying breast cancer control genes and proteins (NCI R01, PIs – Jeffrey Parvin, Kun Huang, Umit Catalyurek), 6/1/2009-4/30/2015.

- **Completed**: PI – Integrated Morphological and Genome Analysis for Computer-Aided Diagnosis and Computer Intervened Personalized Treatment for Lung Cancer, (UK CCTS & OSU CCTS Joint Pilot Award, PIs – Huang/OSU, Lin/UK), 9/1/2012-2/28/2014.

- **Completed**: PI – Cloud Computing and Visualization Tools for Kbase, (Department of Energy SBIR grant, PIs – Baumes/KitWare, Huang/OSU), 2/20/2012-11/19/2012.

- **Completed:** co-Investigator - Lymphocyte functions in the injured spinal cord (NIH R01, PI-Philip Popovich), 09/30/2003 – 01/31/2014.

- **Completed:** co-Investigator - Alginate oligomers to treat infectious microbial biofilms (Department of Defense, PI: Sen), 6/1/2011-5/31/2012.

- **Completed**: co-PI - A comprehensive workflow for large histology segmentation and visualization (NLM contract, PI – Machiraju, Huang), 7/1/2010-12/31/2011.

- **Completed**: co-PI – A comprehensive workflow for robust characterization of microstructure for cancer studies (NLM contract, PI – Machiraju, Huang), 5/1/2011-9/23/2011.

- **Completed**: co-PI - PhenoLIMS – a laboratory information system (LIMS) for gleaning molecular and morphological phenotypes in clinical outcomes (OSU CCTS New Methodology Grant, PI – Machiraju, Huang), 9/1/2010-8/31/2011.

- **Completed**: PI – Build 3D Models for Biomedical Samples at Micron Resolution (The Ohio Supercomputing Center Grant PAS0328-1, 2007, Award: 10000 Resource Units.).

- **Completed**: PI – Experimental and Computational Tools for Analyzing Microcircuitry Development of Ontogentic Radial Units in Mouse Neocortext (multi-PI NIH R21, other PI: Songhai Shi), 7/01/2008-5/31/2011.

- **Completed**: PI - Multi-Resolution Analysis and Visualization of ChIP-seq Data in Genome-Wide Study on the Roles of Estrogen Receptor in Breast Cancer (PhARMA Foundation Young Investigator Grant), 2/1/2009-1/31/2011.

- **Completed**: co-Investigator - Role of PTEN in the tumor microenvironment (Department of Defense BCRP, PI: Gustavo Leone), 10/2006 – 6/15/2009.

- **Completed**: co-Investigator - NIH-BISTI center for grid-enabled medical image analysis (GEMIAC) (PI: Joel Saltz), 07/01/2003 - 07/30/2007.

Grant reviewer

- Maryland Industrial Partnership (MIPS) Grant -2006.

- San Diego State University Grant – 2009

- National Institute of Science Grant - 2010

- National Science Foundation review panel – 2011.

- National Institute of Health Grant Review Study Sections
  - RC4 grant review – 2010 (mail in).
  - ZDE1 study section – June 2012.
  - ZRG1 SBIB – Q80 study section – February 2014, June 2014, February 2015, October 2015, February 2016.
  - BDMA study section – September 2014, June 2015, June 2016, February 2017, October 2018.
  - ITCR special study section – October 2017, February 2018, October 2018, March 2019.
  - IMAT special study section – February 2019.
  - Director's Early Independence Award Review special study section (ZRG1 PSE-H) – March 2019 (mail in).

- GCAT study section – October 2016.
- Special study section on consortium of data discovery – May 2014.
- Innovative Molecular and Cellular Analysis special emphasis panel (ZCA1 TCRB) – February 2019
- Small Business: Computational, Modeling, and Biodata Management (ZRG1 IMST-K (14)) – July 2019
- Academic-Industrial Partnerships Research for Cancer Diagnosis and Treatment (ZRG1 SBIB-Q (57)) – October 2019, February 2020
- HuBMAP Tissue Mapping Centers U54 (ZRG1 BST-U (50)) – May 2019, June 2020, June 2021
- NCI Research Specialist Award R50 (ZCA1 SRB-1 (M1)) – February 2020
- NCI SPORE P50 I Review (ZCA1 RPRB-N (O1)) – May 2020, May 2021
- NCI R21 study section – February 2021
- NIH BDMA slate member – Oct 2021 to June 2024
- Hongkong Research Support Council – 2012, 2013, 2014, 2015, 2017, 2018, 2019, 2020.
- Murtha Cancer Center / Water Reed Hospital research grant – 2015.

Publications:

- **Peer-reviewed journal papers (impact factors are based on the year of publication)**

1. Johnson T, Yu CY, Huang Z, Xu S, Wang T, Dong C, Shao W, Abu Zaid M, Huang X, Wang J, Bartlett C, Zhang Y, Walker B, Liu Y, **Huang K***, **Zhang J***. Diagnostic Evidence GAuge of Single cells (DEGAS): a flexible deep transfer learning framework for prioritizing cells in relation to disease, *Genome Medicine*, 14:11, 2022.

2. George R, Htoo A, Cheng M, Masterson T, **Huang K**, Adra N, Kaimakliotis H, Akgul M, Cheng L. Artificial intelligence in prostate cancer: Definitions, current research, and future directions, accepted to *Urologic Oncology: Seminars and Original Investigations*, 2022.

3. Shao W, Luo X, Zhang Z, Han Z, Chandrasekaran V, Turzhitsky V, Bali V, Roberts A, Metzger M, Baker J, Rosa CL, Weaver J, Dexter P, **Huang K**. Application of unsupervised deep learning algorithms for identification of specific clusters of chronic cough patients from EMR data, *BMC Bioinformatics*, 23(3):140, 2022.

4. Wu Y, Cheng M, Huang S, Pei Z, Zuo Y, Liu J, Yang K, Zhu Q, Zhang J, Hong H, Zhang D, **Huang K**, Cheng L, Shao W. Recent Advances of Deep Learning for Computational Histopathology: Principles and Applications, *Cancers*, 14(5): 1199, 2022.

5. Liu Z, Johnson T, Shao W, Zhang M, **Zhang J***, **Huang K***. Optimal transport- and kernel-based early detection of mild cognitive impairment patients based on magnetic resonance and positron emission tomography images, *Alzheimer's Research & Therapy*, 14:4, 2022.

6. Sharpnack M, Johnson T, Chalkey R, Han Z, Carbone D, **Huang K***, **He K***. TSAFinder: exhaustive tumor-specific antigen detection with RNAseq, *Bioinformatics*, 38(9): 2422-2427, 2022.

7. Cheng J, Pan Y, Huang W, **Huang K**, Cui Y, Hong W, Wang L, Ni D, Tan P. Differentiation

between immune checkpoint inhibitor-related and radiation pneumonitis in lung cancer by CT radiomics and machine learning, accepted to *Medical Physics*, 2022.

8. Storey S, Zhang Z, Luo X, Metzger M, Jakka AR, **Huang K**, Von Ah D. Differences in Health-Related Outcomes and Health Care Resource Utilization in Breast Cancer Survivors With and Without Type 2 Diabetes, *Journal of Patient-Centered Research and Reviews*, 9(1): 15-23, 2022

9. Huang X, **Huang K**, Johnson T, Radovich M, Zhang J, Ma J, Wang Y. ParsVNN: Parsimony Visible Neural Networks for Uncovering Cancer-Specific and Drug-sensitive Genes and Pathways, accepted to *NAR Genomics and Bioinformatics*, 2021.

10. Luo X, Gandhi P, Storey S, Zhang Z, Han Z, **Huang K**. A Computational Framework to Analyze the Associations between Symptoms and Cancer Patient Attributes Post Chemotherapy using EHR data, accepted to *IEEE Journal of Biomedical and Health Informatics*, 2021.

11. Luo X, Gandhi P, Storey S, Zhang Z, Han Z, **Huang K**. A Deep Language Model for Symptom Extraction from Clinical Text and Its Application to Extract COVID-19 symptoms from Social Media, accepted to *IEEE Journal of Biomedical and Health Informatics*, 2021.

12. Luo X, Gandhi P, Zhang Z, Shao W, Han Z, Chandrasekaran V, Turzhitsky V, Bali V, Roberts AR, Metzger M, Baker J, La Rosa C, Weaver J, Dexter Paul, **Huang K**. Applying interpretable deep learning models to identify chronic cough patients using EHR data, *Computer Methods and Programs in Biomedicine*, 210: 106395, 2021.

13. Lu Z, Zhan X, Wu Y, Cheng J, Shao W, Ni D, Han Z, Zhang J, **Feng Q***, **Huang K***. BrcaSeg: A Deep Learning Approach for Tissue Quantification and Genomic Correlations of Histopathological Images, accepted to *Genomics, Proteomics, and Bioinformatics*, 2021.

14. Dong C, Cesarano A, Bombaci G, Reiter JL, Yu CY, Wang Y, Jiang Z, Abu Zaid M, **Huang K**, Lu X, Walker B, Perna F, Liu Y. Intron retention-induced neoantigen load correlates with unfavorable prognosis in multiple myeloma, accepted to *Oncogene*, 2021.

15. Liu Y, Ye X, Zhan X, Yu CY, **Zhang J***, **Huang K***. TPQCI: A topology potential-based method to quantify functional influence of copy number variations, *Methods*, 192: 46-56, 2021.

16. Shao W, Wang T, Huang Z, Han Z, **Zhang J***, **Huang K***. Weakly Supervised Deep Ordinal Cox Model for Survival Prediction from Whole-slide Pathological Images, accepted to *IEEE Transactions on Medical Imaging*, 2021.

17. Wang T, Shao W, Huang Z, Tang H, Zhang J, **Ding Z***, **Huang K***. MOGONET integrates multi-omics data using graph convolutional networks allowing patient classification and biomarker identification, *Nature Communications*, 12 (1): 3445, 2021. (* co-corresponding authors)

18. Saeed O, Mann SA, Luchini C, **Huang K**, Zhang S, Sen Joyashree, Piredda ML, Wang M, Baldrige LA, Sperling RM, Curless KL, Cheng L. Evaluating Mismatch Repair Deficiency for Solid Tumor Immunotherapy Eligibility: Immunohistochemistry versus Microsatellite Molecular Testing. Accepted to *Human Pathology*, 2021.

19. Storey S, Zhang Z, Luo X, Metzger M, Jakka AR, **Huang K**, Von Ah D. Differences in

health-related outcomes and utilization of healthcare resources in breast cancer survivors with and without type 2 diabetes. *Journal of Patient-Centered Research & Reviews* (in press), 2021.

20. Chen D, Abu Zaid M, Reiter JL, Czader M, Wang L, McGuire P, Xuei X, Gao H, **Huang K**, Abonour F, Walker BA, Liu Y. Cryopreservation preserves cell-type composition and gene expression profiles in bone marrow aspirates from multiple myeloma patients. *Frontiers in Genetics*, 12: 583, 2021.

21. Shao W, Xiang S, Zhang Z, **Huang K**, Zhang J. Hyper-graph based Sparse Canonical Correlation Analysis for the Diagnosis of Alzheimer's Disease from Multi-dimensional Genomic Data, *Methods*, 189: 86-94, 2021.

22. Cheng J, Liu Y, Huang W, Hong W, Wang L, Zhan X, Han Z, Ni D, **Huang K**, Zhang J. Computational Image Analysis Identifies Histopathological Image Features Associated With Somatic Mutations and Patient Survival in Gastric Adenocarcinoma. *Frontiers in Oncology*, 11: 1058, 2021.

23. Liu Y, Ye X, Zhan X, Yu C, Zhang J, **Huang K**. TPQCI: A Topology Potential-Based Method to Quantify Functional Influence of Copy Number Variations, in printing for *Methods*, 2021.

24. Storey S, Zhang Z, Luo X, Von Ah D, Metzger M, Zhang J, Jakka AR, **Huang K**. Clinical outcomes and healthcare utilization in colorectal cancer survivors with diabetes. *Oncology Nursing Forum* (in press), 2021.

25. Johnson T, Xiang S, Dong T, Huang Z, Cheng M, Wang T, Yang K, Ni D, **Huang K**, Zhang J. Combinatorial analyses reveal cellular composition changes have different impacts on transcriptomic changes of cell type specific genes in Alzheimer's Disease, *Scientific Reports*, 11(1):353, 2021.

26. Johnson T, Niderker P, **Huang K***, Zhang J*. Spatial Cell Type Composition in Normal and Alzheimers Human Brains is Revealed Using Integrated Mouse and Human Single Cell RNA Sequencing, *Scientific Reports*, 10(1): 108014, 2020. (* co-corresponding authors)

27. Zhan X, Liu Y, Yu C, Wang T-F, Zhang J, Ni D, **Huang K**. A pan-kidney cancer study identifies subtype specific perturbations on pathways with potential drivers in renal cell carcinoma. *BMC Medical Genomics*, 13: 190, 2020.

28. Xu S, Lu Z, Shao W, Yu C, Reiter JL, Feng Q, Feng W, **Huang K***, **Liu Y***. Integrative analysis of histopathological images and chromatin accessibility data for estrogen receptor-positive breast cancer. *BMC Medical Genomics*, 13: 195, 2020.

29. Sun L, Zhang J, Chen W, Chen Y, Zhang X, Yang M, Xiao M, Ma F, Yao Y, Ye M, Zhang Z, Chen K, Chen F, Ren Y, Ni S, Zhang X, Yan Z, Sun Z-R, Zhou H-M, Yang H, Xie S, Haque ME, **Huang K***, Yang Y*. Attenuation of epigenetic regulator SMARCA4 and ERK-ETS signaling suppresses aging-related dopaminergic degeneration. *Aging Cell*, 19(9): e13210, 2020. (* co-corresponding authors)

30. Cao R, Yang F, Ma SC, Liu L, Zhao Y, Li Y, Wu DH, Wang T, Lu WJ, Cai WJ, Zhu HB, Guo XJ, Lu YW, Kuang JJ, Huan WJ, Tang WM, **Huang K**, Huang J, Yao J, Dong ZY. Development and interpretation of a pathomics-based model for the prediction of microsatellite instability in Colorectal Cancer. *Theranostics*, 10(24):11080-11091, 2020.

31. Shao W, Wang T, Sun L, Dong T, Han Z, Huang Z, Zhang J, Zhang D, **Huang K**. Multi-task multi-modal learning for joint diagnosis and prognosis of human cancers. _Medical Image Analysis_, 65: 101795, 2020. (IF: 11.148)

32. Panayides AS, Amini A, Filipovic ND, Sharma A, Tsaftaris SA, Young A, Foran D, Do N, Golemati S, Kurc T, **Huang K**, Nikita KS, Veasey BP, Zervakis M, Saltz JH, Pattichis CS. AI and Medical Imaging Informatics: Current Challenges and Future Directions, accepted to _IEEE Journal of Biomedical and Health Informatics_, 2020.

33. Sharpnack M, Cho JH, Johnson T, Otterson GA, Shields P, **Huang K**, Carbone D, He K. Clinical and Molecular Correlates of Tumor Mutation Burden in Non-Small Cell Lung Cancer, _Lung Cancer_, 146: 36-41, 2020.

34. Lu Z, Xu S, Shao W, Wu Y, Zhang J, Han Z, Feng Q, **Huang K**. Deep learning-based characterization of tumor-infiltrating lymphocytes in breast cancers from histopathology images and multiomics data, accepted to _JCO Clinical Cancer Informatics_, 2020.

35. Cheng J, Han Z, Mehra R, Shao W, Cheng M, Feng Q, Ni D*, **Huang K***, Cheng L*, Zhang J*. Computational analysis of pathological images enables a better diagnosis of TFE3 Xp11.2 translocation renal cell carcinoma, _Nature Communications_, 11(1):1778, 2020. (* co-corresponding authors) PubMed PMID: 32286325; PubMed Central PMCID: PMC7156652.

36. Ge R, Wang Z, Montironi R, Jiang Z, Cheng M, Santoni M, **Huang K**, Massari F, Lu X, Cimadamore A, Lopez-Beltran A, Cheng L. Epigenetic Modulations and Lineage Plasticity in Advanced Prostate Cancer, _Annals in Oncology_ (in press), 2020. (**IF: 14.2**)

37. Wang T, Johnson T, Shao W, Zhang J*, **Huang K***. BERMUDA: a novel deep transfer learning method for single-cell RNA sequencing batch correction reveals hidden high-resolution cellular subtypes, _Genome Biology_, 20(1): 165, 2019. PubMed PMID: 31405383; PubMed Central PMCID: PMC6691531. (**IF: 14.0**)

38. Yang Y, Kaimakliotis H, Williamson S, Michael K, **Huang K**, Barboza M, Idrees M, Grignon D, Eble J, Liang C. Micropapillary Urothelial Carcinoma of Urinary Bladder Displays Immunophenotypic Features of Luminal and p53-like Subtypes and Is Not a Variant of Adenocarcinoma. Accepted to _Urologic Oncology: Seminars and Original Investigations_, 2019. (**IF: 2.86**)

39. Zhan X, Cheng J, Huang Z, Han Z, Helm B, Liu X, Zhang J, Wang T, Ni D, **Huang K**. Correlation Analysis of Histopathology and Proteogenomics Data for Breast Cancer, _Molecular and Cellular Proteomics_, 18(8 suppl 1): S37-S51, 2019. PubMed PMID: 31285282. (**IF: 4.8**)

40. Han Y, Ye X, Wang C, Liu Y, Zhang S, Feng W, **Huang K**, Zhang J. Integration of molecular features with clinical information for predicting outcomes for neuroblastoma patients. _Biology Direct_, 14(1):16, 2019. (**IF: 3.01**)

41. Raman S, Singh S, Pecot T, Caserta E, **Huang K**, Rittscher J, Machiraju J, Leone G. Capturing Variations in Nuclear Phenotypes, accepted to _Journal of Computational Science_, 2019. (**IF: 2.5**)

42. Huang Z, Han Z, Wang T, Shao W, Xiang S, Salama P, Rizkalla M, **Huang K***, Zhang J*. TSUNAMI: Translational Bioinformatics Tool Suite for Network Analysis and Mining,

accepted to *Genomics, Proteomics, and Bioinformatics*, 2019. **(IF: 6.65)**

43. Shao W, Han Z, Cheng J, Cheng L, Wang T, Sun L, Lu Z, Zhang J, Zhang D, **Huang K**. Integrative analysis of pathological images and multi-dimensional genomic data for early-stage cancer prognosis, *IEEE Transactions on Medical Imaging*, 39(1): 99-110, 2019. PubMed PMID: 31170067. **(IF: 7.82)**

44. Johnson T, Wang T, Huang Z, Yu CY, Wu Y, Han Y, Zhang Y, **Huang K***, Zhang J*., LAmbDA: label ambiguous domain adaptation dataset integration reduces batch effects and improves subtype detection, *Bioinformatics*, 35(22): 4696-4706, 2019. PubMed PMID: 31038669; PubMed Central PMCID: PMC6853662. **(IF: 4.53)**

45. Yu CY, Xiang S, Huang Z, Johnson T, Zhan X, Han Z, Abu Zaid M, **Huang K**. Gene Co-expression Network and Copy Number Variation Analyses Identify Transcription Factors Involved in Multiple Myeloma Progression, accept to *Frontiers of Genetics*, 2019. **(IF: 3.52)**

46. Johnson T, Li S, Franz E, Huang Z, Li S, Moray J Campbell MJ, **Huang K**, Zhang Y. PseudoFuN: Deriving functional potentials of pseudogenes from integrative relationships with genes and miRNAs across 32 cancers, *GigaScience*, 8(5): giz046, 2019. PubMed PMID: 31029062 ; PubMed Central PMCID: PMC6486473. **(IF: 7.3)**

47. Smerekanych S, Johnson T, **Huang K**, Zhang Y. Pseudogene-gene functional networks are prognostic of patient survival in breast cancer, accepted to *BMC Medical Genomics*, 2019. **(IF: 2.57)**

48. Abrams Z, Johnson T, **Huang K**, Payne P, Coombes K. A Protocol to Evaluate RNA Sequencing Normalization Methods, accepted to *BMC Bioinformatics*, 2019. **(IF: 2.51)**

49. Huang Z, Johnson T, Han Z, Helm B, Cao S, Zhang C, Salama P, Rizkalla M, Yu CY, Cheng J, Xiang S, Zhan X, Zhang J, **Huang K**. Deep Learning-based Cancer Survival Prognosis from RNA-seq Data: Approaches and Evaluations, accepted to *BMC Medical Genomics*, 2019. **(IF: 2.57)**

50. Helm B, Zhan X, Renbarger J, Murray M, Pollock K, Ferguson M, Pandya P, Han Z, Ni D, Zhang J, **Huang K**. Gene co-expression networks restructured by gene fusion in rhabdomyosarcoma cancers, accepted to *Genes*, 2019. **(IF: 3.33)**

51. Wang T, Zhang J, **Huang K**. Generalized Gene Co-Expression Analysis via Subspace Clustering Using Low-Rank Representation, accepted to *BMC Bioinformatics*, 2019. **(IF: 2.51)**

52. Huang Z, Zhan X, Xiang S, Johnson T, Helm B, Yu C, Zhang J, Salama P, Rizkalla M, Han Z, **Huang K**. SALMON: Survival Analysis Learning with Multi-Omics Neural Networks on Breast Cancer, accepted to *Frontiers in Genetics*, 2019. **(IF: 3.52)**

53. Han Y, Ye X, Cheng J, Zhang S, Feng W, Han Z, Zhang J, **Huang K**. Integrative analysis based on survival associated co-expression gene modules for predicting neuroblastoma patient survival times, *Biology Direct*, in press, 2019. **(IF: 3.01)**

54. Xiang S, Huang Z, Wang T, Han Z, Yu CY, Ni D, **Huang K***, Zhang J*. Condition-specific gene co-expression network mining identifies key pathways and regulators in the brain tissue of Alzheimer's disease patients. *BMC Medical Genomics*. 2018; 11 Suppl 6: 115. (PMID: 30598117; PMCID: PMC6311927) (*co-corresponding authors) **(IF: 2.57)**

55. Srivastava A, Kulkarni C, **Huang K**, Parwani A, Mallick P, Machiraju R. Imitating Pathologist Based Assessment With Interpretable and Context Based Neural Network Modeling of Histology Images. _Biomedical Informatics Insights_. 2018.

56. Li Y, Liu Y, Xu H, Jiang G, Van der Jeught K, Fang Y, Zhou Z, Zhang L, Frieden M, Wang L, Luo Z, Radovich M, Schneider BP, Deng Y, Liu Y, **Huang K**, He B, Wang J, He X, Zhang X, Ji G, Lu X. Heterozygous deletion of chromosome 17p renders prostate cancer vulnerable to inhibition of RNA polymerase II. _Nat Commun_. 2018 Oct 22;9(1):4394. (PMID: 30349055; PMCID: PMC6197287) **(IF: 11.88)**

57. Ding H, Sharpnack M, Wang C, **Huang K***, Machiraju R*. Integrative cancer patient stratification via subspace merging. _Bioinformatics_. 2018 Oct 17. [Epub ahead of print] (PMID: 30329022.) (*co-corresponding authors) **(IF: 4.53)**

58. Gu Y, Servello D, Han Z, Lalchandani RR, Ding JB, **Huang K**, Gu C. Balanced Activity between Kv3 and Nav Channels Determines Fast Spiking in Mammalian Central Neurons. _iScience_. 2018 October 17.

59. Carey HA, Hildreth BE, Geisler JA, Nickel MC, Cabrera J, Ghosh S, Jiang Y, Yan J, Lee J, Makam S, Young NA, Valiente GR, Jarjour WN, **Huang K**, Rosal TJ, Tori Enhancer variants reveal a conserved transcription factornetwork governed by PU.1 during osteoclast differentiation. _Bone Research_, 2018. **(IF: 12.35)**

60. Sharpnack MF, Chen B, Aran D, Kosti I, Sharpnack DD, Carbone DP, Mallick P, **Huang K**. Global Transcriptome Analysis of RNA Abundance Regulation by ADAR in Lung Adenocarcinoma. _EBioMedicine_, 2018 Jan;27:167-175. (PMID: 29273356; PMCID: PMC5828651.)

61. Hankey W, Mclhatton M, Ebede K, Kennedy B, Hancioglu B, Zhang J, Brock G, **Huang K**, Groden J. Mutational mechanisms that activate Wnt signaling and predict outcomes in colorectal cancer patients. Accepted to _Cancer Research_, 2017.

62. Cheng J, Mo X, Wang X, Parwani A, Feng Q§, **Huang K**§. Identification of topological features in renal tumor microenvironment associated with patient survival. Accepted to _Bioinformatics_, 2017. (§co-corresponding authors)

63. Johnson TS, Abrams ZB, Mo X, Zhang Y, **Huang K**. Lack of human cytomegalovirus expression in single cells from glioblastoma tumors and cell lines. In print, _Journal of Neurovirology_, 2017.

64. Zhang X-J, Li Z, Han Z, Sultan KT, **Huang K**, Shi SH. Precise inhibitory microcircuit assembly of developmentally related neocortical interneurons in cluster. _Nature Communications_, 16091, 2017.

65. Shi W, Xianyu A, Han Z*, Tang X, Li Z, Zhong H, Mao T, **Huang K***, Shi S-H*. Ontogenetic establishment of order-specific nuclear organization in the mammalian thalamus. Accepted to _Nature Neuroscience_, 2017. (*co-corresponding authors)

66. Han Z, Johnson T, Zhang J, **Huang K**. Functional Virtual Flow Cytometry – A Visual Analytic Approach for Characterizing Single Cell Gene Expression Patterns, Accepted to _Biomed International_, 2017.

67. Cheng J*, Zhang J*, Han Y, Wang X, Ye X, Meng Y, Pawani A, Han Z, Feng Q§, **Huang K**§, Integrative analysis of histopathological images and genomic data for predicting clear cell renal cell carcinoma prognosis, _Cancer Research_, 77(21): e91-e100, 2017. (*co-first authors, §co-corresponding authors)

68. Tang X, Srivastava A, Liu H, **Huang K***, Leone G*. AnnoPeak: a web application to annotate and visualize peaks from ChIP-seq/ChIP-exo-seq. Accepted to _Bioinformatics_, 2017. (*co-corresponding authors)

69. Syed R, Duggineni, Rutsky JH, Prengasamy, Zhang J, **Huang K**, Needleman B, Mikami D, Perry K, Hazey J, Rajagopalan S. Visceral adipose microRNA 223 is upregulated in human and murine obesity and modulates the inflammatory phenotype of macrophages. Accepted to _PLoS One_, 2016.

70. Kaewprag P, Newton C, Vermillion B, Kim S, **Huang K***, Machiraju R*. Predictive Models for Pressure Ulcers from Intensive Care Unit Electronic Health Records using Bayesian Networks. Accepted to _BMC Medical Informatics and Decision Making_, 2016. (*co-corresponding authors)

71. Taslim C, Weng D, Brasky T, Dumitrescu R, **Huang K**, Kallakury B, Krishnan S, Llanos A, Marian C, McElroy J, Schneider S, Spears L, Troester M, Freuden J, Geyer S, Shields P. Discovery and Replication of microRNAs for Breast Cancer Risk using Genome-Wide Profiling. Accepted to _Oncotarget_, 2016.

72. Sultan KT, Han Z, Zhang X-J, Xianyu A, Li Z, **Huang K***, Shi S-H*. Clonally Related GABAergic Interneurons Do Not Randomly Disperse But Frequently Form Local Clusters in the Forebrain. Accepted to _Neuron_, 2016. (* co-corresponding authors)

73. Kent LN, Rakijas JB, Pandit SK, Westendorp B, Chen HZ, Huntington JT, Tang X, Bae S, Srivastava A, Senapati S, Koivisto C, Martin CK, Cuitino MC, Perez M, Clouse JM, Chokshi V, Shinde N, Kladney R, Sun D, Perez-Castro A, Matondo RB, Nantasanti S, Mokry M, **Huang K**, Machiraju R, Fernandez S, Rosol TJ, Coppola V, Pohar KS, Pipas JM, Schmidt CR, de Bruin A, Leone G. E2f8 mediates tumor suppression in postnatal liver development. _Journal of Clinical Investigation_, 126(8): 2955-69, 2016.

74. Zhang J, **Huang K**. Pan-Cancer Analysis of Frequent DNA Co-Methylation Patterns Reveals Consistent Epigenetic Landscape Changes in Multiple Cancers. To appear in _BMC Genomics_, 2016.

75. Meng N, Machiraju R, **Huang K**. Identification of Recurrent Combinatorial Patterns of Chromatin Modifications at Promoters across Various Tissue Types. To appear in _BMC Bioinformatics_, 2016.

76. Wang J, Xia S, Arand B, Zhu H, Machiraju R, **Huang K**, Ji H, Jiang Q. Single-cell co-expression analysis reveals distinct functional modules, co-regulation mechanisms and clinical outcomes. _PLoS Computational Biology_, 12(4): e1004892, 2016.

77. Han Z, Zhang J, Sun G, Liu G, **Huang K**. A Matrix Rank Based Concordance Index for

Evaluating and Detecting Conditional Specific Co-Expressed Gene Modules, accepted to *BMC Genomics*, special issue for ICIBM'15, 2016.

78. Zhang J, Adams Z, Parvin J, **Huang K**. Integrative Analysis of Somatic Mutations and Transcriptomic Data to Functionally Stratify Breast Cancer Patients, accepted to *BMC Genomics* special issue for ICIBM'15, 2016.

79. Tang X, Liu H, Srivastava A, Pecot T, Chen Z, Wang Q, **Huang K**, Saenz-Robles MT, Cantalupo P, Pipas J, Leone G. Transcriptome regulation and chromatin occupancy by E2F3 and MYC in mice, *Scientific Data*, 16008, 2016.

80. Liu H, Tang X, Srivastava A, Pécot T, Daniel P, Hemmelgarn B, Reyes S, Fackler N, Bajwa A, Kladney R, Koivisto C, Chen Z, Wang Q, **Huang K**, Machiraju R, Saenz-Robles MT, Cantalupo P, Pipas J, Leone G. Redeployment of Myc and E2f1-3 drives Rb deficient cell cycles, accepted to *Nature Cell Biology*, 2015.

81. Ding H, **Huang K**, Machiraju R. GRAPHIE: Graph based Histology Image Explorer, *BMC Bioinformatics*, S11:S10, 2015.

82. Zhang J, **Huang K**. Normalized lmQCM : an Algorithm for Detecting Weak Quasi-clique Modules in Weighted Graph with Application in Functional Gene Cluster Discovery in Cancer, accepted to *Cancer Informatics*, 2015.

83. Meng N, Machiraju R, **Huang K**. Identify Critical Genes in Development with Consistent H3K4me2 Patterns across Multiple Tissues, accepted to *ACM/IEEE Translations on Computational Biology and Bioinformatics*, 2015.

84. Albin A, Ji X, Borlawsky TB, Ye Z, Lin S, Payne PR, **Huang K**, Xiang Y. Enabling online studies of conceptual relationships between medical terms: developing an efficient web platform. *JMIR Med Inform*, 7;2(2):e23, 2015.

85. Gao P, Postiglione MP, Krieger TG, Hernandez L, Wang C, Han Z, Streicher C, Papusheva E, Insolera R, Chugh K, Kodish O, **Huang K**, Simons BD, Luo L, Hippenmeyer S, Shi SH. Deterministic progenitor behavior and unitary production of neurons in the neocortex. *Cell*, 159(4): 775-788, 2014.

86. Ozer HG, Usubalieva A, Dorrance A, Yilmaz AS, Caligiuri M, Marcucci G, **Huang K**. Identification of medium-sized copy number alterations in whole-genome sequencing, *Cancer informatics*, 13(suppl 3): 105-111, 2014.

87. Yates A, Webb A, Chamberlin H, **Huang K**, Machiraju R. Visualizing Relationships in Multidimensional Data with Glyph SPLOMs and Necessity Graphs, *Computer Graphics Forum*, 33(3): 301-310, 2014. (This paper was presented in EuroVis 2014). [*IF: 1.60*]

88. Liu B, Liu J, Wang G, **Huang K**, Li F, Zheng Y, Luo Y, Zhou F. A novel electrocardiogram parameterization algorithm and its application in myocardial infarction detection. *Computers in Biology and Medicine*, S0010-4825(14): 00212-1, 2014.

89. Hu Y, Wang Chao, **Huang K**, Xia F, Parvin JD, Mondal N. Regulation of 53BP1 Protein Stability by RNF8 and RNF168 Is Important for Efficient DNA Double-Strand Break Repair. *PLoS One*, 9 (10):e110522, 2014.

90. Ding H, Wang C, **Huang K**, Machiraju R. A visual analytic system for integrative genomics based cancer patient stratification. Accepted to *BMC Bioinformatics* Special Issue for BioVis

2014.

91.   Moldovan L, Anghelina M, Kantor T, Jones D, Ramadan E, Xiang Y, **Huang K**, Kolipaka A, Malarkey W, Ghasemzadeh N, Mohler P, Quyyumi A, Moldovan N. A module of human peripheral blood mononuclear cell transcriptional network containing primitive and differentiation markers is related to specific cardiovascular health variables. *PLoS One*, 9(4): e95124, 2014.

92.   Xu H-T, Han Z, Gao P, He S, Li Z, Shi W, Kodish O, Shao W, Brown KN, **Huang K**, Shi S-H. Distinct lineage-dependent structural and functional organization of the hippocampus. Accepted to *Cell*, 2014.

93.   Kotian S, Tapahsama B, Lockhart A, **Huang K**, Catalyurek U, Parvin J. NUSAP1 influences the DNA damage response by controlling BRCA1 protein levels. Accepted to *Cancer Biology & Therapy*, 2014. [*IF: 5.243*]

94.   Wang C, Machiraju R, **Huang K**. Breast Cancer Patient Stratification using a Molecular Regularized Consensus Clustering Method. *Methods* (In Press), 2014. [*IF: 3.641*]

95.   Li Q, **Huang K**, Machiraju R. 2013 IEEE Visualization Contest Winner: Observing Genomics and Phenotypical Patterns in the Developing Mouse Brain. Accepted to *IEEE Computer Graphics and Applications Magazine*, 2014. [*IF: 1.760*]

96.   Deiuliis J, Mihai G, Zhang J, Taslim C, Varghese JJ, Maiseyeu A, **Huang K**, Rajagopalan S. Renin-sensitive microRNAs correlate with atherosclerosis plaque progression. Accepted to *Journal of Human Hypertension*, 2013. [*IF: 2.818*]

97.   Wu Y, Kwak K J, Agarwal K, Marras A, Wang C, Mao Y, Huang X, Ma J, Yu B, Lee R, Vachani A, Marcucci G, Byrd J, Muthusamy N, Otterson G, **Huang K**, Castro C, Paulaitis M, Nana-Sinkam S P, Lee, L. Detection of extracellular RNAs in cancer and viral infection via tethered cationic lipoplex nanoparticles containing molecular beacons. Accepted to *Analytical Chemistry*, 2013. [IF: 5.695]

98.   Ren K, Lai A, Mukhopadhyay A, Machiraju R, **Huang K**, Xiang Y. Effectively processing medical term queries on the UMLS Metathesaurus by Layered Dynamic Programming. Accepted to *BMC Medical Genomics*, 2013. [*IF: 3.47*]

99.   Liebner D, **Huang K**, Parvin J. MMAD: Microarray Micro-dissection with Analysis of Differences is a computational tool for deconvoluting cell type specific contributions from tissue samples. Accepted to *Bioinformatics*, 2013. [*IF: 5.4*]

100. Zhang Y, Guan Z, Reader B, Shawler T, Mandrekar-Colucci S, **Huang K**, Weil Z, Bratasz A, Wells J, Powell N, Sheridan J, Whitacre C, Rabchevsky A, Nash M, Popovich P. Autonomic dysreflexia causes chronic immune suppression after spinal cord injury, *Journal of Neuroscience*, 33(32): 12970-12981, 2013. [*IF: 7.115*]

101. Xiang Y, Zhang J, **Huang K**. Mining tissue-tissue gene co-expression network for tumor microenvironment study and biomarker prediction, accepted to *BMC Genomics* special issue for InCoB, 2013. [*IF: 4.4*]

102. Wolock S, Yates A, Petrill SA, Blair C, Li N, Bohland JW, Machiraju R, **Huang K,** Bartlett CW. Gene x smoking interactions on human brain gene expression: finding common

mechanisms in adolescents and adults, *Journal of Child Psychology and Psychiatry*, 54(10): 1109-1119, 2013. [*IF: 4.281*]

103. Hu J, Chen C, **Huang K**，Mitchell T. A distribution pattern assisted method of transcription factor binding site discovery for both yeast and filamentous fungi. *Advances in Bioscience and Biotechnology*, 4:509-517. doi: 10.4236/abb.2013.44067, 2013.

104. Wang C, Pecot T, Zynger D, Shapiro C, Machiraju R, **Huang K**. Identifying survival associated morphological features of triple negative breast cancer using multiple datasets, accepted to *Journal of American Medical Informatics Association* (JAMIA), 2013. [*IF: 3.609*]

105. Taggart D, Camerlengo T, Harrison JK, Sherrer S, Kshetry A, Taylor J, **Huang K**, Suo Z. A High-Throughput and Quantitative Method to Assess the Mutagenic Potential of Translesion DNA Synthesis, accepted to *Nucleic Acid Research*, 2013. [*IF: 8.026*]

106. Wang J, Lan X, Hsu P-Y, Hsu H-K, **Huang K**, Parvin JD, Huang T, Jin VX. Genome-wide analysis uncovers high frequency, strong differential chromosomal interactions and their associated epigenetic patterns in E2-mediated gene regulation, accepted to *BMC Genomics*, 2013. [*IF: 4.07*]

107. Webb A, Papp AC, Sanford JC, **Huang K**, Parvin JD, Sadee W. Expression of mRNA transcripts encoding membrane transporters detected with whole transcriptome sequencing of human brain and liver, *Pharmacogenetics and Genomics*, 23(5): 269-278, 2013. [*IF: 3.485*]

108. Kalluru V, Machiraju R, **Huang K**. Identify condition specific gene co-expression networks, *International Journal of Computational Biology and Drug Design*, 6(1-2): 50-59, 2013.

109. Zhang J, Ni S, Xiang Y, Parvin J, Yang Y, Zhou Y, **Huang K**. Gene co-expression analysis predicts chromosomal aberration loci associated with colon cancer metastasis, *International Journal of Computational Biology and Drug Design*, 6(1-2): 60-71, 2013.

110. Chen HZ, Ouseph MM, Li J, Pecot T, Chokshi V, Kent L, Bae S, Byrne M, Duran C, Comstock G, Trikha P, Mair M, Senpati S, Martin CK, Gandhi S, Wilson N, Liu B, Huang Y-W, Thompson JC, Raman S, Singh S, Leone M, Machiraju R, **Huang K**, Mo X, Fernandez S, Kalaszczynska I, Wolgemuth DJ, Sicinski P, Huang T, Jin V, Leone G. Canonical and atypical E2Fs regulate the mammalian endocyte, *Nature Cell Biology*, 11(14):1192-1202, 2012. [*IF: 19.527*]

111. Yoon SO, Park DJ, Ryu JC, Ozer HG, Tep C, Shin YJ, Lim TH, Pastorino L, Junwar AJ, Walton JC, Nagahara AH, Lu KP, Nelson RJ, Tuszynski MH, **Huang K**. JNK3 perpetuates metabolic stress induced by Ab peptides, *Neuron*, 75(5): 824-837, 2012. [*IF: 14.736*]

112. Liu H-W, Zhang J, Heine G, Arora M, Ozer HG, Onti-Srinivasan R, **Huang K**, Parvin J. Chromatin modification by SUMO-1 stimulates the promoters of translation machinery genes, *Nucleic Acid Research*, 40(20): 10172-10186, 2012. [*IF: 8.026*]

113. Arora M, Zhang J, Heine G, Ozer HG, Liu H-W, **Huang K**, Parvin J. Promoters Active in Interphase are Bookmarked during Mitosis by Ubiquitination, *Nucleic Acid Research*, 40(20): 10187-10202, 2012. [*IF: 8.026*]

114. Zhang J, Lu K, Xiang Y, Islam M, Kotian S, Kais Z, Lee C, Arora M, Liu H-W, Parvin JD, **Huang K**. Weighted frequent gene co-expression network mining to identify genes involved in genome stability, *PLoS Computational Biology*, 8(8): e1002656, 2012. [*IF: 5.215*]

115. Yu Y-C, He S, Chen S, Fu Y, Brown KN, Yao X-H, Ma J, Gao KP, Sosinsky GE, **Huang K**, Shi S-H. Preferential electrical coupling regulates neocortical lineage-dependent microcircuit assembly, *Nature*, 486(7401):113-117, 2012. [*IF: 31.08*]

116. Xiang Y, Fuhry D, Kaya K, Jin R, Catalyurek U, **Huang K**. Merging network patterns: a general framework to summarize biomedical network data, *Network Modeling Analysis in Health Informatics and Bioinformatics*, 1(3): 103-116, 2012.

117. Taslim C, **Huang K**, Lin S, Huang T. Genome-wide novel promoters prediction and chromatin signature analysis using finite mixture models, *BMC Genomics*, 13(S6): S3, 2012. [*IF: 4.21*]

118. Xu RX, Allen D, Hu J, Gnyawali S, Melvin J, Elgharably H, Gordillo G, **Huang K**, Bergdall V, Litorja M, Rice J, Hwang J, Sen CK. Developing digital tissue phantoms for hyperspectral imaging of ischemic wounds, *Biomedical Optics Express*, 3(6): 1433-1445, 2012. [*IF: 2.333*]

119. Zhang P, Mourad R, Xiang Y, **Huang K**, Huang T, Nephew K, Liu Y, Li L. A dynamic time order network for time-series gene expression data analysis, *BMC Systems Biology*, 6(S3): S9, 2012. [*IF: 3.57*]

120. Ozer HG, Parvin J, **Huang K**. DFI: gene feature discovery in RNA-seq experiments from multiple sources, *BMC Genomics*, 13(S8): S11, 2012. [*IF: 4.21*]

121. Zhang J, Parvin J, **Huang K**. Redistribution of H3K4me2 on neural tissue specific genes during mouse brain development, *BMC Genomics*, 13(S8): S5, 2012. [*IF: 4.21*]

122. Taslim C, Chen Z, **Huang K**, Huang T, Wang Q, Lin S. Integrated analysis identifies a class of androgen responsive genes regulated by short combinatorial long-range mechanism facilitated by CTCF, *Nucleic Acid Research*, 40(11): 4754-4764, 2012. [*IF: 8.026*]

123. Ouseph MM, Li J, Chen H-Z, Pecot T, Wenzel P, Thompson J, Comstock G, Chokshi V, Byrne B, Forde B, Chong J-L, **Huang K**, Machiraju R, de Bruin A, Leone G, Atypical E2F repressors and activators coordinate placental development, *Developmental Cell*, 22(4):849-862, 2012. [*IF: 13.946*]

124. Han Z, Lu T, Pecot T, Huang T, Machiraju R, **Huang K**. A signal processing approach for enriched region detection in RNA polymerase II ChIP-seq data, *BMC Bioinformatics*, 13(Suppl 2): S2, 2012. [*IF: 3.03*]

125. Xiang Y, Zhang CQ, **Huang K**. Predicting glioblastoma prognosis networks using weighted gene co-expression network analysis on TCGA data, *BMC Bioinformatics*, 13(Suppl 2), S12, 2012. [*IF: 3.03*]

126. Taslim C, **Huang K**, Huang T, Lin S. Analyzing ChIP-seq data: preprocessing, normalization, differential identification, and binding pattern characterization. *Methods in Molecular Biology*, 802: 275-291, 2012. [*IF: 13.9*]

127. Brown KN, Chen S, Han Z, Lu C-H, Tan X, Ding L, Zhang X-J, Cruz AL, Saur D, Anderson SA, **Huang K**, Shi S-H. Clonal production and organization of inhibitory interneurons in the neocortex, *Science*, 334(6055): 480-486, 2011. [*IF: 31.364*]

128. Xiang Y, Lu K, James S, Bowlasky T, **Huang K**, Payne P. K-neighborhood decentralization: a comprehensive solution to index the UMLS for large scale knowledge discovery, *Journal of Biomedical Informatics*, 45(2): 323-336, 2012. [*IF: 1.719*]

129. Taccioli C, Chen H, Jiang Y, Liu XP, **Huang K**, Smalley KJ, Farber JL, Croce CM, Fong LY. Dietary zinc deficiency fuels esophageal cancer development by inducing a distinct inflammatory signature, advanced online publication, _Oncogene_, 2011. [_IF: 6.373_]

130. Beyer S, Zhang X, Jimenez R, Lee M-L, Richardson A, **Huang K**, Jhiang S. Microarray analysis of genes associated with cell surface NIS protein levels in breast cancer. _BMC Research Notes_, 4:397, 2011.

131. Xu C, Schmitt JM, Akasaka T, Kubo T, **Huang K**. Automatic detection of stent struts with thick neointimal growth in intravascular optical coherence tomography image sequences, _Physics in Medicine and Biology_, 56(20): 6665, 2011. [_IF: 3.056_]

132. Kais Z, Barsky SH, Mathsyaraja H, Zha Alicia, Ransburgh D, He G, Pilarski R, Shapiro C, **Huang K**, Parvin J. KIAA0101 interacts with BRCA1 and regulates centrosome number, _Molecular Cancer Research_, 9(8):1091-1099, 2011. [_IF: 4.16_]

133. Li R, Ackerman WE 4th, Summerfield TL, Yu L, Gulati P, Zhang J, **Huang K**, Romero R, Kniss DA. Inflammatory gene regulatory networks in amnion cells following cytokine stimulation: translational systems approach to modeling human parturition, _PLoS One_, 6(6): e20560, 2011. [_IF: 4.35_]

134. Xiang Y, Payne PRO, **Huang K**. Transactional database transformation and its application in prioritizing human disease genes, _IEEE/ACM Transactions on Bioinformatics and Computational Biology_, 9(1): 294-304, 2012. [_IF: 2.46_]

135. Ozer HG, Huang, Y-W, Wu J, Parvin J, Huang T, **Huang K**. Comparing multiple ChIP-sequencing experiments, _Journal of Bioinformatics and Computational Biology_, 9(2):269-282, 2011.

136. Wang G, Wang Y, Shen C, Huang, Y-W, **Huang K**, Huang T, Nephew KP, Li L, Liu Y. RNA polymerase II binding patterns reveal genomic regions involved in microRNA gene regulation, _PLoS One_, 5(11):e13798, 2010. [_IF: 4.35_]

137. Wan SG, Taccioli C, Jiang Y, Chen H, Smalley KJ, **Huang K**, Liu XP, Farber JL, Croce CM, Fong LY. Zinc deficiency activates S100A8 inflammation in the absence of COX-2 and promotes murine oral-esophageal tumor progression, _International Journal of Cancer_, 129(2): 331-345, 2011. [_IF: 4.722_]

138. Zhang J, Xiang Y, Ding L, Keen-Circle K, Borlawsky T, Ozer HG, Jin R, Payne PRO, **Huang K**. Using gene co-expression network analysis to predict biomarkers for chronic lymphocytic leukemia special issue on AMIA Summit of Translational Bioinformatics, _BMC Bioinformatics_, 11(suppl 9): S5, 2010. [_IF: 3.43_]

139. Payne PRO, **Huang K**, Keen-Circle K, Kundu A, Zhang J, Borlawsky T. Multi-dimensional discovery of biomarker and phenotype, special issue on AMIA Summit of Translational Bioinformatics, _BMC Bioinformatics_, 11(suppl 9): S3, 2010. [_IF: 3.43_]

140. Xu R, **Huang K**, Qin R, Huang J, Xu JS, Ding L, Gnyawali US, Gnyawali SC, Sen CK, Dual-mode imaging of cutaneous tissue oxygenation and tissue vascular thermal reactivity, _Journal of Visual Experiments_, 46: 2095, 2010.

141. Guo Y, Yuan C, Tian F, **Huang K**, Weghorst C, Tsai, M-D, Li J. Contributions of conserved TPLH tetrapeptides to the conformational stability of ankyrin repeat proteins, *Journal of Molecular Biology*, accepted, 2010. [*IF: 4.2*]

142. Zabuawala T, Taffany D, Shama SM, Merchant A, Adair B, Rosol T, Fernandez S, **Huang K**, Leone K, Ostrowski MC. An ets2-driven transcriptional program in tumor-associated macrophages promotes tumor metastasis, *Cancer Research*, 70(4): 1323-1333, 2010. [*IF: 7.514*]

143. Schwartzbaum J, **Huang K**, Lawler S, Ding B, Yu J. Allergy and inflammatory transcriptome is predominantly negatively correlated with CD133 expression, *Neuro-Oncology*, in press, 2010. [*IF: 5.00*]

144. Taslim C, Wu J, Yan P, Singer G, Parvin J, Huang T, Lin S, **Huang K**. Comparative study on ChIP-seq data: normalization and binding pattern characterization, *Bioinformatics*, 25(18): 2334-2340, 2009. [*IF: 4.328, the third most read article in Bioinformatics in September 2009*]

145. Cooper L, Sertel O, Kong J, **Huang K**, Gurcan M. Feature-based registration of distinct stained histopathology images: an application for computerized follicular lymphoma prognosis, *Computer Methods and Programs in Biomedicine*, 96(3):182-192, 2009. [*IF: 1.22*]

146. Yu J, Ershler M, Yu L, Wei M, Hackanson B, Yokohama A, Mitsui T, Liu C, Mao C, Liu S, Liu Z, Liu C-G, Liu X, **Huang K**, Visser J, Guido M, Plass C, Belyavsky A, Caligiuri M. TSC-22 contributes to hematopoietic stem cell proliferation and repopulation and is epigenetically silenced in large granular lymphocyte leukemia, *Blood*, 113(22): 5558-5567, 2009. [*IF: 10.432*]

147. Rybaczyk L, Rozmiarek A, Circle K, Grants I, Needleman B, Wunderlich JE, **Huang K**, Christofi FL. New bioinformatics approach to analyze gene expressions and signaling pathways reveals unique purine gene dysregulation profiles that distinguish between CD and UC, *Inflammatory Bowel Diseases*, 15(7): 971-984, 2009. [*IF: 4.975*]

148. Ruiz A, Ujaldon M, Cooper L, **Huang K**. Non-rigid registration for large sets of microscopic images on graphics processors, *Journal of Signal Processing Systems*, 55(1-3): 229-250, 2009. [*IF: 0.779*]

149. Mosaliganti K, Janoos F, Irfanoglu O, Ridgway R, Machiraju R, **Huang K**, Saltz J, Leone G, Ostrowski M. Tensor classification of *N*-point correlation function features for histology tissue segmentation, *Medical Image Analysis*, 13(1): 156-166, 2009. [*IF: 3.602*]

150. Janoos F, Mosaliganti K, Xu X, Machiraju R, Wong S, **Huang K**. Robust 3D reconstruction and identification of dendritic spines from optical microscopy imaging, *Medical Image Analysis*, 13(1): 167-179, 2009. [*IF: 3.602*]

151. Mosaliganti K, Cooper L, Sharp R, Machiraju R, Leone G, **Huang K**, Saltz J. Reconstruction of cellular biological structures from optical microscopy data, *IEEE Transactions on Visualization and Computer Graphics*, 14(4): 863-876, 2008. [*IF: 2.445*]

152. Mosaliganti K, Sharp R, Machiraju R, **Huang K**, Leone G. Geometry-driven visualization of microscopic structures in biology, *Computer Graphics Forum, the International Journal of the Eurographics Association*, 27(3): 871-878, 2008. [*IF: 1.86*]

153. Mosaliganti K, Pan T, Ridgway R, Sharp R, Cooper L, Culacy A, Sharma A, Irfanoglu O, Machiraju R, Kurc T, Wenzel P, deBruin A, Leone G, Saltz J, **Huang K**. An imaging workflow for characterizing phenotypical change in terabyte sized mouse model datasets, *Journal of Biomedical Informatics*, 41(6): 863-873, 2008. [*IF: 1.924*]

154. Rybaczyk L, Bashaw M, Pathak D, **Huang K**. An indicator of cancer: downregulation of monoamine oxidase-A in multiple organs and species, *BMC Genomics*, 9: 134, 2008. [*IF: 3.93, Designated as Highly Accessed*]

155. Mosaliganti K, Janoos F, Sharp R, Ridgway R, Machiraju R, **Huang K**, Wenzel P, deBruin A, Leone G, Saltz J. Detection and visualization of surface-pockets to enable phenotyping studies. *IEEE Transactions on Medical Imaging,* 26(9):1283-1290, 2007. [*IF: 4.004*]

156. Wenzel PL, Wu L, de Bruin A, Chong JL, Chen WY, Dureska G, Sites E, Pan T, Sharma A, **Huang K**, Ridgway R, Mosaliganti K, Sharp R, Machuraju R, Saltz J, Yamamoto H, Cross JC, Robinson ML, Leone G. *Rb* is critical in a mammalian tissue stem cell population. *Genes and Development*, 21:85-97, 2007. [*IF: 14.795*]

157. Sharp R, Ridgway R, Mosalignati K, Wenzel P, Pan T, de Bruin A, Machuraju R, **Huang K**, Leone G, Saltz J. Volume rendering phenotype differences in mouse placenta microscopy data. *Computing in Science & Engineering,* 9(1):38-47, 2007. [*IF: 0.71*]

158. Hong W, Wright J, **Huang K**, Ma Y. A multi-scale hybrid linear model for lossy image representation. *IEEE Transaction on Image Processing,* 15(12):3655-3671, 2006. [*IF: 3.315*]

159. Yang AY, Rao S, **Huang K**, Hong W, Ma Y. Symmetry-based 3-D reconstruction from perspective images, *Computer Vision and Image Understanding (CVIU)*, 99(2): 210-240, August 2005. [*IF: 2.22*]

160. Hastings S, Ribeiro M, Langella S, Oster S, Catalyurek U, Pan T, **Huang K**, Ferreira R, Saltz J, Kurc T, XML database support for distributed execution of data-intensive scientific workflows, *ACM SIGMOD Record*, 34(3): 50-55, 2005. [*IF: 1.455*]

161. Mosaliganti K, Pan T, Machiraju R, **Huang K**, Saltz J, ITK-based registration of large images from light microscopy: a biomedical application, *The Insight Journal*, 19, 2005.

162. **Huang K**, Hong W, Ma Y. Symmetry-based photo editing, *Pattern Recognition*, 38(6): 825-834, 2004. [*IF: 3.279*]

163. Hong W, Yang AY, **Huang K**, Ma Y. On symmetry and multiple view geometry: structure, pose, and calibration from a single image, *International Journal Computer of Vision*, 60(3): 241-265, 2004. [*IF: 5.358*]

164. Ma Y, **Huang K**, Vidal R, Kosecka J, Sastry S. Rank conditions of the multiple-view matrix in multiple-view geometry, *International Journal of Computer Vision*, 59(2):115-137, 2004. [*IF: 5.358*]

- **Peer-reviewed papers in conference papers**

165. Liu Z, Shao W, Zhang J, Zhang M, **Huang K**. Transfer Learning via Optimal Transportation for Integrative Cancer Patient Stratification, accepted to *Proceedings of International Joint Conference on AI (IJCAI)*, 2021. (acceptance rate 13.9%).

166. Wang T, Ding Z, **Huang K**. Towards Fair Cross-Domain Adaptation via Generative Learning, accepted to the *Proceedings of the IEEE Winter Conference on Applications of Computer Vision (WACV) 2021,* Waikoloa (virtual), 2021.

167. Wang T, Lu W, Yang F, Liu L, Dong Z, Tang W, Chang J, Huan W, **Huang K**, Yao J. Microsatellite Instability Prediction of Uterine Corpus Endometrial Carcinoma Based on H&E Histology Whole-slide Imaging, accepted to the *Proceedings of the IEEE International Symposium on Biomedical Imaging (ISBI)*, Iowa City, 2020.

168. Srivastava A, Sharpnack M, **Huang K**, Mallick P, Machiraju R. PTR Explorer: An approach to identify and explore Post Transcriptional Regulatory mechanisms using proteogenomics. Accepted to the *Proceedings of the Pacific Symposium of Biocomputing (PSB)*, Hawaii, 2020.

169. Gandhi P, Luo X, Storey S, Zhang Z, Han Z, **Huang K**. Identifying Symptom Clusters in Breast Cancer and Colorectal Cancer Patients using EHR Data. Accepted to *Proceedings of the 10th ACM Conference on Bioinformatics, Computational Biology, and Health Informatics* (ACM BCB), Niagara Falls, 2019. (**Best Paper Award**)

170. Shao W, Wang T, Huang Z, Cheng J, Han Z, Zhang D, **Huang K**. Diagnosis-guided multi-modal feature selection for prognosis prediction of lung squamous cell carcinoma. Accepted to *Proceedings of Medical Image Computing and Computer Aided Intervention Conference (MICCAI)*, Shenzhen, 2019.

171. Wang T, Johnson T, Zhang J, **Huang K**. Topological Methods for Visualization and Analysis of High Dimensional Single-Cell RNA Sequencing Data. *Pacific Symposium on Biocomputing,* 24:350-361, 2019. (Oral presentation)

172. Shao W, Cheng J, Sun L, Han Z, Zhang D, **Huang K**. Ordinal multi-modal feature selection for survival analysis of early-stage renal cancer. Accepted to the *Proceedings of Medical Image Computing and Computer Aided Intervention Conference (MICCAI)*, Spain, 2018.

173. Johnson T, Li S, **Huang K**, Zhang Y. Evaluating relationships between pseudogenes and genes: from pseudogene evolution to their functional potentials. Accepted to the *Proceedings of the Pacific Symposium of Biocomputing (PSB)*, Hawaii, 2018. (Oral presentation)

174. Srivastava A, Kulkarni C, **Huang K**, Mallick P, Machiraju R. Building Trans-omics Evidence: Using Imaging and `Omics" to Characterize Cancer Profiles. Accepted to the *Proceedings of the Pacific Symposium of Biocomputing (PSB)*, Hawaii, 2018.

175. Li Q, **Huang K**, Machiraju R. Spatiotemporal Visualization of Gene Expression in the Developing Mouse Brain. *Proceedings of the Eurographics and Visualization Conference*, 121-125, 2017. Thttps://doi.org/10.2312/eurovisshort.20171144

176. Wang C, Yang L, **Huang K**. Integrative Analysis for Lung Adenocarcinoma Predicts Morphological Features Associated with Genetic Variations. Accepted to the *Proceedings of the Pacific Symposium of Biocomputing (PSB)*, Hawaii, 2017. (Oral presentation)

177. Johnson T, Abrahams Z, Zhang Y, **Huang K**. Mapping Neuronal Cell Types Using Integrative Multi-species Modeling of Human and Mouse Single Cell RNA Sequencing Data. Accepted to the *Proceedings of the Pacific Symposium of Biocomputing (PSB)*, Hawaii, 2017.

178. Shroff S, Zhang J, **Huang K**. Gene Co-Expression Analysis Predicts Genetic Variants Associated with Drug Responsiveness in Lung Cancer. Accepted to *Proceedings of the AMIA*

Annual Summit on Translational Bioinformatics, San Francisco, 2016. (Winner of the Marco Ramoni Distinguished Paper award)

179. Hatem A, Kaya K, Parvin J, **Huang K**, and Çatalyürek Ü. MICA: MicroRNA Integration for Active Module Discovery, *6th ACM Conference on Bioinformatics, Computational Biology and Health Informatics (ACM-BCB)*, Sep 2015.

180. Sharpnack A, **Huang K**. Detecting Cancer Pathway Crosstalk with Distance Correlation. Accepted to *Proceedings of the AMIA Annual Summit on Translational Bioinformatics*, San Francisco, 2015. (One of the four finalists for Marco Ramoni Distinguished Paper award)

181. Kaewprag P, Newton C, Vermillion B, Hyun S, **Huang K**, Machiraju R. Predictive Modeling for Pressure Ulcers from Intensive Care Unit Electronic Health Records. Accepted to *Proceedings of the AMIA Annual Summit on Clinical Research Informatics*, San Francisco, 2015.

182. Wang Y, Ozer GH, **Huang K**, Agrawal G. Removing Sequential Bottlenecks in Analysis of Next-Generation Sequencing Data. Accepted to *Proceedings of the IEEE International Parallel and Distributed Processing Symposium: Workshop on High Performance Computational Biology* (HiCOMB), 2014.

183. Webb A, Albin A, Ye Z, Rastegar-Mojarad M, **Huang K**, Parvin J, Sadee W, Li L, Lin S, Xiang Y. Mining massive SNP data for identifying associated SNPs and uncovering gene relationships. *Proceedings of the 5th ACM Conference on Bioinformatics, Computational Biology, and Health Informatics* (ACM-BCB), 304-313, 2014.

184. Wang C, Machiraju R, **Huang K**. Cancer Patient Integrative Stratification via a Two-step Consensus Clustering of Molecular Expression and Clinical Attributes. *Proceedings of the AMIA Summit of Translational Bioinformatics* (In Press), 2014.

185. Xiang Y, Fuhry D, Jin R, Zhao Y, **Huang K**. Visualizing clusters in parallel coordinates for visual knowledge discovery, *Lecture Notes in Computer Science*, 7301/2012: 505-516 (*Proceedings of the 16th Pacific-Asia Conference on Knowledge Discovery and Data Mining*), 2012. [*Peer Reviewed, acceptance rate less than 30%*]

186. Pecot T, Singh S, Caserta E, **Huang K**, Machiraju R, Leone, G. Non-parametric cell nuclei segmentation based on tracking over depth from 3D fluorescence confocal images, accepted to *Proceedings of IEEE International Symposium on Biomedical Imaging*, Barcelona, Spain, 2012.

187. Camerlengo T, Ozer HG, Onti-Srinivasan R, Yan P, Huang T, Parvin J, **Huang K**. From sequencer to supercomputer: an automatic pipeline for managing and processing next generation sequencing data. Accepted to Proceedings of the *AMIA Summit on Translational Bioinformatics*, San Francisco, 2012. [*Peer Reviewed*]

188. Wenzke K, Cantemir C, Zhang J, Marsh C, **Huang K**. Identifying Common Genes and Networks in Multi-Organ Fibrosis. In the Proceedings of the *AMIA Summit on Translational Bioinformatics*, San Francisco,CA, United States:AMIA (2012):106-115. [*Peer reviewed*]

189. Gnyawali S, Elghrably H, Melvin J, **Huang K**, Bergdall V, Allen D, Hwang J, Litorja M, Shirley E, Sen C, Xu R. Hyperspectral imaging of ischemic wounds. In: *Optical Diagnostics and Sensing XII: Toward Point-of-Care Diagnostics and Design and Performance*

Validation of Phantoms Used in Conjunction with Optical Measurement of Tissue IV, 822910, SPIE Optical Engineering, 2012. [*Peer Reviewed*]

190. Taslim C, Lin S, **Huang K**. Chromatin signature analysis and prediction of genome-wide novel promoters using finite mixture model. Accepted to *Proceedings of the IEEE International Workshop on Genomic Signal Processing and Statistics (GENSIPS)*, San Antonio, 2011. [*Peer Reviewed*]

191. Xu RX, Melvin J, Huang J, Elgharably H, Gnyawali S, **Huang K**, Bergdall V, Allen D, Hwang J, Litorja M, Shirley E, Sen C. Hyperspectral imaging of ischemic wounds. Accepted to the SPIE photonics West, San Francisco, SPIE. (2012):8229B-47.

192. Zhang J, Ni S, Parvin J, Yang Y, **Huang K**. Predicting Parkinson's disease related genes using frequent gene co-expression analysis. Accepted to *Proceedings of the IEEE Bioinformatics and Biomedicine (BIBM)*, Atlanta, 2011. [*Editor Reviewed*]

193. Zhang J, Knobloch T, Parvin J, Weghorst C, **Huang K**. Identifying smoking associated gene co-expression networks related to oral cancer initiation. Accepted to *Proceedings of the IEEE Bioinformatics and Biomedicine (BIBM)*, Atlanta, 2011. [*Editor Reviewed*]

194. Singh S, Janoos F, Pecot T, Caserta E, Rittscher J, Leone G, **Huang K**, Machiraju R. Non-parametric Population Analysis of Cellular Phenotypes. Accepted to *Proceedings of the 14th International Conference on Medical Image Computing and Computer Assisted Intervention (MICCAI)*, Toronto, Canada, Sep 2011. [*Peer Reviewed, acceptance rate ~30%*]

195. Cooper L, Saltz J, Catalyurek U, **Huang K**. Acceleration of two point correlation function calculation for pathology image, accepted to *Proceedings of IEEE Conference on Health Informatics and Systems Biology*, San Jose, California, 2011. [*Peer Reviewed, oral presentation, acceptance rate less than 30%*]

196. Cooper L, **Huang K**, Ujaldon M. Parallel automatic registration of large scale microscopic images on multiprocessor CPUs and GPUs, accepted to *Proceedings of the 12th IEEE International Workshop on Parallel and Distributed Scientific and Engineering Computing (PDSEC)*, Anchorage, 2011. [*Peer Reviewed*]

197. Ding L, Insolera R, Shi S, **Huang K**. Detecting cellular events in brain cortex using time-lapse microscopy, in *Proceedings of the IEEE International Symposium on Biomedical Imaging (ISBI)*, 1553-1556, Chicago, 2011. [*Peer Reviewed, oral presentation*]

198. Wu H-Y, Zhang J, **Huang K**. Peak detection on ChIP-Seq data using wavelet transformation, in *Proceedings of the Workshop on Data Mining in Next Generation Sequencing Data* in IEEE International Conference on Bioinformatics and Biomedicine (BIBM), Hong Kong, 2010. [*Peer Reviewed*]

199. Ozer H-G, Wu J, Huang Y-W, Parvin J, Huang T, **Huang K**. Comparing multiple protein binding profiles in ChIP-seq experiments, in *Proceedings of the Computational Systems Bioinformatics (CSB)*, Palo Alto, California, 2010. [*Peer Reviewed*, acceptance rate less than 30%].

200. Hong H, Xiang Y, Jin R, **Huang K**. Block Interaction: A Generative Summarization Schem for Frequent Pattern Mining, in *Proceedings of the ACM SIGKDD Frequent Patter Mining Workshop*, Washington DC, United States:ACM. (2010):55-64. [*Invited with Peer Review*]

201. Uppalapati P, Yang X, **Huang K**. Predicting prognostic markers for glioma using gene co-expression network analysis, in *Proceedings of the Workshop of Gene Network and Pathway Generation and Analysis* in ACM Bioinformatics and Computational Biology Conference, 2010. [*Peer Reviewed*]

202. Cooper L, Saltz J, Machiraju R, **Huang K**. Two-point correlation functions: feature space manifolds and correlation updating, in *Proceedings of the Workshop on Mathematical Methods in Biomedical Image Analysis (MMBIA)* in IEEE International Conference of Computer Vision and Pattern Recognition (CVPR), 2010. [*Peer Reviewed*]

203. Zhang J, Ding L, Keen-Circle K, Borlawsky T, Xiang Y, Ozer HG, Jin R, Payne PRO, **Huang K**. Predicting biomarkers for chronic lymphocytic leukemia using gene co-expression network analyses for ZAP70, in *Proceedings of the AMIA Summit of Translational Bioinformatics*, 2010. [*Peer Reviewed, selected to be published in BMC Bioinformatics*]

204. Payne PRO, **Huang K**, Keen-Circle K, Kundu A, Zhang J, Borlawsky T. Multi-dimensional discovery of biomarker and phenotype complexes, in *Proceedings of the AMIA Summit of Translational Bioinformatics*, 2010. [*Peer Reviewed*]

205. Qin R, Huang J, Xu J, Gnyawali S, Ding L, Sen C, **Huang K**, Xu R. Multi-modal quantitative imaging of wound tissue oxygenation and perfusion, in *Proceedings of the SPIE Photonics West*, 2010. [*Abstract of this paper was peer reviewed*]

206. Ruan N, Jin R, Lee V, **Huang K**. A sparsification approach for temporal graphical model decomposition, in *Proceedings of the IEEE International Conference on Data Minding (ICDM)*, 2009. [Peer Reviewed, *Acceptance Rate: 8.9%*]

207. Kundu A, Ozer HG, Borlawsky T, Circle K, **Huang K**, Payne P. Clinical attribute network for chronic lymphocytic leukemia, in *Proceedings of the IEEE International Conference on Bioinformatics & Biomedicine (BIBM)*, 297-282, 2009. [Peer Reviewed, *Acceptance Rate: 35%*]

208. Camerlengo T, Ozer HG, Teng M, Perez F, Yan P, Li L, Parvin J, Huang T, Kurc T, Liu Y, **Huang K**. Enabling data analysis on high-throughput data in large data depository using web-based analysis platform – a case study on integrating QUEST with GenePattern in epigenetics research, in *Proceedings of the IEEE International Conference on Bioinformatics & Biomedicine (BIBM)*, 392-395, 2009. [Peer Reviewed, *Acceptance Rate: 35%*]

209. Kong J, Boyer K, Dunham P, Saltz J, **Huang K**. A new model-based estimation of ellipses for object representation, in *Proceedings of the IEEE Engineering in Medicine and Biology Conference (EMBC)*, IEEE Press, Minneapolis, MN, 2009. [Peer Reviewed]

210. Zhang J, Xiang Y, Jin R, **Huang K**. Using frequent co-expression network to identify gene clusters for breast cancer prognosis, in *Proceedings of the ISIBM International Joint Conferences on Bioinformatics, Systems Biology and Intelligent Computing*, 428-434, IEEE Press, 2009. [Peer Reviewed]

211. Camerlengo T, Ozer HG, Zhang G, Joobeur T, Meulia T, Trgovcich J, **Huang K**. Computational challenges and solutions to the analysis of microRNA profiles in virally-infected cells derived by massively parallel sequencing, to appear in

Proceedings of the Ohio Collaborative Conference on Bioinformatics (OCCBIO), 32-36, IEEE Press, 2009. [Peer Reviewed]

212. Ozer HG, Camerlengo T, Huang T, Parvin J, **Huang K**. A new method for mapping short DNA sequencing reads by using quality scores, to appear in *Proceedings of the Ohio Collaborative Conference on Bioinformatics (OCCBIO)*, 21-25, IEEE Press, 2009. [Peer Reviewed]

213. Parvin J, Kais Z, Arora M, Kotian S, Zha A, Ransburgh D, Bozdag D, Catalyurek U, **Huang K**. Identification of a breast cancer associated regulatory network, to appear in *Proceedings of the Ohio Collaborative Conference on Bioinformatics (OCCBIO)*, 71-75, IEEE Press, 2009. [Peer Reviewed]

214. Ozer H, Bozdag D, Camerlengo T, Wu J, Huang Y-W, Hartley T, Parvin J, Huang T, Catalyurek U, **Huang K**. A comprehensive analysis workflow for genome-wide screening data from ChIP-sequencing experiments, in *Proceedings of the First International Conference on Bioinformatics and Computational Biology, Lecture Notes in Computer Science*, 5642:320-330, Springer-Verlag, 2009. [Peer Reviewed]

215. Mosaliganti K, Machiraju R, **Huang K.** Geometry-driven visualization of microscopic structures, in *Proceedings of the IEEE International Symposium of Biomedical Imaging (ISBI'08),* 828-831, IEEE Press, 2008. [Peer Reviewed]

216. Ruiz A, Ujaldon M, Andrades JA, Becerra J, **Huang K**, Pan T, Saltz J. The GPU on biomedical image processing for color and phenotype analysis, in *Proceedings of IEEE 7th International Symposium on BioInformatics & BioEngineering (BIBE'07)*, 1124-1128, IEEE Press, Cambridge, Massachusetts, October 2007. [Peer Reviewed, *Acceptance Rate: 13%*]

217. Mosaliganti K, Chen J, Janoos F, Machiraju R, Xia W, **Huang K**. Automated quantification of colony growth in clonogenic assays, *in Proceedings of International Workshop on Microscopic Image Analysis with Applications in Biology (MIAAB'07)*, New Jersey, September 2007. [Peer Reviewed]

218. Cooper L, Naidu S, Leone G, Saltz J, **Huang K**. Registering high resolution microscopic images with different histochemical stainings - a tool for mapping gene expression with cellular structures, *in Proceedings of International Workshop on Microscopic Image Analysis with Applications in Biology (MIAAB'07)*, New Jersey, September 2007. [Peer Reviewed]

219. Janoos F, Irfanoglu O, Mosaliganti K, Machiraju R, **Huang K**, Wenzel P, de Bruin A, Leone G. Multiple-resolution image segmentation using the 2-point correlation functions, in *Proceedings of the IEEE International Symposium on Biomedical Imaging*, 300-303, IEEE Press, Washington, DC, April 2007. [Peer Reviewed]

220. Mosaliganti K, Jonoos F, Xu X, Machiraju R, Wong STC, **Huang K**, Temporal matching of dentritic spines in confocal microscopy images of neuronal tissue, in *Proceedings of the Microscopic Image Analysis with Applications in Biology (MIAAB) Workshop in MICCAI,* October 2006. [Peer Reviewed]

221. Ridgeway R, Irfanoglu O, Machiraju R, **Huang K**. Image segmentation with tensor-based classification of N-point correlation functions, in *Proceedings of the Microscopic Image*

Analysis with Applications in Biology (MIAAB) Workshop in MICCAI, October 2006. [Peer Reviewed]

222. Cooper L, **Huang K**, Sharma A, Mosaliganti R, Pan T. Registration vs. reconstruction: Building 3-D models from 2-D microscopy images, in *Proceedings of the Bioimage Informatics Workshop*, 57-58, Santa Barbara, CA, September 2006. [Peer Reviewed]

223. **Huang K**, Cooper L, Sharma A, Pan T. Fast automatic registration algorithm for large microscopy images, in *Proceedings of the IEEE/NLM Life Science Systems & Applications Workshop*, 128-129, IEEE Computer Society, Bethesda, MD, July 2006. [Peer Reviewed]

224. Sharp R, Ridgway R, Mosalignati K, Irfanoglu O, Wenzel P, Machiraju R, Pan T, de Bruin A, Machuraju R, Leone G, **Huang K**, Saltz J. Examining Phenotype Differences in Mouse Placenta with Volume Rendering and Segmentation, in *Proceedings of the IEEE/NLM Life Science Systems & Applications Workshop*, 70-71, IEEE Computer Society, July 2006. [Peer Reviewed]

225. Prescott J, Clary M, Wiet G, Pan T, **Huang K**. Automatic registration of large set of microscopic images using high-level features, in *Proceedings of the IEEE International Symposium on Medical Imaging (ISBI)*, 1284-1287, IEEE Press, Arlington, VA, April 2006. [Peer Reviewed]

226. Mosaliganti R, Pan T, Sharp R, Ridgway R, Iyengar S, Gulacy A, Wenzel P, de Bruin A, Machiraju R, **Huang K**, Leone G, Saltz J. Registration and 3D visualization of large microscopy images, in *Proceedings of the SPIE Annual Medical Imaging Meetings*, 923-934, SPIE, San Diego, CA, February 2006. [Peer Reviewed]

227. Catalyurek U, Hastings S, **Huang K**, Kumar VS, Kurc T, Langella S, Narayanan S, Oster S, Pan T, Rutt B, Zhang X, Saltz J. Supporting large scale medical and scientific datasets, *Proceedings of the International Conference ParCo*, 33:3-14, 2005. [Peer Reviewed,]

228. Cooper L, Liu J, **Huang K**. Spatial segmentation of temporal texture using mixture linear models, in *Proceedings of the Dynamical Vision Workshop in the International Conference of Computer Vision*, *Lecture Notes in Computer Science,* 4358:142-150, Springer-Verlag, Beijing, China, October 2005. [Peer Reviewed, *Acceptance Rate: 12.5%*]

229. Hong W, Wright J, **Huang K**, Ma Y. A multi-scale hybrid linear model for lossy image representation, in *Proceedings of the IEEE International Conference on Computer Vision (ICCV)*, 1:764-771, IEEE Press, Beijing, China, October 2005. [Peer Reviewed, *Acceptance Rate: 16.2%*]

230. Pan T, **Huang K**. Virtual mouse placenta: tissue layer segmentation, in *Proceedings of the IEEE EMBC*, 3112-3116, IEEE Press, September 2005. [Peer Reviewed]

231. **Huang K**, Wagner A, Ma Y. Hybrid linear system identification via subspace embedding and segmentation, in *Proceedings of the 43th IEEE Conference on Decision and Control*, 3:3227-3234, Nassau, Bahamas, December 2004. [Peer Reviewed]

232. **Huang K**, Yang AY, Ma Y. Sparse Representation of Images with Hybrid Linear models, in *Proceedings of the International Conference on Image Processing*, 2: 1281-1284, IEEE Press, Singapore, October 2004. [Peer Reviewed, Top 15% papers]

233. **Huang K**, Ma Y. Robust GPCA algorithm with applications in video segmentation via hybrid system identification, in *Proceedings of the Sixteenth International Symposium on Mathematical Theory of Networks and Systems (MTNS2004)*, Leuven, Belgium, July 2004. [Peer Reviewed]

234. **Huang K**, Ma Y ,Vidal R. Minimum effective dimension for mixtures of subspaces: a robust GPCA algorithm and its applications, in *Proceedings of the IEEE International Conference on Computer Vision and Pattern Recognition (CVPR'04)*, 631-638, IEEE Press, Washington DC, June 2004. [Peer Reviewed, *Acceptance Rate: 23.6%*]

235. **Huang K**, Yang AY, Hong W, Ma Y. Large baseline matching and reconstruction from symmetry cells, in *Proceedings of the IEEE International Conference on Robotics and Automation (ICRA'04)*, 2:1418-1423, New Orleans, USA, April 2004. [Peer Reviewed]

236. Yang AY, Rao S, **Huang K**, Hong W, Ma Y. Geometric segmentation of perspective images based on symmetry groups, in *Proceedings of the International Conference on Computer Vision*, 2:1251-1258, Nice, France, October, 2003. [Peer Reviewed, *Acceptance Rate: 16.1%*]

237. **Huang K**, Hong W, Ma Y. Symmetry-based photoediting, in *the International Conference on Computer Vision*, *Workshop on Higher Level Knowledge*, 21-28, Nice, France, October, 2003. [Peer Reviewed]

238. Brand M, **Huang K**. A unifying theorem for spectral embedding and clustering, in *Proceedings of the 9th International Conference on Artificial Intelligence and Statistics*, Key West, Florida, January, 2003. [Peer Reviewed]

239. **Huang K**, Fossum R, Ma Y. Generalized rank conditions in multiple view geometry with application to dynamic scenes, in *Proceedings of the 6th European Conference on Computer Vision*, *Lecture Notes in Computer Science*, 2:201-216, Copenhagen, Denmark, May 2002. [Peer Reviewed, *Acceptance Rate: 30.2*]

240. Ma Y, **Huang K**, Yang Y. Classification of rank conditions for multiple views of dynamical scenes, in *6th European Conference on Computer Vision*, Workshop on Vision and Modeling of Dynamic Scenes, Copenhagen, Denmark, May 2002. [Peer Reviewed, *Acceptance Rate: 36%*]

241. Ma Y, Kosecka J, **Huang K**. Rank deficiency condition of the multiple view matrix for mixed point and line features, in *Proceeding of the 5th Asian Conference on Computer Vision*, Melbourne, Australia, January 2002. [Peer Reviewed]

242. **Huang K**, Kumar PR. Hierarchical and integrated algorithms: comparison and applications in motion estimation and recognition, in *Proceedings of the 39th IEEE Conference on Decision and Control*, 1: 674-679, IEEE Press, Sydney, Australia, December 2000. [Peer Reviewed]

- **Editorial**

1. **Huang K**, Liu Y, Huang Y, Li L, Cooper L, Ruan J, Zhao Z. Intelligent biology and medicine in 2015: advancing interdisciplinary education, collaboration, and data science. *BMC Genomics*, Suppl 7:524, 2016.

2. Zhao Z, Liu Y, Huang Y, **Huang K**, Ruan J. Advancing Systems Biology in the International Conference on Intelligent Biology and Medicine (ICIBM) 2015. *BMC Systems Biology.* Suppl 3:61, 2016.

3. Xu D, **Huang K**, Schmidt J. Guest editors introduction to the special section on software and databases. *IEEE/ACM Transactions on Computational Biology and Bioinformatics (TCBB)*, 12(4): 793-794, 2015.

4. Zhao Z, Sanfilippo A, **Huang K**. Gene network and pathway generation and analysis, *International Journal of Computational Biology and Drug Design*, 4(1):1-4, 2011.

- **Book chapters**

1. Hai T, Dominic J, **Huang K**. ATF3 activating transcription factor 3, in *Encyclopedia of Signaling Molecules*, Springer New York, 2012.

2. **Huang K**, Mosaliganti K, Cooper L, Machiraju R. Quantitative phenotyping using microscopic images, in *Microscopic Image Analysis for Life Science Applications*, Artech House Publishers, 2008.

3. Cooper L, Ruiz A, Ujaldon M, **Huang K**. Scalable image registration and 3D reconstruction at microscopic resolution, in *High Throughput Image Reconstruction and Analysis*, Artech House Publishers, 2008.

4. Ribeiro M, Kurç T, Pan T, **Huang K**, Çatalyürek U, Zhang X, Langella S, Hastings S, Oster S, Ferreira R, Saltz J. 2006. Tools for efficient subsetting and pipelined processing of large scale, distributed biomedical image data. In *Grid Computing: The New Frontier Of High Performance Computing*. Advances in Parallel Computing. Vol. 14. Edited by Grandinetti L. Amsterdam, Netherlands: Elsevier Science.

5. **Huang K**, Ma Y. A survey on geometric vision, in *Handbook of Robotics*, CRC Press, 2004.

- **Abstracts**

1. **Huang K**, Leung A, Zhang J, Zhang CQ. Tissue-tissue gene co-expression network for tumor microenvironment study. Accepted to *Proceedings of the AMIA Summit of Translational Bioinformatics*, San Francisco, March, 2010. [Peer Reviewed]

2. Taslim C, **Huang K**, Lin S, Huang T. Chromatin signature analysis and prediction of genome-wide novel proximal/distal promoters. In *Proceedings of the Cold Spring Harbor Laboratory Genome Informatics*. CSHL Press: Cold Spring Harbor, October, 2009. [Editor Reviewed]

3. Taslim C, Huang T, Lin S, **Huang K**. Comparative analysis of ChIP-seq data using mixture model, in Critical Assessment of Massive Data Analysis Conference (CAMDA2009), Chicago, October, 2009. [Peer Reviewed]

4. Bozdag D, Camerlengo T, Ozer HG, Trgovicich J, Meulia T, **Huang** K, Catalyurek U. Parallel computing strategies for sequence mapping of NGS data, in Critical Assessment of Massive Data Analysis Conference (CAMDA2009), Chicago, October, 2009. [Peer Reviewed]

5. Xiang Y, Zhang J, Ruan N, Jin R, Parvin J, **Huang K**. A study on frequent co-expression networks in cancers, *AMIA Annual Summit on Translational Bioinformatics*, San Francisco, March 2009. [Peer Reviewed]

6. **Huang K**, Wu J, Zhang J, Huang T, Parvin J. GenomeScape: a universal 3D visualization tool for genomic data, *AMIA Annual Summit on Translational Bioinformatics*, San Francisco, March 2009. [Peer Reviewed]

7. Cooper L, Wright J, Singh S, Bluestein E, Ma Y, **Huang K**. GeneSubspace - a tool for clustering the gene expression profiles using mixture linear models, *AMIA Annual Summit on Translational Bioinformatics*, San Francisco, March 2009. [Peer Reviewed]

8. Rybaczyk L, Pathak D, Cooper L, Circle K, **Huang K**. Four common gene expression changes across multiple cancers in multiple species. *AACR annual meeting* (Abstract#4266), 2008. [Peer Reviewed]

9. Rybaczyk L, Wunderlich J, Circle K, Needleman B, Melvin S, Cardounel A, Grants I, **Huang K**, Christofi F. Differential dysregulation of ADORA3, ADORA2A, ADORA2B, and P2RY14 expression profiles from 37 purine genes in mucosal biopsies and peripheral blood mononuclear cells in IBD, *Gastroenterology* 132: Suppl. 2, A-246, 2007. [Peer Reviewed]

10. Circle K, Rybaczyk L, Grants I, Wunderlich J, **Huang K**, Christofi F: A new comparative analysis of gene expression and selection (CAGES) reveals purine gene signature profiles that distinguish between crohn's and ulcerative colitis. *6th Annual Advances in the Inflammatory Bowel Diseases*, 2007. [Peer Reviewed]

11. **Huang K**, Sharma A, Cooper L, Pan T, Gurcan M, Saltz J. A novel image registration pipeline for 3-D reconstruction from microscopy images, *Advancing Practice, Instruction and Innovation Through Informatics (APIII),* Vancouver, Canada, August 2006. [Peer Reviewed]

12. Sharma A, **Huang K**, Pan T, Gurcan M, Saltz J. A parallel image registration framework for terabyte sized microscopy datasets, *Advancing Practice, Instruction and Innovation Through Informatics (APIII),* Vancouver, Canada, August 2006. [Peer Reviewed]

13. Pan T, Sharma A, Gurcan M, **Huang K**, Leone G, Saltz J. GridCAD Microscopy: a caBIG based system for image processing and quantitative analysis, *Advancing Practice, Instruction and Innovation Through Informatics (APIII),* Vancouver, Canada, August 2006. [Peer Reviewed]

14. **Huang K**, Iyengar S, Radecki R, Mahmoud AM, Twa MD, Lembach RG, Roberts CJ. Comparison of corneal scattering properties pre- and post-LASIK using orbscan images, *in Proceedings of the 2006 Annual Meeting for Research in Vision and Ophthalmology (ARVO)*, Fort Lauderdale, FL, April 2006. [Peer Reviewed]

15. Pan T, Masaliganti K, Sharp R, Ridgeway R, **Huang K**, Machuraju R, Saltz J. Virtual placenta: computational phenotyping through image analysis, *Advancing Practice, Instruction and Innovation through Informatics (APIII),* Vancouver, Canada, August 2005. [Peer Reviewed]

16. **Huang K**, Moroz LL, Sudlow L, Gillette R. Nitric oxide and 5-HT may regulate feeding network arousal state via intracellular Ca2+ and H+ in *Pleurobranchae Californica*, in *Abstracts of 28th Annual Meeting of Society for Neuroscience*, Los Angeles, USA, October 1998. [Editor Reviewed]

- **Technical reports**

1. **Huang K**, Hong W, Yang AY, Rao S, Ma Y. Symmetry-based 3-D reconstruction from perspective images (Part I and II), *Technical Report*, UILU-ENG-03-2204, April, 2003.

2. Brand M, **Huang K**. A Unifying Theorem for spectral embedding and clustering, *Technical Report of Mitsubishi Electric Research Laboratory*, TR2002-42, October, 2002.

3. Fossum R, **Huang K**, Ma Y. General Rank conditions in multiple view geometry, *Technical Report*, UILU-ENG-01-2222, October 8, 2001.

4. Ma Y, **Huang K**, Vidal R, Kosecka J, Sastry S. New rank conditions of the multiple view matrix in multiple view geometry, *Technical Report*, UILU-ENG-01-2214 (DC-220), June 18, 2001.

5. Ma Y, Vidal R, **Huang K**, Sastry S. New rank deficiency condition for multiple view geometry of point features, *Technical Report*, UILU-ENG-01-2208 (DC-200), May 8, 2001.

6. Ma Y, **Huang K**, Kosecka J. New rank deficiency condition for multiple view geometry of line features, *Technical Report*, UILU-ENG-01-2209 (DC-201), May 8, 2001.

- **Thesis and dissertations**

1. **Huang K**, Geometric principles of visual sensor networks, Ph.D. Dissertation, University of Illinois, 2004.

2. **Huang K**, Hierarchical and integrated algorithms: comparison and applications in motion estimation and recognition, Master Thesis, University of Illinois, 2000.

3. **Huang K**, Computer-aided analysis of electrophysiological signals, Bachelor Degree Thesis, Tsinghua University, 1996.

Professional Activities:

- **Invited seminar presentations**

1. University of Hawaii, 2021
2. University of Alabama at Birmingham, 2021
3. University of Southern Florida, California, 2018
4. Mayo Clinic, Rochester, Minnesota, 2017
5. Moffitt Cancer Center, Florida, 2016
6. Northshore Health System, Illinois, 2016
7. Indiana State University, Indiana, 2016
8. Southern Medical University, Guangzhou, China, 2015
9. Guangdong Lung Cancer Institute, Guangzhou, China, 2015
10. Shanghai Jiaotong University, Shanghai, China, 2015
11. University of Texas Health Science Center, Texas, 2015
12. University of Alabama at Birmingham, Alabama, 2015
13. Fudan University, Shanghai, China, 2015
14. Dalian Medical University, Dalian, China, 2015
15. West Virginia University, Morgantown, West Virginia, 2015

16. George Washington University, Biophysics Program, Washington DC, February, 2015.

17. ShanghaiTech University, College of Electronic and Information Technology, Shanghai, China, October, 2014, 2015.

18. Harbin Engineering University, Department of Automation, Harbin, China, August, 2014.

19. Rutgers University, Department of Computer Science, Brunswick, New Jersey, May, 2014.

20. Peking University, Beijing , China, 2013

21. Northeastern Normal University, School of Computer Science, Changchun, China, July, 2013.

22. University of North Carolina at Charlotte, Department of Bioinformatics, Charlotte, North Carolina, March, 2013.

23. University of Georgia, Department of Computer Science, Athens, Georgia, October, 2012.

24. Methodist Hospital, Department of Systems Medicine and Bioengineering, Houston, Texas, October, 2012.

25. Soochow University, Department of Electrical Engineering, Suzhou, China, December, 2012.

26. Biomedical Informatics Research Institute, Shanghai, China, September, 2012.

27. National Key Laboratory of Systems Biology, Shanghai, China, September, 2012.

28. Tongji University, Department of Automation, Shanghai, China, September, 2012.

29. University of Science and Technology of China, Department of Bioengineering, Hefei, China, September 2012.

30. Soochow University, Institute of Systems Biology, Suzhou, China, September, 2012.

31. Chinese Academy of Science Shenzhen Advanced Research Institute, Shenzhen, China, September, 2012.

32. Indiana University, Medical School, Indiana, 2011

33. Microsoft Research Asia, Beijing, China, 2011

34. Fuzhou University, Institute of Life Science, Fuzhou, China, 2010.

35. West Virginia University, Department of Mathematics, Morgantown, 2009.

36. University of Illinois at Chicago, Department of Biomedical Engineering, Chicago, 2008.

- **Conference and meeting presentations**

1. International Symposium on Image Computing and Digital Medicine (Plenary Speaker), Chengdu, China, 2017

2. IEEE International Conference on Biomedical and Health Informatics (BHI), Pathology Image Informatics Workshop (Invited Speaker), Las Vegas, 2016

3. iBRIGT Conference (Invited Speaker), Texas, 2015

4. ACM-BCB Workshop on Computational Pathology: Linking Tissue Phenotypes with Genomics and Clinical Outcomes (Invited Speaker), Georgia, 2015

5. ACM-BCB Workshop on Novel enabling technologies in mining massive biomedical data (Invited Speaker), Georgia, 2015

6. International Conference on Translational Bioinformatics (Plenary Speaker), Taicang, China, December, 2015.

7. International Conference on Translational Bioinformatics (Plenary Speaker), Taicang, China, December, 2014.

8. International Conference on Translational Bioinformatics (Invited Speaker), Taicang, China, December, 2013.

9. Bioimage Informatics Session (Invited Speaker), Biomedical Engineering Society Annual Conference, Atlanta, GA, October, 2012.

10. International Conference on Translational Bioinformatics (Invited Speaker), Taicang, China, December, 2012.

11. AMIA Annual Summit on Translational Bioinformatics, San Francisco, California, March, 2012.

12. AMIA Annual Summit on Translational Bioinformatics, San Francisco, California, March, 2012.

- **Editorial position**

1. Section editor, BMC Medical Genomics, 2016 – 2019.

2. Associate editor, BMC Medical Genomics, 2011 – 2016.

3. Editorial Board, Journal of Translational Bioinformatics, 2013-2015

4. Guest editor, Special issue on Software and Tools for IEEE/ACM Transactions on Bioinformatics and Computational Biology, 2015.

5. Guest editor, Special issue on Gene Network and Pathway Generation and Analysis for the International Journal of Computational Biolology and Drug Design, January 2011.

- **Conference organizer**

1. Steering Committee Member, International Conference on Intelligence in BioMedicine (ICIBM), 2021

2. Steering Committee Member, International Conference on Intelligence in BioMedicine (ICIBM), 2020

3. Steering Committee Member, International Conference on Intelligence in BioMedicine (ICIBM), 2019

4. Steering Committee Member, International Conference on Intelligence in BioMedicine (ICIBM), 2018

5. Steering Committee Member, International Symposium on Image Computing and Digital Medicine (ISICDM), 2018

6. Co-Chair of the 1st Computational Pathology Workshop: Linking Tissue Phenotypes with Genomics and Clinical Outcomes, ACM International Conference on Bioinformatics, Computational Biology, and Health Informatics (ACM-BCB 2015)

7. Co-Chair of the 8th International Workshop on High Performance Computing for Biomedical Image Analysis (HPC-MICCAI), the 18th International Conference on Medical Image Computing and Computer Assisted Intervention (MICCA)

8. Program Chair, International Conference on Intelligence in Biology and Medicine (ICIBM), Indianapolis, IN, 2015.

9. Program co-Chair, International Conference on Translational Bioinformatics, Harbin, China, 2015.

10. Chair of Workshop on Next Generation Sequencing Data Analysis and Applications, in International Conference on Intelligence in Biology and Medicine (ICIBM), Nashville, TN, 2013.

11. Program co-Chair of the Sino-US Workshop on Bioinformatics at Soochow University, 2013

12. Industry and Exhibition co-Chair for IEEE BioVis Symposium, 2012.

13. Co-Chair of the Zing Conference on Computational Biology, 2012.

14. Publicity co-Chair for IEEE International Conference on Health Informatics and Systems Biology (HISB), 2012.

15. Workshop co-Chair for IEEE International Conference on BioIformatics in BioMedicine (BIBM) 2012.

16. Chair of Workshop on Next Generation Sequencing Data Analysis and Applications, in International Conference on Intelligence in Biology and Medicine (ICIBM) 2012.

17. Co-Chair of Workshop on Data Mining in Next Generation Sequencing in IEEE International Conference on BioIformatics in BioMedicine (BIBM) 2011.

18. Co-Chair of Workshop on Microscopic Image Analysis with Applications in Biomedicine (MIAAB) in ACM Conference on Bioinformatics and Computational Biology (BCB) 2011.

19. Co-Chair of Workshop on Data Mining in Next Generation Sequencing in IEEE International Conference on BioIformatics in BioMedicine (BIBM) 2010.

20. Co-Chair of Workshop on Gene Network and Pathway Analysis in ACM International Conference on Biocomputing and Bioinformatics (ACM BCB) 2010.

21. Organizer of the Massive Parallel Sequencing session in OCCBIO 2009.

22. Chair of Systems Biology Session of International Joint Conference on Bioinformatics, Systems Biology and Intelligent Computing 2009

- **Session chair**

1. Special session on Computational Epigenetics, IEEE Workshop on Genome Signal Processing (GENSIP), 2011.

2. Chair of Brain Imaging session in the IEEE International Symposium of Biomedical Imaging (ISBI) 2011.

3. Chair of the Systems Biology session in the ISIBM International Joint Conferences on Bioinformatics, Systems Biology and Intelligent Computing (IJCBS) 2009.

4. Chair of the Massive Parallel Sequencing session in OCCBIO 2009.

- **Conference tutorial**

1. Tutorial on Bioimaging Informatics, International Conference on Intelligence in Biology and Medicine (ICIBM), Indianapolis, IN, 2015.

2. Tutorial on Next Generation Sequencing, International Conference on Intelligence in Biology and Medicine (ICIBM), San Antonio, TX, 2014.

3. Tutorial on Epigenomics at IEEE GENSIP, San Antonio, TX, 2011.

4. Tutorial on Epigenomics at IEEE BIBM, Hong Kong, 2010.

5. Tutorial on Analysis of ChIP-seq Data at ACM BCB, Niagara Falls, NY, 2010.

6. Tutorial on Epigenetics and ChIP-seq Data Analysis at International Conference on Computational Systems Bioinformatics (CSB), Stanford University, CA, 2010.

7. Tutorial on Epigenomics at the Computational Systems Bioinformatics (CSB) Conference, Palo Alto, CA, 2010

- **Program committee member**

1. Program committee in the International Conference on Bioinformatics and Computational Biology (BIcoB), 2016.

2. Program committee in the International Conference on Bioinformatics and Computational Biology (BIcoB), 2015.

3. Program committee in the International Conference on Bioinformatics and Computational Biology (BIcoB), 2014.

4. Program committee in the IEEE International Conference on Health Informatics (ICHI) 2013.

5. Program committee in the IEEE International Conference in Intelligent Computing (ICIC) 2013.

6. Program committee in the International Conference on Bioinformatics and Computational Biology (BIcoB), 2013.

7. Program committee in the IEEE International Conference on Computer Vision and Pattern Recognition (CVPR) 2012.

8. Program committee in the IEEE International Conference in Intelligent Computing (ICIC) 2012.

9. Program committee in the International Conference on Bioinformatics and Computational Biology (BIcoB), 2012.

10. Program committee in the ACM Conference on Bioinformatics and Computational Biology (BCB) 2011.

11. Program committee in the IEEE International Conference in Intelligent Computing (ICIC) 2011.

12. Program committee in the IEEE International Conference in Computer Vision (ICCV) 2011.

13. Program committee in the IEEE International Conference in Computer Vision and Pattern Recognition (CVPR) 2011.

14. Program committee in the 3rd International Conference on Bioinformatics and Computational Biology (BICoB) 2011.

15. Program committee in the International Conference on Information Science and Technology (ICIST) 2011.

16. Program committee in the 4th International Workshop on Mining Multiple Information Sources in conjunction with the IEEE International Conference on Data Mining (ICDM) 2010.

17. Program committee in the International Conference on Intelligent Computing (ICIC) 2010.

18. Program committee of the IEEE Pacific Rim Symposium on Image Video and Technology (PSIVT'09).

19. Program committee of the Dynamical Vision Workshop of the 2009 International Conference in Computer Vision (ICCV'09).

20. Program committee of the Workshop on Microscopic Image Analysis with Applications in Biomedicine (MIAAB'09).

21. Program committee of the 2008 IEEE International Conference in Computer Vision and Pattern Recognition (CVPR'08).

22. International program committee of the International Symposium on Volume Graphics (VG'08) in the 2008 EUROGRAPHICS Conference.

23. Program committee of the Workshop on Microscopic Image Analysis with Applications in Biomedicine (MIAAB'08).

24. Program committee of the Dynamical Vision Workshop of the 2007 International Conference in Computer Vision (ICCV'07).

25. Program committee of the 2007 International Conference in Computer Vision (ICCV'07).

26. International program committee of the International Symposium on Volume Graphics (VG'07) in the 2007 EUROGRAPHICS Conference.

27. Program committee of the Microscopic Image Analysis with Application in Biomedicine Workshop (MIAAB'07).

28. Program committee of the IEEE Pacific Rim Symposium on Image Video and Technology (PSIVT'07).

29. Program committee of the International Conference on Computer Vision Theory and Applications (VISAPP'07).

30. Program committee of the 2006 European Conference in Computer Vision (ECCV'06).

31. Program committee of the 2006 IEEE International Conference in Computer Vision and Pattern Recognition (CVPR'06).

32. Program committee of the Dynamical Vision Workshop of the 2006 European Conference in Computer Vision (ECCV'06).

33. Program committee of the 2005 IEEE International Conference in Computer Vision and Pattern Recognition (CVPR'05).

34. Program committee of the Dynamical Vision Workshop of the 2005 International Conference in Computer Vision (ICCV'05).

- **Book reviewer**

    MIT Press.

- **Paper reviewer**

    Bioinformatics. (Journal)

    BMC Systems Biology. (Journal)

    Elsevier Editorial System for Methods. (Journal)

    International Journal on Alzheimer Research. (Journal)

    Gene, Chromosomes and Cancer. (Journal)

    Genome Research. (Journal)

    IEEE Transactions on Pattern Analysis and Machine Intelligence (TPAMI). (Journal)

    IEEE Transactions on Robotics and Automation. (Journal)

    IEEE Transaction on Image Processing (TIP). (Journal)

    SPIE Optical Engineering. (Journal)

    Journal of Image Engineering. (Journal)

    Journal of Neuroscience Methods. (Journal)

    Journal of Proteome. (Journal)

    Information Sciences. (Journal)

    IEEE Signal Processing Letters. (Journal)

    Journal of Optical Society American A. (Journal)

    Journal of Biomedical Informatics. (Journal)

    International Journal of Pattern Recognition. (Journal)

    International Journal of Computer Vision (IJCV). (Journal)

    Journal of Visual Communication and Image Representation. (Journal)

    Neurocomputing. (Journal)

    IEEE Transactions on Circuits and Systems for Video Technology. (Journal)

    International Journal of Biomedical Imaging. (Journal)

    IEEE International Conference on Computer Vision. (Papers In Proceedings)

    Europen Conference on Computer Vision. (Papers In Proceedings)

IEEE International Conference on Computer Vision and Pattern Recognition. (Papers In Proceedings)

IEEE International Conference on Decision and Control. (Papers In Proceedings)

IEEE International Conference on Robotics and Automation. (Papers In Proceedings)

AMIA Summit on Translational Bioinformatics. (Papers In Proceedings)

Pacific Symposium on Biocomputing (PSB). (Papers In Proceedings)

International Conference on Computer Vision Theory and Applications (VISAPP). (Papers In Proceedings)

- **Professional Societies**

Institute of Electrical and Electronics Engineers (1999 – Current).

Societies and Working Groups:

1. Board of Directors, International Association of Intelligence in Biology and Medicine, 2018
2. National Cancer Institute ICBP Data and Software Sharing Working Group.
3. National Cancer Institute CCSB Tumor Heterogeneity Working Group.
4. National Cancer Institute CPTAC Data Analysis Working Group.
5. National Cancer Institute TCGA PanCancer Working Group.

Teaching:

- **Course director**
1. BMI7830 (2014 - 2016) – Advanced Bioinformatics for Human Diseases, 3 credits
2. BMI5730 (2006 – 2010, 2013) – Bioinformatics for Human Diseases, 3 credits
3. IBGP705 (2006 – 2011) – Introductory bioinformatics course for BSGP students, 1 credit
- **Co-taught courses and guest lectures (2012-2016)**
1. BMI5730 (2012, 2014-2016)
2. BMI5740 (2013)
3. BSGP7000 (2012 - 2014)
4. BMI7840 (2013)
5. CSE5544 (Scientific Visualization, 2012)
6. BMI5710 (2012)
7. IBGP705 (2012)

Trainees:

- **PhD students as dissertation advisor/co-advisor**
1. Justin Couetil – MD/PhD, IUSM

2. Zanyu Shi - Biostatistics, IUPUI

3. Ziyan Song - Biostatistics, IUPUI

4. Xiaoqing Huang (co-advised with Dr. Jie Zhang) – Biostatistics, IUPUI

5. Ziyu Liu (co-advised with Dr. Min Zhang) – Statistics, Purdue University

6. Tianhan Dong – Pharmacology, IUSM

7. Zhi Huang (co-advised with Dr. Paul Salama) – Electrical and Computer Engineering, IUPUI, postdoctoral researcher at Stanford University

8. Tongxin Wang (co-advised with Dr. Haixu Tang) – Computer Science, IUB, data scientist at Facebook, Inc.

9. Christina Yu (PhD 2020, co-advised with Dr. Jeffrey Parvin) – BSGP / MIDAS Fellow, postdoctoral researcher at Rutgers University

10. Travis Johnson (PhD 2020, co-advised with Dr. Yan Zhang) – BSGP / MIDAS Fellow / NIH F31 Fellow, currently Assistant Research Professor in Biostatistics at IU School of Medicine

11. Michael Sharpnack (PhD 2018) – MSTP / BSGP / NLM T15 Fellow, currently Resident in UCSF

12. Arunima Srivastiva (PhD 2020, co-advised with Dr. Machiraju) – Computer Science and Engineering

13. Qihang Li (PhD 2017, co-advised with Dr. Machiraju) – OSU Computer Science and Engineering

14. Brian Arand (co-advised with Dr. Machiraju) – OSU Computer Science and Engineering

15. Parchamon Kaewprag (PhD 2019, co-advised with Dr. Machiraju) – OSU Computer Science and Engineering

16. Hao Ding (PhD 2016, co-advised with Dr. Machiraju) – Currently Research Scientist at Walmart Labs

17. Nan Meng (PhD 2016, co-advised with Dr. Machiraju) – Currently Quantitative Data Analyst at Two Sigma, New York

18. Chao Wang (PhD 2015) – Currently Principal Software Engineer at Thermal Fisher (HHMI Med-to-Grad Fellow, Pelotonia Fellow)

19. Shantanu Singh (PhD 2011, co-advised with Dr. Machiraju) – currently Senior Group Leader at Broad Institute.

20. Lee Cooper (PhD 2009) – currently Associate Professor in Pathology at Northerwestern University (NLM K22 and NCI U24 grants awardee).

21. Kishore Mosaliganti (PhD 2008, co-advised with Dr. Machiraju) – formerly Research Fellow at Harvard Medical School (NIH K25 grant awardee), currently VP at Fidelity

22. Leszek Rybaczyk (PhD 2008, deceased) – was Postdoctoral Researcher in Nationwide Children's Hospital.

- **Visiting PhD students**

1. Yusong Liu (HEU, 10/2018 – 10/2020)

2. Tao Lian (SMU, 11/2019 – 01/2021)

3. Yatong Han (HEU, 10/2016 – 03/2018)

4. Jun Cheng – currently Assistant Professor in Shenzhen University (SMU, 05/2016 – 03/2018)

5. Zixiao Lu (SMU, 03/2018 – 09/2020)

6. Peng Zhao (UEST, 11/2018 – 11/2019)

- **PhD students as dissertation committee member**

1. Chuanpeng Dong – IUPUI BioHealth Informatics (PhD 2022)

2. Ruohong Li – IUPUI Biostatistics (PhD 2021)

3. Brynn Hollingsworth – OSU BSGP (PhD 2010)

4. Mohammad Ali Rezaei – OSU Pharmacy

5. Muhtadi Islam – OSU BSGP/MSTP (PhD 2016)

6. Cindy Lee – OSU BSGP (PhD 2015)

7. Mucahid Kutlu – OSU CSE (PhD 2015)

8. Anas AbuDoleh – OSU ECE (PhD 2015)

9. Zach Abrams – OSU BSGP (PhD 2016)

10. Jinnan Hu – OSU Plant Pathology (PhD 2013)

11. Selnur Erdal – OSU Radiology (PhD 2012)

12. Huameng Li – OSU Pharmacy (PhD 2011)

13. Sasha Beyer – OSU BSGP (PhD 2011)

14. Jun Kong – OSU ECE (PhD 2008) – currently Associate Professor in Mathematics and Statistics at Georgia State University

15. Ruohong Li – IU Public Health Biostatistics (PhD 2021)

16. Jiannan Liu – IUPUI BioHealth Informatics (PhD expected 2022)

- **MS students**

1. Brian Kennedy (2016 – current) – Biomedical Informatics

2. Eric Skinner (2014 – current) – Biomedical Informatics

3. Travis Johnson (2014 – 2016) – Biomedical Informatics, current PhD student in the BSGP program at OSU

4. Daniel Morgan (2014) – Biomedical Informatics, currently PhD student in Sweden

5. Terry Camerlengo (2008 – 2013) – Biophysics, currently IT consultant

6. Raghuram Onti-Srinivasan (co-advised with Dr. Machiraju) – Computer Science and Engineering

7. Jinchao Di (2012-2013) – Electrical and Computer Engineering

8. Zhiwei Ma (2011-2012) – Biophysics, currently Ph.D. student in University of Massachusetts

9. Vikram Kalluru (2011-2012) – Electrical and Computer Engineering, currently engineer in Boston area

10. Lizhi Li (2011) – Biophysics

11. Randall Ridgway (2005-2007), currently industry researcher

12. Iyengar Srinivasan (2006-2007), currently software engineer at Mathworks Inc.

13. Kristin Keen-Circle (2007-2008), currently Registered Nurse at Nationwide Children's Hospital

14. Heng-Yi Wu (2010), currently research assistant in Indiana University (IUPUI)

15. Kewei Lu (2010-2011), currently PhD student at OSU

16. Renuka Panchagavi (2011- 2012)

- **Postdoctoral researchers and fellows**

1. Dr. Wei Shao (2019 – 2021)

2. Dr. Bryan Helm (2018 – 2021) – NIH T32 Fellow

3. Dr. Xiaohui Zhang (2018 – 2021)

4. Dr. Shunian Xiang (2018 – 2020) – co-supervised with Dr. Jie Zhang

5. Dr. Xing Tang (2014 – 2016) – co-supervised with Dr. Leone, currently Research Scientist in St. Jude Children's Hospital

6. Dr. Cenny Taslim (2008 – 2016) – co-supervised with Dr. Peter Shields, currently Bioinformatics Scientist at Nationwide Children's Hospital Research Institute

7. Dr. Xingyan Kuang (2014 – 2016) – co-supervised with Dr. Peter Shields, currently postdoctoral researcher at OSU

8. Dr. Jinyu Hu (2014- 2015) – co-supervised with Dr. Craig Burd, currently postdoctoral researcher at Stanford University

9. Dr. Amy Webb (2010 – 2015) – co-supervised with Dr. Parvin, currently Research Scientist at OSU Biomedical Informatics Shared Resource

10. Dr. David Liebner (2011 – 2014) – co-supervised with Dr. Parvin, currently Assistant Professor in Department of Medicine at the Ohio State University

11. Dr. Theirry Pecot (2009 – 2014) – co-supervised with Dr. Machiraju, currently Research Scientist at INRIA, France

12. Dr. Dias Kurmshev (2011 – 2013) – co-supervised with Dr. Ostrowski

13. Dr. Yang Xiang (2010 – 2012, NSF CIFellow) – currently Research Assistant Professor in Biomedical Informatics at the Ohio State University

14. Dr. Hatice Gulcin Ozer (2008 – 2012) – currently Research Scientist in Biomedical Informatics at the Ohio State University

15. Dr. Liya Ding (2009 – 2010) – currently Scientist and Image Analyst at Allen Institute for Cell Sciences

16. Dr. Onur Hamcisi (2009) – currently academic researcher

17. Dr. Li Wang (2006-2007) – currently industry research

18. Dr. Anand Merchant (2008-2011) – currently academic researcher

- **Undergraduate interns and high school volunteers**

1. Michael Cheng (2019-2021) – Senior in Biology, Indiana University at Bloomington

2. Allen Zhao (2019) – Sophomore in Washington University

3. Sanaya Shroff (2014, 2015) – junior in Chemical Engineering, Cornell University (Currently at PhD program in Boston University)

4. Peter Niedeker (2014, 2015) – senior in Mathematics, University of Notre Dame

5. Frederick Zhang (2014) – junior in Economy, Vanderbilt University

6. Muzi Zhang (2012) – senior in Mathematics, OSU

7. Zhiyan Gu (2012 – 2013) senior in Mathematics, OSU

8. Shiman Liu (2012 – 2013) – senior in Actuarial Sciences, OSU

9. Junyi Zhang (2013 – current) – senior in Actuarial Sciences, OSU

10. Laura Lin (2012) – junior in Dublin Jerome High School (Currently at OSU)

11. Nitish Aggawal (2011-2014) – senior in Actuarial Sciences, OSU

12. Kelly Pan (2015 - 2016) – student in Dublin Coffman High School (Currently at Brown University)