JUW WON PARK, PH.D.

Associate Professor
Brown Cancer Center
Department of Medicine
University of Louisville

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EDUCATION

Ph.D. in Computer Science — July 2009
University of Iowa, Iowa City, IA, USA
Advisors: Prof. Alberto Segre and Prof. James Cremer

M.S. in Computer Science — May 1999
University of Iowa, Iowa City, IA, USA

B.S. in Computer Science — February 1995
Korea University, Seoul, Republic of Korea

WORK EXPERIENCE

Associate Professor: Department of Medicine, University of Louisville, KY — 08/2023 – current

- Bigdata and systems approaches to RNA regulatory network
- Developing Bioinformatics and genomics methods for cancer studies using high-throughput sequencing data

Director: Bioinformatics Core, Brown Cancer Center, University of Louisville, KY — 08/2023 – current

- Bioinformatics support and training Brown Cancer Center researchers

Associate Professor: Department of Computer Science and Engineering, University of Louisville, KY — 08/2021 – 07/2023
Assistant Professor: Department of Computer Science and Engineering, University of Louisville, KY — 08/2015 – 07/2021

- Bioinformatics and genomics
- Computer graphics

Co-Director: CIEHS (Center for Integrative Environmental Health Sciences) Biostatistics & Informatics Facility Core (BIFC), University of Louisville, KY — 08/2022 – current

- Bioinformatics support and training for CIEHS members
- Providing intellectual input required for rigorous data analysis

Faculty: KY INBRE (Kentucky IDeA Networks of Biomedical Research Excellence) Bioinformatics Core, University of Louisville, KY 08/2015 – current

- Algorithms for next-generation sequence analysis
- Analyses of various genomic data

Postdoctoral fellow: Department of Microbiology, Immunology, & Molecular Genetics, UCLA, CA 12/2012 – 07/2015

- Novel computational and statistical methods for analysis of massive genome and transcriptome data
- Alternative mRNA splicing and its regulation in eukaryotic cells using high-throughput RNA sequencing and related genomic technologies
- Transcriptome-wide landscape of alternative splicing associated with metastasis of cancer cells
- The regulation of alternative splicing by chromatin or RNA factors

Postdoctoral fellow: Department of Internal Medicine, University of Iowa, IA 08/2009 – 12/2012

- Identification of differential alternative splicing events from high-throughput RNA sequencing
- Genome-wide spectrum of alternative splicing events regulated by the epithelial-specific splicing regulatory proteins (ESRP1 and ESRP2)
- Robust computational and statistical methods for analyzing regulatory variation of alternative splicing using RNA sequencing data

Graduate Research Assistant: Department of Computer Science, Center for Statistical Genetic Research, University of Iowa, IA 01/2003 – 07/2009

- Clustering algorithm for genetically homogeneous subsets of pedigrees by exploring the shape information implicit in the linkage likelihood space
- Efficient visualization and navigation of high-dimensional linkage likelihood space
- Online biotic database for Tropical American biodiversity (collaboration with geoscience department: http://nmita.iowa.uiowa.edu/)

RESEARCH GRANTS

2R01ES027778-06A1 (PI: Chris States), $3,314,460 1/23/2024 – 03/31/2028
Mechanism of Arsenic Carcinogenesis
Goals: To identify additional miR-186 targets contributing to chromosomal instability (CIN) and to characterize the impact of the 5 additional miRNAs overexpressed in iAs-induced squamous cell carcinoma (SCC).
Role: **CO-I**

HT94252310018 DOD/CMDRP/USAMRAA (PI: Carolyn Klinge), $1,015,291 3/1/2023 – 2/28/2026
m6A Epitranscriptome Drivers of Endocrine-Resistant Breast Cancer

Goals: To identify progression to endocrine resistance and increased metastatic risk for targeted intervention in BC patients by examining N6-methyladenosine (m6A) epitranscriptome.
Role: **CO-I**

2R01AT008617-06A1 NIH/NCCIH (PI: Huang-ge Zhang), $3,228,120 7/20/2022 – 5/31/2027
Mechanisms underlying edible exosome-like nanoparticles for prevention of brain inflammation
Goals: The purpose of this grant is to provide cellular and molecular insight into how ELNs (exosome-like nanoparticles) modulate neuroimmune function via a gut-brain axis by targeting microglial cells that benefits the brain.
Role: **CO-I**

1P30ES030283-01A1 NIH/NIEHS (PI: Chris States), $6,473,751 8/1/2020 – 3/31/2025
University of Louisville Center for Integrative Environmental Health Sciences
Goals: The University of Louisville's (UofL) Center for Integrative Environmental Health Science (CIEHS) brings together a multidisciplinary group of investigators working together to develop a framework to understand the complexities of and to integrate the interactions between environmental toxicants, lifestyle factors, life stage, genetics and gender and their roles in human health and disease. The CIEHS is uniquely positioned to build transdisciplinary teams to tackle these problems by virtue of the multidisciplinary expertise of its members and its geographic location.
Role: **Director of Biostatistics & Informatics Facility Core**

R15GM140427 (PI: Juw Won Park) NIH/NIGMS, $460,156 9/21/2021-7/31/2023
Identifying and characterizing translation of circular RNAs using high-throughput sequencing data
Goals: The major goals of this project are to develop a computation method to detect and characterize translated circular RNAs using non-polyA RNA-seq data along with Ribo-seq data and to develop a new web server for aggregating, cataloging, and visualizing translated circular RNAs derived from public repositories like GEO.
Role: **sole PI**

KY INBRE Post-Doctoral Fellow Awards from NIH/NIGMS (PI: Juw Won Park), $142,760
9/21/2021-07/31/2023
Goals: This funding provides partial support (50%) for a post-doctoral research associate for NIH-R15 funded investigators.
Role: **sole PI**

P20GM103436 (PI: Juw Won Park) NIH/NIGMS 5/01/2021-04/30/2022
KY INBRE Bridge Funding Awards
Goals: The purpose of this program is to enable NIH-funded faculty to maintain their research program for short periods of time between the lapse of initial grant funding and the start of a new or renewal NIH grant award.

Role: **sole PI**

1R21ES030334-01A1 NIH/NIEHS (PI: Chris States), $429,000 7/14/2020 – 06/30/2022
Alternative splicing in arsenical skin carcinogenesis
Goals: The major goals of this project are to examine the contribution towards the process of carcinogenesis of significant differential splicing events at three time points in human keratinocytes chronically exposed to low levels of arsenite and to correlate these events with changes in the proteomic profiles.
Role: **CO-I**

1U19AI142762-01 NIH/NIAID (PI: Colleen B Jonsson), $25,159,198 3/06/2019 – 02/29/2020
In vitro evaluation and characterization of novel lead therapeutic candidates for encephalitic alphavirus treatment
Goals: The major goals of this project are to detect and map antiviral treatment-resistant mutations in RNA virus using high-throughput sequencing data as well as to design new compounds using such mutation information which can induce therapeutic efficacy in human trials.
Role: **CO-I** In collaboration with Colleen Jonsson (University of Tennessee Health Science Center), Jennifer Golden (University of Wisconsin), and Donghoon Chung (University of Louisville)

R15GM126446 NIH/NIGMS (PI: Juw Won Park), $462,2000 09/15/2017-08/31/2021
Detecting and characterizing circular RNAs using high-throughput sequencing data
Goals: To develop a computation method to detect, characterize, and quantify differentially expressed circular RNAs between various biological conditions using non-polyA RNA-seq data and to develop a new web server for aggregating, cataloging, and visualizing circular RNAs derived from public repositories like GEO.
Role: **sole PI**

KY INBRE Post-Doctoral Fellow Awards from NIH/NIGMS (PI: Juw Won Park), $142,760
09/15/2017-08/31/2020
Goals: This funding provides partial support (50%) for a post-doctoral research associate for NIH-R15 funded investigators.
Role: **sole PI**

P20GM103436 KBRIN IDeA, NIH/NIGMS (PI: Juw Won Park), $120,000 05/01/2017-04/30/2019
Identification of circular RNAs.
Goals: To improve our understanding of a recently discovered circular form of RNA (circular RNA or circRNA) using high-throughput sequencing data to identify and characterize these structures from the existing publicly available datasets.
Role: **sole PI**

SELECTED JOURNAL PUBLICATIONS

1. Hwang JY, Kook TL, Paulus SM, **Park JW**. Translation of Circular RNAs: Functions of Translated Products and Related Bioinformatics Approaches. ***Curr Bioinform***. 2024;19(1):3–13. doi: 10.2174/1574893618666230505101059. PMCID: PMC10947221.
2. Xu F, Ren Y, Teng Y, Mu J, Tang J, Sundaram K, Zhang L, **Park JW**, Hwang JY, Yan J, Dryden G, Zhang HG. Tryptophan As a New Member of RNA-Induced Silencing Complexes Prevents Colon Cancer Liver Metastasis. ***Adv Sci***. 2024 Jun 20:e2307937. doi: 10.1002/advs.202307937. Epub ahead of print. PMID: 39031551.
3. Sundaram K, Teng Y, Mu J, Xu Q, Xu F, Sriwastva MK, Zhang L, **Park JW**, Zhang X, Yan J, Zhang SQ, Merchant ML, Chen SY, McClain CJ, Dryden GW, Zhang HG. Outer Membrane Vesicles Released from Garlic Exosome-like Nanoparticles (GaELNs) Train Gut Bacteria that Reverses Type 2 Diabetes via the Gut-Brain Axis. ***Small***. 2024 May;20(20):e2308680. doi: 10.1002/smll.202308680. Epub 2024 Jan 15. PMID: 38225709; PMCID: PMC11102339.
4. Sayed M, **Park JW**. miRinGO: Prediction of Biological Processes Indirectly Targeted by Human microRNAs. ***Noncoding RNA***. 2023 Jan 22;9(1):11. doi: 10.3390/ncrna9010011. PMID: 36827544; PMCID: PMC9962180.
5. Petri BJ, Piell KM, Wahlang B, Head KZ, Rouchka EC, **Park JW**, Hwang JY, Banerjee M, Cave MC, Klinge CM, Altered splicing factor and alternative splicing events in a mouse model of diet- and polychlorinated biphenyl-induced liver disease. ***Environ Toxicol Pharmacol*** 2023 Oct;103:104260. doi: 10.1016/j.etap.2023.104260. Epub 2023 Sep 7. PMID: 37683712; PMCID: PMC10591945.
6. Sriwastva MK, Teng Y, Mu J, Xu F, Kumar A, Sundaram K, Malhotra RK, Xu Q, Hood JL, Zhang L, Yan J, Merchant ML, **Park JW**, Dryden GW, Egilmez NK, Zhang HG. An extracellular vesicular mutant KRAS-associated protein complex promotes lung inflammation and tumor growth. ***J Extracell Vesicles***. 2023 Feb;12(2):e12307. doi: 10.1002/jev2.12307. PMID: 36754903; PMCID: PMC9908562.
7. Koo HY, Kim MA, Min H, Hwang JY, Prajapati-DiNubila M, Kim KS, Matzuk MM, **Park JW**, Doetzlhofer A, Kim UK, Bok J. Follistatin regulates the specification of the apical cochlea responsible for low-frequency hearing in mammals. ***Proc Natl Acad Sci***. 2023 Jan 3;120(1):e2213099120.
8. Sayed M, Hwang JY, **Park JW**, "Circular RNA detection and effect of sequence homology", ***Applied Computing Review*** (2022) 22(1):24-30
9. Teng Y, Mu J, Xu F, Zhang X, Sriwastva MK, Liu QM, Li X, Lei C, Sundaram K, Hu X, Zhang L, **Park JW**, Hwang JY, Rouchka EC, Zhang X, Yan J, Merchant ML, Zhang HG. Gut bacterial isoamylamine promotes age-related cognitive dysfunction by promoting microglial cell death. ***Cell Host Microbe***. 2022 Jul 13;30(7):944-960.e8. doi: 10.1016/j.chom.2022.05.005. Epub 2022 Jun 1. PMID: 35654045; PMCID: PMC9283381.
10. Sundaram K, Mu J, Kumar A, Behera J, Lei C, Sriwastva MK, Xu F, Dryden GW, Zhang L, Chen S, Yan J, Zhang X, **Park JW**, Merchant ML, Tyagi N, Teng Y, Zhang HG. Garlic exosome-like nanoparticles reverse high-fat diet induced obesity via the gut/brain axis. ***Theranostics***. 2022 Jan 1;12(3):1220-1246. doi: 10.7150/thno.65427. PMID: 35154484; PMCID: PMC8771565.
11. Kumar A, Sundaram K, Teng Y, Mu J, Sriwastva MK, Zhang L, Hood JL, Yan J, Zhang X, **Park JW**, Merchant ML, Zhang HG. Ginger nanoparticles mediated induction of Foxa2 prevents high-fat diet-induced insulin resistance. ***Theranostics***. 2022 Jan 1;12(3):1388-1403. doi: 10.7150/thno.62514. PMID: 35154496; PMCID: PMC8771553.
12. Peart NJ, Hwang JY, Quesnel-Vallières M, Sears MJ, Yang Y, Stoilov P, Barash Y, **Park JW**, Lynch KW, Carstens RP, The global Protein-RNA interaction map of ESRP1 defines a post-transcriptional program that is essential for epithelial cell function. ***iScience*** (2022) Sep 23;25(10):105205. doi: 10.1016/j.isci.2022.105205. PMID: 36238894; PMCID: PMC9550651.

13. Ferragut Cardoso AP, Banerjee M, Al-Eryani L, Sayed M, Wilkey DW, Merchant ML, **Park JW**, States JC. Temporal Modulation of Differential Alternative Splicing in HaCaT Human Keratinocyte Cell Line Chronically Exposed to Arsenic for up to 28 Wk. ***Environ Health Perspect***. 2022 Jan;130(1):17011. doi: 10.1289/EHP9676. Epub 2022 Jan 24. PMID: 35072517; PMCID: PMC8785870.
14. Sriwastva MK, Deng ZB, Wang B, Teng Y, Kumar A, Sundaram K, Mu J, Lei C, Dryden GW, Xu F, Zhang L, Yan J, Zhang X, **Park JW**, Merchant ML, Egilmez NK, Zhang HG. Exosome-like nanoparticles from Mulberry bark prevent DSS-induced colitis via the AhR/COPS8 pathway. ***EMBO Rep***. 2022 Feb 3;23(3):e53365. doi: 10.15252/embr.202153365. Epub 2022 Jan 7. PMID: 34994476; PMCID: PMC8892346.
15. Koo H, Hwang JY, Jung S, Park H, Bok J, **Park JW**. Position Specific Alternative Splicing and Gene Expression Profiles Along the Tonotopic Axis of Chick Cochlea. ***Front Mol Biosci***. 2021 Sep 8;8:726976. doi: 10.3389/fmolb.2021.726976. PMID: 34568429; PMCID: PMC8456117.
16. Kumar A, Sundaram K, Mu J, Dryden GW, Sriwastva MK, Lei C, Zhang L, Qiu X, Xu F, Yan J, Zhang X, **Park JW**, Merchant ML, Bohler HCL, Wang B, Zhang S, Qin C, Xu Z, Han X, McClain CJ, Teng Y, Zhang HG. High-fat diet-induced upregulation of exosomal phosphatidylcholine contributes to insulin resistance. ***Nat Commun***. 2021 Jan 11;12(1):213. doi: 10.1038/s41467-020-20500-w. PMID: 33431899; PMCID: PMC7801461.
17. Chaabane M, Andreeva K, Hwang JY, Kook TL, **Park JW***, Cooper NGF*. seekCRIT: Detecting and characterizing differentially expressed circular RNAs using high-throughput sequencing data. PLoS ***Comput Biol***. 2020 Oct 20;16(10):e1008338. doi: 10.1371/journal.pcbi.1008338. PMID: 33079938; PMCID: PMC7598922. ***co-corresponding authors**
18. Hwang JY, Jung S, Kook TL, Rouchka EC, Bok J, **Park JW**. rMAPS2: an update of the RNA map analysis and plotting server for alternative splicing regulation. ***Nucleic Acids Res***. 2020 Jul 2;48(W1):W300-W306. doi: 10.1093/nar/gkaa237. PMID: 32286627; PMCID: PMC7319468.
19. Chaabane M, Williams RM, Stephens AT, **Park JW**. circDeep: deep learning approach for circular RNA classification from other long non-coding RNA. ***Bioinformatics***. 2020 Jan 1;36(1):73-80. doi: 10.1093/bioinformatics/btz537. PMID: 31268128; PMCID: PMC6956777.
20. Sundaram K, Miller DP, Kumar A, Teng Y, Sayed M, Mu J, Lei C, Sriwastva MK, Zhang L, Yan J, Merchant ML, He L, Fang Y, Zhang S, Zhang X, **Park JW**, Lamont RJ, Zhang HG. Plant-Derived Exosomal Nanoparticles Inhibit Pathogenicity of Porphyromonas gingivalis. ***iScience***. 2019 Nov 22;21:308-327. doi: 10.1016/j.isci.2019.10.032. Epub 2019 Oct 21. Erratum in: iScience. 2020 Feb 21;23(2):100869. doi: 10.1016/j.isci.2020.100869. PMID: 31678913; PMCID: PMC6838522.
21. Alugubelly N, Mohammad AN, Edelmann MJ, Nanduri B, Sayed M, **Park JW***, Carr RL*. Proteomic and transcriptional profiling of rat amygdala following social play. ***Behav Brain Res***. 2019 Dec 30;376:112210. doi: 10.1016/j.bbr.2019.112210. Epub 2019 Sep 4. PMID: 31493430; PMCID: PMC6783381. ***co-corresponding authors**
22. Alugubelly N, Mohammed AN, Edelmann MJ, Nanduri B, Sayed M, **Park JW***, Carr RL*. Adolescent rat social play: Amygdalar proteomic and transcriptomic data. ***Data Brief.*** 2019 Sep 30;27:104589. doi: 10.1016/j.dib.2019.104589. PMID: 31673590; PMCID: PMC6817652. ***co-corresponding authors**
23. Choi C, Palmieri F, Chen HC, **Park JW**, "Guest Editorial: Soft Computing Applications for Novel and Upcoming Distributed and Parallel Systems, from Cloud Computing and Beyond." ***IEEE Transactions on Industrial Informatics.*** 2019 15(10):5646-5647
24. Harrison BJ, **Park JW**, Gomes C, Petruska JC, Sapio MR, Iadarola MJ, Chariker JH, Rouchka EC. Detection of Differentially Expressed Cleavage Site Intervals Within 3' Untranslated Regions Using CSI-UTR Reveals Regulated Interaction Motifs. ***Front Genet.*** 2019 Mar 12;10:182. doi: 10.3389/fgene.2019.00182. PMID: 30915105; PMCID: PMC6422928.

25. Teng Y, Ren Y, Sayed M, Hu X, Lei C, Kumar A, Hutchins E, Mu J, Deng Z, Luo C, Sundaram K, Sriwastva MK, Zhang L, Hsieh M, Reiman R, Haribabu B, Yan J, Jala VR, Miller DM, Van Keuren-Jensen K, Merchant ML, McClain CJ, **Park JW**, Egilmez NK, Zhang HG. Plant-Derived Exosomal MicroRNAs Shape the Gut Microbiota. ***Cell Host Microbe***. 2018 Nov 14;24(5):637-652.e8. doi: 10.1016/j.chom.2018.10.001. Epub 2018 Oct 25. PMID: 30449315; PMCID: PMC6746408 **(featured on the journal cover)**
26. Lee J, Park N, Park JY, Kaplan BLF, Pruett SB, **Park JW**, Park YH, Seo KS. Induction of Immunosuppressive CD8+CD25+FOXP3+ Regulatory T Cells by Suboptimal Stimulation with Staphylococcal Enterotoxin C1. ***J Immunol***. 2018 Jan 15;200(2):669-680. doi: 10.4049/jimmunol.1602109. Epub 2017 Dec 13. PMID: 29237775; PMCID: PMC5757107.
27. Jung S, Chang DJ, **Park JW**. Large Scale Document Inversion using a Multi-threaded Computing System. ***ACM SIGAPP Appl Comput Rev***. 2017 Jun;17(2):27-35. doi: 10.1145/3131080.3131083. Epub 2017 Aug 3. PMID: 29861701; PMCID: PMC5983369.
28. Park JY, Moon BY, **Park JW**, Thornton JA, Park YH, Seo KS. Genetic engineering of a temperate phage-based delivery system for CRISPR/Cas9 antimicrobials against Staphylococcus aureus. ***Sci Rep***. 2017 Mar 21;7:44929. doi: 10.1038/srep44929. PMID: 28322317; PMCID: PMC5359561.
29. **Park JW**, Jung S, Rouchka EC, Tseng YT, Xing Y. rMAPS: RNA map analysis and plotting server for alternative exon regulation. ***Nucleic Acids Res***. 2016 Jul 8;44(W1):W333-8. doi: 10.1093/nar/gkw410. Epub 2016 May 12. PMID: 27174931; PMCID: PMC4987942.
30. Zhou R*****, **Park JW***, Chun RF, Lisse TS, Garcia AJ, Zavala K, Sea JL, Lu ZX, Xu J, Adams JS, Xing Y, Hewison M. Concerted effects of heterogeneous nuclear ribonucleoprotein C1/C2 to control vitamin D-directed gene transcription and RNA splicing in human bone cells. ***Nucleic Acids Res***. 2017 Jan 25;45(2):606-618. doi: 10.1093/nar/gkw851. Epub 2016 Sep 26. PMID: 27672039; PMCID: PMC5314791. ***<u>These authors contributed equally</u>**
31. Bebee TW, Sims-Lucas S, **Park JW**, Bushnell D, Cieply B, Xing Y, Bates CM, Carstens RP. Ablation of the epithelial-specific splicing factor Esrp1 results in ureteric branching defects and reduced nephron number. ***Dev Dyn***. 2016 Oct;245(10):991-1000. doi: 10.1002/dvdy.24431. Epub 2016 Jul 28. PMID: 27404344; PMCID: PMC5096029.
32. Lin L, **Park JW**, Ramachandran S, Zhang Y, Tseng YT, Shen S, Waldvogel HJ, Curtis MA, Faull RL, Troncoso JC, Pletnikova O, Ross CA, Davidson BL, Xing Y. Transcriptome sequencing reveals aberrant alternative splicing in Huntington's disease. ***Hum Mol Genet***. 2016 Aug 15;25(16):3454-3466. doi: 10.1093/hmg/ddw187. Epub 2016 Jul 4. PMID: 27378699; PMCID: PMC5179942.
33. Yang Y*****, **Park JW***, Bebee TW, Warzecha CC, Guo Y, Shang X, Xing Y, Carstens RP. Determination of a Comprehensive Alternative Splicing Regulatory Network and Combinatorial Regulation by Key Factors during the Epithelial-to-Mesenchymal Transition. ***Mol Cell Biol***. 2016 May 16;36(11):1704-19. doi: 10.1128/MCB.00019-16. PMID: 27044866; PMCID: PMC4959312. ***<u>These authors contributed equally</u>**
34. Cieply B*****, **Park JW***, Nakauka-Ddamba A, Bebee TW, Guo Y, Shang X, Lengner CJ, Xing Y, Carstens RP. Multiphasic and Dynamic Changes in Alternative Splicing during Induction of Pluripotency Are Coordinated by Numerous RNA-Binding Proteins. ***Cell Rep***. 2016 Apr 12;15(2):247-55. doi: 10.1016/j.celrep.2016.03.025. Epub 2016 Mar 31. PMID: 27050523; PMCID: PMC5718363. ***<u>These authors contributed equally</u>**
35. Ji X*****, **Park JW***, Bahrami-Samani E, Lin L, Duncan-Lewis C, Pherribo G, Xing Y, Liebhaber SA. αCP binding to a cytosine-rich subset of polypyrimidine tracts drives a novel pathway of cassette exon splicing in the mammalian transcriptome. ***Nucleic Acids Res***. 2016 Mar 18;44(5):2283-97. doi: 10.1093/nar/gkw088. Epub 2016 Feb 20. PMID: 26896798; PMCID: PMC4797308. ***<u>These authors contributed equally</u>**

36. Lin L*, Jiang P*, **Park JW***, Wang J, Lu ZX, Lam MP, Ping P, Xing Y. The contribution of Alu exons to the human proteome. ***Genome Biol***. 2016 Jan 28;17:15. doi: 10.1186/s13059-016-0876-5. PMID: 26821878; PMCID: PMC4731929. ***These authors contributed equally**
37. Ruscetti M, Dadashian EL, Guo W, Quach B, Mulholland DJ, **Park JW**, Tran LM, Kobayashi N, Bianchi-Frias D, Xing Y, Nelson PS, Wu H. HDAC inhibition impedes epithelial-mesenchymal plasticity and suppresses metastatic, castration-resistant prostate cancer. ***Oncogene***. 2016 Jul 21;35(29):3781-95. doi: 10.1038/onc.2015.444. Epub 2015 Dec 7. PMID: 26640144; PMCID: PMC4896852.
38. Stein S, Lu ZX, Bahrami-Samani E, **Park JW**, Xing Y. Discover hidden splicing variations by mapping personal transcriptomes to personal genomes. ***Nucleic Acids Res***. 2015 Dec 15;43(22):10612-22. doi: 10.1093/nar/gkv1099. Epub 2015 Nov 17. PMID: 26578562; PMCID: PMC4678817.
39. Bebee TW*, **Park JW***, Sheridan KI, Warzecha CC, Cieply BW, Rohacek AM, Xing Y, Carstens RP. The splicing regulators Esrp1 and Esrp2 direct an epithelial splicing program essential for mammalian development. ***Elife***. 2015 Sep 15;4:e08954. doi: 10.7554/eLife.08954. PMID: 26371508; PMCID: PMC4566030. ***These authors contributed equally. Selected and recommended by "Faculty of 1000" (http://f1000.com/prime/725787938)**
40. Lu ZX*, Huang Q*, **Park JW***, Shen S, Lin L, Tokheim CJ, Henry MD, Xing Y. Transcriptome-wide landscape of pre-mRNA alternative splicing associated with metastatic colonization. ***Mol Cancer Res***. 2015 Feb;13(2):305-18. doi: 10.1158/1541-7786.MCR-14-0366. Epub 2014 Oct 1. PMID: 25274489; PMCID: PMC4336826. ***These authors contributed equally. This paper was highlighted by the journal**
41. Shen S*, **Park JW***, Lu ZX, Lin L, Henry MD, Wu YN, Zhou Q, Xing Y. rMATS: robust and flexible detection of differential alternative splicing from replicate RNA-Seq data. ***Proc Natl Acad Sci U S A***. 2014 Dec 23;111(51):E5593-601. doi: 10.1073/pnas.1419161111. Epub 2014 Dec 5. PMID: 25480548; PMCID: PMC4280593. ***These authors contributed equally**
42. Guo R, Zheng L, **Park JW**, Lv R, Chen H, Jiao F, Xu W, Mu S, Wen H, Qiu J, Wang Z, Yang P, Wu F, Hui J, Fu X, Shi X, Shi YG, Xing Y, Lan F, Shi Y. BS69/ZMYND11 reads and connects histone H3.3 lysine 36 trimethylation-decorated chromatin to regulated pre-mRNA processing. ***Mol Cell***. 2014 Oct 23;56(2):298-310. doi: 10.1016/j.molcel.2014.08.022. Epub 2014 Sep 25. PMID: 25263594; PMCID: PMC4363072.
43. Tokheim C, **Park JW**, Xing Y. PrimerSeq: Design and visualization of RT-PCR primers for alternative splicing using RNA-seq data. ***Genomics Proteomics Bioinformatics***. 2014 Apr;12(2):105-9. doi: 10.1016/j.gpb.2014.04.001. Epub 2014 Apr 18. PMID: 24747190; PMCID: PMC4411361.
44. **Park JW**, Tokheim C, Shen S, Xing Y. Identifying differential alternative splicing events from RNA sequencing data using RNASeq-MATS. ***Methods Mol Biol***. 2013;1038:171-9. doi: 10.1007/978-1-62703-514-9_10. PMID: 23872975.
45. Zhao K, Lu ZX, **Park JW**, Zhou Q, Xing Y. GLiMMPS: robust statistical model for regulatory variation of alternative splicing using RNA-seq data. ***Genome Biol***. 2013 Jul 22;14(7):R74. doi: 10.1186/gb-2013-14-7-r74. PMID: 23876401; PMCID: PMC4054007.
46. Dittmar KA*, Jiang P*, **Park JW***, Amirikian K, Wan J, Shen S, Xing Y, Carstens RP. Genome-wide determination of a broad ESRP-regulated posttranscriptional network by high-throughput sequencing. ***Mol Cell Biol***. 2012 Apr;32(8):1468-82. doi: 10.1128/MCB.06536-11. Epub 2012 Feb 21. PMID: 22354987; PMCID: PMC3318588. ***These authors contributed equally**
47. Shen S, **Park JW**, Huang J, Dittmar KA, Lu ZX, Zhou Q, Carstens RP, Xing Y. MATS: a Bayesian framework for flexible detection of differential alternative splicing from RNA-Seq data. ***Nucleic Acids Res***. 2012 Apr;40(8):e61. doi: 10.1093/nar/gkr1291. Epub 2012 Jan 20. PMID: 22266656; PMCID: PMC3333886.
48. Budd AF, Adrain TS, **Park JW**, Klaus JS, Johnson KG, "The Neogene Marine Biota of Tropical America ('NMITA') Database: Integrating Data from the Dominican Republic Project". ***Evolutionary Stasis and***

<u>Changes in the Dominican Republic Neogene</u>, 2008 Ch.13, pp 301-310 Springer Science + Business Media B.V.

INVITED TALKS

1. **Park JW,** "Big Data and Systems Biology Approaches to Explore RNA Regulatory Networks in Cancer Genomics", Baylor University, Waco, TX, USA, March 2019
2. **Park JW,** "Big Data and Systems Biology Approaches to Explore RNA Regulatory Networks in Cancer Genomics", Gettysburg College, Gettysburg, PA, USA, November 2018
3. **Park JW,** "Effects of RNA-binding Proteins on Alternative Splicing", KBRIN Bioinformatics Retreat, Harrodsburg, KY, USA, August 2017
4. **Park JW,** "Alternative splicing and circular RNAs", UT-KBRIN Bioinformatics Summit, Burns, TN, USA, April 2017
5. **Park JW,** "Big Data and Systems Biology approaches to Explore RNA Regulatory Networks in Cancer Genomics", Department of Physics, Western Kentucky University, Bowling Green, KY, USA, April 2017
6. **Park JW,** "High-throughput Sequencing and Systems Biology approaches to Cancer Genomics", Department of Biology, Western Kentucky University, Bowling Green, KY, USA, May 2016
7. **Park JW,** "Circular RNA and its biogenesis", UT-KBRIN Bioinformatics Summit, Lake Barkley State Resort Park, Cadiz, KY, USA, April 2016
8. **Park JW,** "High-throughput Sequencing and Systems Biology approaches to explore RNA Regulatory Networks in Cancer Genomics", James Graham Brown Cancer Center, University of Louisville, Louisville, KY, USA, March 2016
9. **Park JW,** "Big Data and Bioinformatics approaches to Cancer Genomics", Department of Basic Sciences, Mississippi State University, Mississippi State, MS, USA, March 2016
10. **Park JW,** "Bioinformatics Approaches to Explore RNA Regulatory Networks", Department of Computer Science, University of Kentucky, Lexington, KY, USA, February 2016
11. **Park JW,** "Big Data and Systems Biology Approaches to Explore Transcriptome and RNA Regulatory Networks", Systems Biology & Omics Integration, University of Kentucky, Lexington, KY, USA, September 2015
12. **Park JW,** "Identifying Alternative Splicing Events from RNA-Seq Data", Department of Anatomy, Yonsei University, Seoul, Korea, July 2012
13. **Park JW**, "RNA-Seq and bioinformatics", Department of Anatomy, Yonsei University, Seoul, Korea, July 2010

CONFERENCE PROCEEDINGS

1. Lee S, Kim J, Kim B, Shin SY, **Park JW**, Hong J, "Adjusting inference time for power efficiency in neuromorphic architectures.", Proceedings of the 37th Annual ACM Symposium on Applied Computing (***SAC***), 1102-1108, Virtual Event, April 2022
2. Lee H, Kim Y, **Park JW**, Shin SY, Hong J, "An efficient deep learning platform for detecting objects.", Proceedings of the 34th Annual ACM Symposium on Applied Computing (***SAC***), 1353-1354, Limassol, Cyprus, April 2019
3. Shon M, Kim H, Park K, **Park JW**, Won K, Hong J, "A robust and secure backup system for protecting malware.", Proceedings of the 34th Annual ACM Symposium on Applied Computing (***SAC***), 2125-2131, Limassol, Cyprus, April 2019
4. Sayed M, Hwang JY, **Park JW**, "Sequence homology in circular RNA detection", *Proceedings of the 2018 Conference on Research in Adaptive and Convergent Systems (**RACS**)*, 195-198, Honolulu, HI, USA, October 2018

5. Baniata M, Heo M, Lee J, **Park JW**, Hong J, " Energy-efficient unequal chain length clustering for WSN.", Proceedings of the 33rd Annual ACM Symposium on Applied Computing (***SAC***), 2125-2131, Pau, France, April 2018
6. Chaabane M, Rouchka EC, **Park JW**, "Circular RNA Detection from High-throughput Sequencing". *Proceedings of the 2017 Conference on Research in Adaptive and Convergent Systems (**RACS**)*, Krakow, Poland, September 2017
7. Jung S, Chang D, **Park JW**, "Parallel Document Inversion using GPU". *Proceedings of the 2016 Conference on Research in Adaptive and Convergent Systems (**RACS**)*, Odense, Denmark, October 2016
8. **Park JW**, Chariker J, Xing Y, "Strand specific RNA-seq data for higher specificity". *Proceedings of the 2015 Conference on Research in Adaptive and Convergent Systems (**RACS**)*, Prague, Czech Republic, October 2015
9. **Park JW**, Cremer J, Segre A, Logue M, Vieland V, "Visual Exploration of Genetic Likelihood Space". *In the Proceedings of ACM Symposium on Applied Computing (**SAC**)*, Dijon, France, April 2006
10. **Park JW**, Logue M, Ni J, Cremer J, Segre A, Vieland V, "Scientific Visualization of Multidimensional Data: Genetic likelihood Visualization". *In the Proceedings of High Performance Computing and Applications (**HPCA**) – **Current Trends in High Performance Computing and Its Applications,*** Springer-Verlag ISBN 3-540-25785-3 (2005)
11. Kwon M, Hong J, **Park JW**, Cho Y, "InCore: Accounting and Charging Heterogeneous Unix Systems". *In the Proceedings of the 17th International Conference on Computers and Their Applications (**ISCA**)*, March 2002
12. Hong J, Kim S, **Park JW**, Park T, Yeom HY, Cho Y, "An Effective Checkpoint Scheme Based on Memory Profile and Time Series Analysis". *In the Proceedings of the 16th International Conference on Computers and Their Applications (**ISCA**)*, Seattle, WA, March 2001

OTHER PRESENTATIONS (EXTENDED ABSTRACT/WORKSHOP/SYMPOSIUM)

1. Chaabane M, Williams R, Stephens A, Rouchka EC, **Park JW**, "Circular RNA Detection from High-throughput Sequencing", International Society for Computational Biology (**ISMB**), Chicago, IL, July 2018
2. Sayed M, Hwang J, Cardoso A, Al-Eryani L, States JC, **Park JW**, " RBP Motif Enrichment Analysis of Alternative Splicing Events in Arsenic-induced Skin Cancer", International Society for Computational Biology (**ISMB**), Chicago, IL, July 2018
3. Chaabane M, Rouchka EC, **Park JW**, "Circular RNA Detection from High-throughput Sequencing", Southeast Regional IDeA Conference, Morgantown, WV, October 2017
4. Lee J, **Park JW**, Park N, Park JY, Seo KS, "Transcriptome analysis of functional CD4+CD25+ regulatory T cells and CD8+CD25+ suppressive T cells induced by superantigens", 6th Biennial National IDeA Symposium of Biomedical Research Excellence (**NISBRE**), Washington, DC, June 2016
5. **Park JW**, "Transcriptome-wide Landscape of Pre-mRNA Alternative Splicing Associated with Metastatic Colonization", 5th Annual Southern California Systems Biology Conference (**SCSB**), Irvine, CA, January 2015
6. **Park JW**, "RNA-Seq detection of differential alternative splicing", Department of Internal Medicine Research Day, Iowa City, IA, February 2011
7. Wan J, **Park JW**, "Transcriptome-wide identification of alternative polyadenylation events regulated by epithelial splicing factor Esrp1", Annual Genetics Retreat, Iowa City, IA, October 2010

8. Logue M, **Park JW**, Cremer J, Segre A, Vieland V, "Exploiting Genetic Model Information to Identify Homogeneous Pedigrees". *The American Society of Human Genetics 56th Annual Meeting* (***ASHG***), October 2006
9. Logue M, **Park JW**, Ni J, Cremer J, Segre A, Knosp B, Beck S, Vieland V, "Interactive Visualization Tools for Genetic Data". *The American Society of Human Genetics 54th Annual Meeting* (***ASHG***), 2004

TEACHING EXPERIENCE

Instructor: Department of Computer Science and Engineering, University of Louisville, KY Spring 2016 – current
Courses: Object Oriented Programming Design with Java, Capstone Design, Independent Study, Current Topics in Bioinformatics

Guest Instructor: Department of Biomedical Engineering, University of Iowa, IA Fall 2011, Fall 2012
Course: Bioinformatics Techniques

- Taught 1-month module to introduce the various computational techniques in bioinformatics field and programming skills to senior undergraduate students from biology, engineering, and molecular biology background

Teaching Assistant: Department of Computer Science, University of Iowa, IA 08/1997 – 06/1999
Courses: Introduction to Programming, Programming with Java II

SERVICE & PROFESSIONAL ACTIVITIES

1. **School/Community/Outreach**
    a. Undergraduate Student Advising
        i. Sydney Paulus, Undergraduate research assistant, Department of Neuroscience, University of Louisville, Project: detection of translated circular RNAs, 2022-2023
        ii. Austin Stephens, Undergraduate research assistant, Department of Computer Engineering and Computer Science, University of Louisville, Project: circular RNA classification, 2017-2018
        iii. Robert Max Williams, Undergraduate research assistant, Department of Computer Engineering and Computer Science, University of Louisville, Project: circular RNA detection, 2017-2018
        iv. Kelly Morris, Undergraduate research assistant, Department of Computer Engineering and Computer Science, University of Louisville, Project: differentially expressed genes, Spring 2019
        v. John Kinney, Undergraduate research assistant, Department of Computer Engineering and Computer Science, University of Louisville, Project: differentially expressed genes, Spring 2019
    b. Executive Committee
        i. Member, Ph.D. Program in Interdisciplinary Studies: Specialization in Bioinformatics, Spring 2018 – current
        ii. Chair, Ph.D. Program in Interdisciplinary Studies: Specialization in Bioinformatics, Fall 2018 – current

2. **Department**
    a. PhD Fellowship Committee (2017 - 2019)
    b. Faculty Search Committee (2019-2023)

3. **Professional**
    a. Grant Proposal Reviewer
        i. Breast Cancer Now, UK, 2018, 2019, 2020
        ii. The National Caner Institute, France, 2022
    b. Selected Journal Refereeing
        i. Guest Editor; IEEE Transactions on Industrial Informatics (TII), 2019
        ii. Guest Editor; Frontiers in Genetics, 2020
        iii. Guest Editor; Frontiers in Cell and Developmental Biology, 2020
        iv. Reviewer; PLOS Computational Biology, 2017
        v. Reviewer; Scientific Report, 2017, 2018, 2024
        vi. Reviewer; BMC Plant Biology, 2018
        vii. Reviewer; The FEBS Journal, 2018
        viii. Reviewer; BMC Genomics, 2018, 2019
        ix. Reviewer; BMC Bioinformatics, 2019
        x. Reviewer; Bioinformatics, 2019
        xi. Reviewer; IEEE Access, 2019
        xii. Reviewer; Frontiers in Genetics, 2020
        xiii. Reviewer; BMC Plant Biology, 2020
        xiv. Reviewer; BMC Bioinformatics, 2020
        xv. Reviewer; Microorganisms, 2020
        xvi. Reviewer; Bioinformatics, 2021,2023
        xvii. Reviewer; Mobile Information Systems, 2022
        xviii. Reviewer; BMC Genome Biology, 2023
        xix. Reviewer; Nature Chemical Biology, 2023
        xx. Reviewer; International Journal Of Biological Macromolecules, 2024
        xxi. Reviewer; Scientific Reports, 2024
    c. Conference Organizing Committee
        i. Program Co-Chair; ACM/SIGAPP Symposium on Applied Computing (SAC), 2022, 2023, 2024, 2025
        ii. Steering Committee; ACM International Conference on Research in Adaptive and Convergent Systems (RACS), 2023, 2024
        iii. Program Co-Chair; ACM International Conference on Research in Adaptive and Convergent Systems (RACS), 2018, 2019, 2020
        iv. Publicity Co-Chair; ACM SIGAPP Symposium On Applied Computing (SAC), 2020
        v. Poster Co-Chair; ACM SIGAPP Symposium On Applied Computing (SAC), 2021

4. **Resources (data, publications, and developed software are available online):**
    a. Bioinformatics Lab (http://bioinformatics.louisville.edu/lab/index.php)

MENTORING

1. Sungbo Jung, Ph.D. student, Department of Computer Science and Engineering, University of Louisville, Project: RNA-binding protein motif enrichment analysis, 2016-2024
2. Tae Lim Kook, Ph.D. student, Interdisciplinary Studies: Specialization in Bioinformatics, University of Louisville, Project: Machine learning approach for analysis of alternative splicing in transcriptome, 2020-2023
3. Mohammed Sayed, Ph.D. student, Department of Computer Engineering and Computer Science, University of Louisville, Project: Analysis of alternative splicing and its regulation, 2015-2021
4. Jae Yeon Hwang, Postdoc, Department of Computer Engineering and Computer Science, University of Louisville, Project: Translation of circular RNA, 2018-2023
5. Kalina Andreeva, Postdoc, Department of Anatomical Sciences and Neurobiology, University of Louisville, Project: Circular RNAs in Gene Regulation, 2015-2022
6. Kelly Morris, Undergraduate research assistant, Department of Computer Engineering and Computer Science, University of Louisville, Project: differentially expressed genes, Spring 2019
7. John Kinney, Undergraduate research assistant, Department of Computer Engineering and Computer Science, University of Louisville, Project: differentially expressed genes, Spring 2019
8. Austin Stephens, Undergraduate research assistant, Department of Computer Engineering and Computer Science, University of Louisville, Project: circular RNA classification, 2017-2018
9. Robert Max Williams, Undergraduate research assistant, Department of Computer Engineering and Computer Science, University of Louisville, Project: circular RNA detection, 2017-2018
10. Aanchal Malhotra, Ph.D. student, Interdisciplinary Studies: Specialization in Bioinformatics, University of Louisville, Project: Analysis of alternative splicing in transcriptome, 2016-2019
11. Mohammed Chaabane, M.S. student, Department of Computer Engineering and Computer Science, University of Louisville, Project: Enrichment analysis of RBP (RNA-binding protein) motifs, 2016-2018
12. Tahlia Hodes, Summer intern, Department of Computer Engineering and Computer Science, University of Louisville, Project: Combined p-value calculation for tissue specific circular RNA detection, 2016
13. Maha Soliman, Postdoc, KBRIN, University of Louisville, Project: Analysis of circular RNAs and their regulatory roles, 2015-2016
14. Shayna Stein, Undergrad student, Department of Mathematics of Computation, UCLA, Project: Effects of SNPs on alternative splicing and RNA-seq alignment, 2013-2015
15. Zijun Zhang, Ph.D. student, Department of Bioinformatics, UCLA, Project: Genome-wide motif prediction map for known splicing factors, 2014
16. Kevin Le, Undergrad student, Department of Microbiology, Immunology, & Molecular Genetics, UCLA, Project: Understanding and processing RNA sequencing, 2014

THESIS COMMITTEE

1. Uddalok Jana, Ph.D., Interdisciplinary Studies: Specialization in Bioinformatics, University of Louisville, 2024-current
2. Roxanne Hayes, Ph.D., Biology, University of Louisville, 2024-current
3. Swati Saha, Ph.D., Interdisciplinary Studies: Specialization in Bioinformatics, University of Louisville, 2023-current
4. Aryan Neupane, Ph.D., Interdisciplinary Studies: Specialization in Bioinformatics, University of Louisville, 2020-2023
5. Tae Lim Kook, Ph.D., Interdisciplinary Studies: Specialization in Bioinformatics, University of Louisville, 2020-2023

6. Asma Baccouche, Ph.D., Computer Science and Engineering, University of Louisville, 2020-present
7. Babak Joze Abbaschian, Ph.D., Computer Science and Engineering, University of Louisville, 2019-present
8. Fadoua Khmaissia, Ph.D., Computer Science and Engineering, University of Louisville, 2019-present
9. Mahdi Moalla, Ph.D., Computer Science and Engineering, University of Louisville, 2019-present
10. Ahmed Sleman, Ph.D., Computer Science and Engineering, University of Louisville, 2019-2023
11. Mohsen Asghari, Ph.D., Computer Science and Engineering, University of Louisville, 2018-2022
12. Kalpani de Silva, Ph.D., Interdisciplinary Studies: Specialization in Bioinformatics, University of Louisville, 2018-2022
13. Mohammed Sayed, Ph.D., Computer Science and Engineering, University of Louisville, 2015-2021
14. Ali Shahrjoo, Ph.D., Computer Science and Engineering, University of Louisville, 2017-2021
15. Mohamed Shehata, Ph.D., Computer Science and Engineering, University of Louisville, 2017-2022
16. Mehdi Farhangi, Ph.D., Computer Science and Engineering, University of Louisville, 2018-2019
17. Anju Panicker, Ph.D., Computer Engineering and Computer Science, University of Louisville, 2017-2018
18. Patrick Trainor, Ph.D., Interdisciplinary Studies: Specialization in Bioinformatics, University of Louisville, 2017-2018
19. Shade Elhadik, Ph.D., Computer Engineering and Computer Science, University of Louisville, 2016-2017
20. Faezeh Tafazzoli, Ph.D., Computer Engineering and Computer Science, University of Louisville, 2016-2017
21. Ernur Saka, Ph.D., Computer Engineering and Computer Science, University of Louisville, 2016-2018
22. Andrey Smelter, Ph.D., Interdisciplinary Studies: Specialization in Bioinformatics, University of Louisville, 2016-2017
23. Ameni Trabelsi, M.S., Computer Engineering and Computer Science, University of Louisville, 2016-2018
24. Mohamed Chaabane, M.S., Computer Engineering and Computer Science, University of Louisville, 2016-2018