Stanford

Wing Hung Wong

Stephen R. Pierce Family Goldman Sachs Professor of Science and Human Health and Professor of Biomedical Data Science

Statistics

Curriculum Vitae available Online

Bio

BIO

I am a professor at Stanford University with joint appointments in the Department of Statistics and the Department of Biomedical Data Science. My current research interests are Bayesian Statistics, Computational Biology, Precision Medicine and Semiconductor-based automation of biological experiments.

ACADEMIC APPOINTMENTS

- Professor, Statistics
- Professor, Department of Biomedical Data Science
- Member, Bio-X
- Member, Cardiovascular Institute
- Member, Maternal & Child Health Research Institute (MCHRI)
- Member, Institute for Computational and Mathematical Engineering (ICME)
- Member, Stanford Cancer Institute
- Member, Wu Tsai Neurosciences Institute

HONORS AND AWARDS

- Grace Wahba Award and Lecture, Institute of Mathematic Statistics (2023)
- COPSS Distinguished Achievement Award and Lectureship, Committee of Presidents of Statistical Societies (2021)
- Founding Member, The Academy of Sciences of Hong Kong (2015)
- Academician, Academia Sinica (2010)
- Member, National Academy of Sciences (2009)
- Bahadur Lecturer, The University of Chicago (2006)
- Fellow, American Association for the Advancement of Science (2002)
- Neyman Lecturer, Institute of Mathematical Statistics (2002)
- Fellow, American Statistical Association (1998)
- COPSS Award, Committee of Presidents of Statistical Societies (1993)
- Fellow, Institute of Mathematical Statistics (1991)
- Fellow, Guggenheim Foundation (1986)

LINKS

- My lab site: https://web.stanford.edu/group/wonglab/
- faculty page: https://statistics.stanford.edu/people/wing-hung-wong

Research & Scholarship

CURRENT RESEARCH AND SCHOLARLY INTERESTS

My lab is interested in statistics and genomics. Past contributions include the use of Monte Carlo algorithms in Bayesian computation, asymptotic inference in high or infinite dimensional problems, and bioinformatics tools for the analysis microarray data and sequencing data. Current interests include i) gene regulatory analysis based on integrative modeling of data from diverse cell types and from single cells, and ii) use of semiconductor technology to enable novel biological experiments.

Teaching

COURSES

2025-26

- Bayesian Statistics: STATS 270, STATS 370 (Spr)
- Biomedical Data Science Student Seminar: BMDS 201A, BMDS 201B, BMDS 201C (Win)
- Consulting Workshop: STATS 390 (Win)
- Workshop in Biomedical Data Science: BMDS 280B, STATS 260B (Win)

2024-25

- Applied Bayesian Statistics: STATS 271, STATS 371 (Spr)
- Biomedical Data Science Student Seminar: BIOMEDIN 201 (Win)
- Consulting Workshop: STATS 390 (Win)
- Workshop in Biostatistics: BIODS 260B, STATS 260B (Win)

2023-24

- Bayesian Statistics: STATS 270, STATS 370 (Spr)
- Biomedical Data Science Student Seminar: BIODS 201, BIOMEDIN 201 (Win)
- Literature of Statistics: STATS 319 (Spr)
- Workshop in Biostatistics: BIODS 260B, STATS 260B (Win)

2022-23

- Bayesian Statistics: STATS 270, STATS 370 (Aut)
- Biomedical Informatics Student Seminar: BIODS 201, BIOMEDIN 201 (Win)

STANFORD ADVISEES

Doctoral Dissertation Reader (AC)

Ian Christopher Tanoh

Postdoctoral Faculty Sponsor

Zhanying Feng

Doctoral Dissertation Advisor (AC)

Sophia Lu

Master's Program Advisor

Ayeeshi Poosarla, Minh Truong

Doctoral (Program)

Wei Deng

Postdoctoral Research Mentor

Hanmin Guo

GRADUATE AND FELLOWSHIP PROGRAM AFFILIATIONS

- Biomedical Data Science (Phd Program)
- Biomedical Data Science (Masters Program)

Publications

PUBLICATIONS

- **EpiGePT: a pretrained transformer-based language model for context-specific human epigenomics.** *Genome biology*
  Gao, Z., Liu, Q., Zeng, W., Jiang, R., Wong, W. H.
  2024; 25 (1): 310
- **IMPLICATION OF COMPLEX STRUCTURAL GENOME VARIATION IN THE GENETIC ARCHITECTURE OF NEUROPSYCHIATRIC DISORDERS: INSIGHTS FROM HUMAN POPULATION ANALYSIS AND FROM POSTMORTEM BRAINS OF INDIVIDUALS WITH PSYCHIATRIC DISORDERS**
  Zhou, B., Arthur, J., Guo, H., Kim, T., Huang, Y., Pattni, R., Song, G., Palejev, D., Dohna, H., Roussos, P., Kundaje, A., Hallmayer, J., Snyder, et al
  ELSEVIER.2024: 93
- **Prioritizing disease-related rare variants by integrating gene expression data.** *PLoS genetics*
  Guo, H., Urban, A. E., Wong, W. H.
  2024; 20 (9): e1011412
- **Resolving the 22q11.2 deletion using CTLR-Seq reveals chromosomal rearrangement mechanisms and individual variance in breakpoints.** *Proceedings of the National Academy of Sciences of the United States of America*
  Zhou, B., Purmann, C., Guo, H., Shin, G., Huang, Y., Pattni, R., Meng, Q., Greer, S. U., Roychowdhury, T., Wood, R. N., Ho, M., Dohna, H. Z., Abyzov, et al
  2024; 121 (31): e2322834121
- **An encoding generative modeling approach to dimension reduction and covariate adjustment in causal inference with observational studies.** *Proceedings of the National Academy of Sciences of the United States of America*
  Liu, Q., Chen, Z., Wong, W. H.
  2024; 121 (23): e2322376121
- **Prioritizing disease-related rare variants by integrating gene expression data.** *Research square*
  Guo, H., Urban, A. E., Wong, W. H.
  2024
- **Author Correction: Cost-effective methylome sequencing of cell-free DNA for accurately detecting and locating cancer.** *Nature communications*
  Stackpole, M. L., Zeng, W., Li, S., Liu, C. C., Zhou, Y., He, S., Yeh, A., Wang, Z., Sun, F., Li, Q., Yuan, Z., Yildirim, A., Chen, et al
  2024; 15 (1): 3693
- **Prioritizing disease-related rare variants by integrating gene expression data.** *bioRxiv : the preprint server for biology*
  Guo, H., Urban, A. E., Wong, W. H.
  2024
- **Genetic effects of sequence-conserved enhancer-like elements on human complex traits.** *Genome biology*
  Zhu, X., Ma, S., Wong, W. H.

2024; 25 (1): 1

- **Detection and analysis of complex structural variation in human genomes across populations and in brains of donors with psychiatric disorders** *Cell*
  Zhou, B., Arthur, J. G., Guo, H., et al
  2024; Published online September 30, 2024

- **Data integration and inference of gene regulation using single-cell temporal multimodal data with scTIE.** *Genome research*
  Lin, Y., Wu, T. Y., Chen, X., Wan, S., Chao, B., Xin, J., Yang, J., Wong, W. H., Wang, Y. X.
  2023

- **Mutations in human DNA methyltransferase DNMT1 induce specific genome-wide epigenomic and transcriptomic changes in neurodevelopment.** *Human molecular genetics*
  Davis, K. N., Qu, P. P., Ma, S., Lin, L., Plastini, M., Dahl, N., Plazzi, G., Pizza, F., O'Hara, R., Wong, W. H., Hallmayer, J., Mignot, E., Zhang, et al
  2023

- **EpiGePT: a Pretrained Transformer model for epigenomics.** *bioRxiv : the preprint server for biology*
  Gao, Z., Liu, Q., Zeng, W., Wong, W. H., Jiang, R.
  2023

- **Comprehensive tissue deconvolution of cell-free DNA by deep learning for disease diagnosis and monitoring.** *Proceedings of the National Academy of Sciences of the United States of America*
  Li, S., Zeng, W., Ni, X., Liu, Q., Li, W., Stackpole, M. L., Zhou, Y., Gower, A., Krysan, K., Ahuja, P., Lu, D. S., Raman, S. S., Hsu, et al
  2023; 120 (28): e2305236120

- **scTIE: data integration and inference of gene regulation using single-cell temporal multimodal data.** *bioRxiv : the preprint server for biology*
  Lin, Y., Wu, T. Y., Chen, X., Wan, S., Chao, B., Xin, J., Yang, J. Y., Wong, W. H., Wang, Y. X.
  2023

- **NeuronMotif: Deciphering cis-regulatory codes by layer-wise demixing of deep neural networks.** *Proceedings of the National Academy of Sciences of the United States of America*
  Wei, Z., Hua, K., Wei, L., Ma, S., Jiang, R., Zhang, X., Li, Y., Wong, W. H., Wang, X.
  2023; 120 (15): e2216698120

- **Revealing Free Energy Landscape From MD Data via Conditional Angle Partition Tree.** *IEEE/ACM transactions on computational biology and bioinformatics*
  Jiang, H., Li, H., Wong, W. H., Fan, X.
  2023; 20 (2): 1384-1394

- **Statins improve endothelial function via suppression of epigenetic-driven EndMT** *Nature Cardiovascular Research*
  Liu, C., Shen, M., Tan, W. L., Chen, I. Y., Liu, Y., Yu, X., Zhang, A., Liu, Y., Zhao, M., Ameen, M., Zhang, M., Gross, E. R., Lei, et al
  2023

- **Current and future perspectives of single-cell multi-omics technologies in cardiovascular research.** *Nature cardiovascular research*
  Tan, W. L., Seow, W. Q., Zhang, A., Rhee, S., Wong, W. H., Greenleaf, W. J., Wu, J. C.
  2023; 2 (1): 20-34

- **Convergence Rates of a Class of Multivariate Density Estimation Methods Based on Adaptive Partitioning** *JOURNAL OF MACHINE LEARNING RESEARCH*
  Liu, L., Li, D., Wong, W.
  2023; 24

- **Heritability enrichment in context-specific regulatory networks improves phenotype-relevant tissue identification.** *eLife*
  Feng, Z., Duren, Z., Xin, J., Yuan, Q., He, Y., Su, B., Wong, W. H., Wang, Y.
  2022; 11

- **Author Correction: Regulatory analysis of single cell multiome gene expression and chromatin accessibility data with scREG.** *Genome biology*
  Duren, Z., Chang, F., Naqing, F., Xin, J., Liu, Q., Wong, W. H.
  2022; 23 (1): 213

- **HiChIPdb: a comprehensive database of HiChIP regulatory interactions.** *Nucleic acids research*
  Zeng, W., Liu, Q., Yin, Q., Jiang, R., Wong, W. H.
  2022
- **DETECTION OF COMPLEX STRUCTURAL GENOME VARIANTS USING ARC-SV AND THEIR ENRICHMENT INSIDE GENES OF NEURODEVELOPMENTAL PATHWAYS**
  Hughes, C., Zhou, B., Arthur, J. G., Kim, T., Song, G., Palejev, D., Wong, W. H., Urban, A. E.
  ELSEVIER.2022: E177-E178
- **Cost-effective methylome sequencing of cell-free DNA for accurately detecting and locating cancer.** *Nature communications*
  Stackpole, M. L., Zeng, W., Li, S., Liu, C. C., Zhou, Y., He, S., Yeh, A., Wang, Z., Sun, F., Li, Q., Yuan, Z., Yildirim, A., Chen, et al
  2022; 13 (1): 5566
- **Unfolding the genotype-to-phenotype black box of cardiovascular diseases through cross-scale modeling.** *iScience*
  Xi, X., Li, H., Chen, S., Lv, T., Ma, T., Jiang, R., Zhang, P., Wong, W. H., Zhang, X.
  2022; 25 (8): 104790
- **Nested epistasis enhancer networks for robust genome regulation.** *Science (New York, N.Y.)*
  Lin, X., Liu, Y., Liu, S., Zhu, X., Wu, L., Zhu, Y., Zhao, D., Xu, X., Chemparathy, A., Wang, H., Cao, Y., Nakamura, M., Noordermeer, et al
  2022: eabk3512
- **Regulatory analysis of single cell multiome gene expression and chromatin accessibility data with scREG.** *Genome biology*
  Duren, Z., Chang, F., Naqing, F., Xin, J., Liu, Q., Wong, W. H.
  2022; 23 (1): 114
- **scJoint integrates atlas-scale single-cell RNA-seq and ATAC-seq data with transfer learning.** *Nature biotechnology*
  Lin, Y., Wu, T., Wan, S., Yang, J. Y., Wong, W. H., Wang, Y. X.
  1800
- **Coupled generation.** *Journal of the American Statistical Association*
  Dai, B., Shen, X., Wong, W.
  2022; 117 (539): 1243-1253
- **Leveraging cell-type-specific regulatory networks to interpret genetic variants in abdominal aortic aneurysm.** *Proceedings of the National Academy of Sciences of the United States of America*
  Ma, S., Chen, X., Zhu, X., Tsao, P. S., Wong, W. H.
  1800; 119 (1)
- **On the identifiability of the isoform deconvolution problem: application to select the proper fragment length in an RNAseq library.** *Bioinformatics (Oxford, England)*
  Ferrer-Bonsoms, J. A., Morales, X., Afshar, P. T., Wong, W. H., Rubio, A.
  1800
- **AN EQUATION FOR THE IDENTIFICATION OF AVERAGE CAUSAL EFFECT IN NONLINEAR MODELS** *STATISTICA SINICA*
  Wong, W.
  2022; 32: 539-545
- **DeepCAGE: Incorporating transcription factors in genome-wide prediction of chromatin accessibility.** *Genomics, proteomics & bioinformatics*
  Liu, Q., Hua, K., Zhang, X., Wong, W. H., Jiang, R.
  2022
- **Collaborative Multilabel Classification** *JOURNAL OF THE AMERICAN STATISTICAL ASSOCIATION*
  Zhu, Y., Shen, X., Jiang, H., Wong, W.
  2021
- **Sc-compReg enables the comparison of gene regulatory networks between conditions using single-cell data.** *Nature communications*
  Duren, Z., Lu, W. S., Arthur, J. G., Shah, P., Xin, J., Meschi, F., Li, M. L., Nemec, C. M., Yin, Y., Wong, W. H.
  2021; 12 (1): 4763
- **Dynamic chromatin regulatory landscape of human CAR T cell exhaustion.** *Proceedings of the National Academy of Sciences of the United States of America*

Gennert, D. G., Lynn, R. C., Granja, J. M., Weber, E. W., Mumbach, M. R., Zhao, Y., Duren, Z., Sotillo, E., Greenleaf, W. J., Wong, W. H., Satpathy, A. T., Mackall, C. L., Chang, et al
2021; 118 (30)

- **Sensitive detection of tumor mutations from blood and its application to immunotherapy prognosis.** *Nature communications*
  Li, S., Noor, Z. S., Zeng, W., Stackpole, M. L., Ni, X., Zhou, Y., Yuan, Z., Wong, W. H., Agopian, V. G., Dubinett, S. M., Alber, F., Li, W., Garon, et al
  2021; 12 (1): 4172

- **MIMIC: an optimization method to identify cell type-specific marker panel for cell sorting.** *Briefings in bioinformatics*
  Zou, M., Duren, Z., Yuan, Q., Li, H., Hutchins, A. P., Wong, W. H., Wang, Y.
  2021

- **Simultaneous deep generative modeling and clustering of single cell genomic data.** *Nature machine intelligence*
  Liu, Q., Chen, S., Jiang, R., Wong, W. H.
  2021; 3 (6): 536-544

- **Modeling regulatory network topology improves genome-wide analyses of complex human traits.** *Nature communications*
  Zhu, X., Duren, Z., Wong, W. H.
  2021; 12 (1): 2851

- **Simultaneous deep generative modelling and clustering of single-cell genomic data** *NATURE MACHINE INTELLIGENCE*
  Liu, Q., Chen, S., Jiang, R., Wong, W.
  2021

- **Density estimation using deep generative neural networks.** *Proceedings of the National Academy of Sciences of the United States of America*
  Liu, Q., Xu, J., Jiang, R., Wong, W. H.
  2021; 118 (15)

- **hReg-CNCC reconstructs a regulatory network in human cranial neural crest cells and annotates variants in a developmental context.** *Communications biology*
  Feng, Z., Duren, Z., Xiong, Z., Wang, S., Liu, F., Wong, W. H., Wang, Y.
  2021; 4 (1): 442

- **Coupled Generation** *JOURNAL OF THE AMERICAN STATISTICAL ASSOCIATION*
  Dai, B., Shen, X., Wong, W.
  2020

- **Mini-Batch Metropolis-Hastings With Reversible SGLD Proposal** *JOURNAL OF THE AMERICAN STATISTICAL ASSOCIATION*
  Wu, T., Rachel Wang, Y. X., Wong, W. H.
  2020

- **Time course regulatory analysis based on paired expression and chromatin accessibility data.** *Genome research*
  Duren, Z., Chen, X., Xin, J., Wang, Y., Wong, W.
  2020

- **Integrated functional genomic analyses of Klinefelter and Turner syndromes reveal global network effects of altered X chromosome dosage.** *Proceedings of the National Academy of Sciences of the United States of America*
  Zhang, X., Hong, D., Ma, S., Ward, T., Ho, M., Pattni, R., Duren, Z., Stankov, A., Bade Shrestha, S., Hallmayer, J., Wong, W. H., Reiss, A. L., Urban, et al
  2020

- **Chromatin accessibility landscape and regulatory network of high-altitude hypoxia adaptation.** *Nature communications*
  Xin, J. n., Zhang, H. n., He, Y. n., Duren, Z. n., Bai, C. n., Chen, L. n., Luo, X. n., Yan, D. S., Zhang, C. n., Zhu, X. n., Yuan, Q. n., Feng, Z. n., Cui, et al
  2020; 11 (1): 4928

- **A method for scoring the cell type-specific impacts of noncoding variants in personal genomes.** *Proceedings of the National Academy of Sciences of the United States of America*
  Li, W. n., Duren, Z. n., Jiang, R. n., Wong, W. H.
  2020

- **Xrare: a machine learning method jointly modeling phenotypes and genetic evidence for rare disease diagnosis** *GENETICS IN MEDICINE*
  Li, Q., Zhao, K., Bustamante, C. D., Ma, X., Wong, W. H.
  2019; 21 (9): 2126–34

- **DeepTACT: predicting 3D chromatin contacts via bootstrapping deep learning.** *Nucleic acids research*
  Li, W., Wong, W. H., Jiang, R.
  2019

- **DC3 is a method for deconvolution and coupled clustering from bulk and single-cell genomics data.** *Nature communications*
  Zeng, W. n., Chen, X. n., Duren, Z. n., Wang, Y. n., Jiang, R. n., Wong, W. H.
  2019; 10 (1): 4613

- **Extensive and deep sequencing of the Venter/HuRef genome for developing and benchmarking genome analysis tools** *SCIENTIFIC DATA*
  Zhou, B., Arthur, J. G., Ho, S. S., Pattni, R., Huang, Y., Wong, W. H., Urban, A. E.
  2018; 5

- **Extensive and deep sequencing of the Venter/HuRef genome for developing and benchmarking genome analysis tools.** *Scientific data*
  Zhou, B., Arthur, J. G., Ho, S. S., Pattni, R., Huang, Y., Wong, W. H., Urban, A. E.
  2018; 5: 180261

- **Towards high performance data analytic on heterogeneous many-core systems: A study on Bayesian Sequential Partitioning** *JOURNAL OF PARALLEL AND DISTRIBUTED COMPUTING*
  Lai, B., Wu, T., Chiu, T., Li, K., Lee, C., Chien, W., Wong, W.
  2018; 122: 36–50

- **CRISPhieRmix: a hierarchical mixture model for CRISPR pooled screens.** *Genome biology*
  Daley, T. P., Lin, Z., Lin, X., Liu, Y., Wong, W. H., Qi, L. S.
  2018; 19 (1): 159

- **CRISPR Activation Screens Systematically Identify Factors that Drive Neuronal Fate and Reprogramming.** *Cell stem cell*
  Liu, Y., Yu, C., Daley, T. P., Wang, F., Cao, W. S., Bhate, S., Lin, X., Still, C. 2., Liu, H., Zhao, D., Wang, H., Xie, X. S., Ding, et al
  2018

- **Integrative analysis of single-cell genomics data by coupled nonnegative matrix factorizations.** *Proceedings of the National Academy of Sciences of the United States of America*
  Duren, Z., Chen, X., Zamanighomi, M., Zeng, W., Satpathy, A. T., Chang, H. Y., Wang, Y., Wong, W. H.
  2018

- **Unsupervised clustering and epigenetic classification of single cells** *NATURE COMMUNICATIONS*
  Zamanighomi, M., Lin, Z., Daley, T., Chen, X., Duren, Z., Schep, A., Greenleaf, W. J., Wong, W.
  2018; 9: 2410

- **A 1.86mJ/Gb/Query Bit-Plane Payload Machine Learning Processor in 90nm CMOS**
  Ku, F., Wu, T., Liao, Y., Chang, H., Wong, W., Lee, C., IEEE
  IEEE.2018

- **DIABETIC RETINOPATHY DETECTION BASED ON DEEP CONVOLUTIONAL NEURAL NETWORKS**
  Chen, Y., Wu, T., Wong, W., Lee, C., IEEE
  IEEE.2018: 1030–34

- **CORRELATION-BASED FACE DETECTION FOR RECOGNIZING FACES IN VIDEOS**
  Hsu, H., Wu, T., Wong, W., Lee, C., IEEE
  IEEE.2018: 3101–5

- **CONFNET: PREDICT WITH CONFIDENCE**
  Wan, S., Wu, T., Wong, W. H., Lee, C., IEEE
  IEEE.2018: 2921–25

- **Challenges and recommendations for epigenomics in precision health** *NATURE BIOTECHNOLOGY*

Carter, A. C., Chang, H. Y., Church, G., Dombkowski, A., Ecker, J. R., Gil, E., Giresi, P. G., Greely, H., Greenleaf, W. J., Hacohen, N., He, C., Hill, D., Ko, et al

2017; 35 (12): 1128–32

- **Simultaneous inference of phenotype-associated genes and relevant tissues from GWAS data via Bayesian integration of multiple tissue-specific gene networks** *JOURNAL OF MOLECULAR CELL BIOLOGY*

  Wu, M., Lin, Z., Ma, S., Chen, T., Jiang, R., Wong, W.

  2017; 9 (6): 436–52

- **Gaining comprehensive biological insight into the transcriptome by performing a broad-spectrum RNA-seq analysis** *NATURE COMMUNICATIONS*

  Sahraeian, S., Mohiyuddin, M., Sebra, R., Tilgner, H., Afshar, P. T., Au, K., Asadi, N., Gerstein, M. B., Wong, W., Snyder, M. P., Schadt, E., Lam, H. Y. K.

  2017; 8: 59

- **COSINE: non-seeding method for mapping long noisy sequences.** *Nucleic acids research*

  Afshar, P. T., Wong, W. H.

  2017

- **Predicting transcription factor binding motifs from DNA-binding domains, chromatin accessibility and gene expression data.** *Nucleic acids research*

  Zamanighomi, M., Lin, Z., Wang, Y., Jiang, R., Wong, W. H.

  2017; 45 (10): 5666-5677

- **Modeling gene regulation from paired expression and chromatin accessibility data.** *Proceedings of the National Academy of Sciences of the United States of America*

  Duren, Z., Chen, X., Jiang, R., Wang, Y., Wong, W. H.

  2017

- **Phased Genome Sequencing Through Chromosome Sorting.** *Methods in molecular biology (Clifton, N.J.)*

  Chen, X., Yang, H., Wong, W. H.

  2017; 1551: 171-188

- **Convergence rates of a partition based Bayesian multivariate density estimation method**

  Liu, L., Li, D., Wong, W.

  edited by Guyon, Luxburg, U. V., Bengio, S., Wallach, H., Fergus, R., Vishwanathan, S., Garnett, R.

  NEURAL INFORMATION PROCESSING SYSTEMS (NIPS).2017

- **Scalable multi-sample single-cell data analysis by Partition-Assisted Clustering and Multiple Alignments of Networks.** *PLoS computational biology*

  Li, Y. H., Li, D. n., Samusik, N. n., Wang, X. n., Guan, L. n., Nolan, G. P., Wong, W. H.

  2017; 13 (12): e1005875

- **Simultaneous dimension reduction and adjustment for confounding variation** *PROCEEDINGS OF THE NATIONAL ACADEMY OF SCIENCES OF THE UNITED STATES OF AMERICA*

  Lin, Z., Yang, C., Zhu, Y., Duchi, J., Fu, Y., Wang, Y., Jiang, B., Zamanighomi, M., Xu, X., Li, M., Sestan, N., Zhao, H., Wong, et al

  2016; 113 (51): 14662-14667

- **Modeling the causal regulatory network by integrating chromatin accessibility and transcriptome data** *NATIONAL SCIENCE REVIEW*

  Wang, Y., Jiang, R., Wong, W. H.

  2016; 3 (2): 240-251

- **Stable 5-Hydroxymethylcytosine (5hmC) Acquisition Marks Gene Activation During Chondrogenic Differentiation** *JOURNAL OF BONE AND MINERAL RESEARCH*

  Taylor, S. E., Li, Y. H., Smeriglio, P., Rath, M., Wong, W. H., Bhutani, N.

  2016; 31 (3): 524-534

- **Computational Aspects of Optional Polya Tree** *JOURNAL OF COMPUTATIONAL AND GRAPHICAL STATISTICS*

  Jiang, H., Mu, J. C., Yang, K., Du, C., Lu, L., Wong, W. H.

  2016; 25 (1): 301-320

- **The primate-specific noncoding RNA HPAT5 regulates pluripotency during human preimplantation development and nuclear reprogramming** *NATURE GENETICS*

  Durruthy-Durruthy, J., Sebastiano, V., Wossidlo, M., Cepeda, D., Cui, J., Grow, E. J., Davila, J., Mall, M., Wong, W. H., Wysocka, J., Au, K. F., Pera, R. A.

  2016; 48 (1): 44-?

- **A Hardware-Efficient Sigmoid Function With Adjustable Precision for a Neural Network System** *IEEE TRANSACTIONS ON CIRCUITS AND SYSTEMS II-EXPRESS BRIEFS*

  Tsai, C., Chih, Y., Wong, W. H., Lee, C.

  2015; 62 (11): 1073-1077

- **Characterization of fusion genes and the significantly expressed fusion isoforms in breast cancer by hybrid sequencing** *NUCLEIC ACIDS RESEARCH*

  Weirather, J. L., Afshar, P. T., Clark, T. A., Tseng, E., Powers, L. S., Underwood, J. G., Zabner, J., Korlach, J., Wong, W. H., Au, K. F.

  2015; 43 (18)

- **An ensemble approach to accurately detect somatic mutations using SomaticSeq** *GENOME BIOLOGY*

  Fang, L. T., Afshar, P. T., Chhibber, A., Mohiyuddin, M., Fan, Y., Mu, J. C., Gibeling, G., Barr, S., Asadi, N. B., Gerstein, M. B., Koboldt, D. C., Wang, W., Wong, et al

  2015; 16

- **MetaSV: an accurate and integrative structural-variant caller for next generation sequencing** *BIOINFORMATICS*

  Mohiyuddin, M., Mu, J. C., Li, J., Asadi, N. B., Gerstein, M. B., Abyzov, A., Wong, W. H., Lam, H. Y.

  2015; 31 (16): 2741-2744

- **Genome-Wide Mapping of DNA Hydroxymethylation in Osteoarthritic Chondrocytes** *ARTHRITIS & RHEUMATOLOGY*

  Taylor, S. E., Li, Y. H., Wong, W. H., Bhutani, N.

  2015; 67 (8): 2129-2140

- **VarSim: a high-fidelity simulation and validation framework for high-throughput genome sequencing with cancer applications** *BIOINFORMATICS*

  Mu, J. C., Mohiyuddin, M., Li, J., Asadi, N. B., Gerstein, M. B., Abyzov, A., Wong, W. H., Lam, H. Y.

  2015; 31 (9): 1469-1471

- **Leveraging long read sequencing from a single individual to provide a comprehensive resource for benchmarking variant calling methods.** *Scientific reports*

  Mu, J. C., Tootoonchi Afshar, P., Mohiyuddin, M., Chen, X., Li, J., Bani Asadi, N., Gerstein, M. B., Wong, W. H., Lam, H. Y.

  2015; 5: 14493-?

- **Learning regulatory programs by threshold SVD regression** *PROCEEDINGS OF THE NATIONAL ACADEMY OF SCIENCES OF THE UNITED STATES OF AMERICA*

  Ma, X., Xiao, L., Wong, W. H.

  2014; 111 (44): 15675-15680

- **Human tRNA synthetase catalytic nulls with diverse functions.** *Science*

  Lo, W., Gardiner, E., Xu, Z., Lau, C., Wang, F., Zhou, J. J., Mendlein, J. D., Nangle, L. A., Chiang, K. P., Yang, X., Au, K., Wong, W. H., Guo, et al

  2014; 345 (6194): 328-332

- **Modeling stochastic noise in gene regulatory systems.** *Quantitative biology (Beijing, China)*

  Meister, A., Du, C., Li, Y. H., Wong, W. H.

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