Stanford

Wing Hung Wong

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

Statistics

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 and Precision Medicine.

ACADEMIC APPOINTMENTS

- Professor, Statistics
- Professor, 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

- 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

The current emphasis of my lab includes gene regulatory analysis and analysis of high throughput genomics data. These areas require new methods in statistical analysis, mathematical modeling and computation. Past contributions to mainstream statistics and bioinformatics 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. Recently we have made a major effort to analyze gene regulatory networks based on integrative modeling of multiple types of genomics data from diverse cell types and from single cells.We have also interested in the analysis of electronic medical records.

Teaching

COURSES

2021-22

- A Course in Bayesian Statistics: STATS 270, STATS 370 (Spr)

2020-21

- A Course in Bayesian Statistics: STATS 270, STATS 370 (Win)

2019-20

- A Course in Bayesian Statistics: STATS 270, STATS 370 (Win)
- Theory of Probability: STATS 116 (Aut)

2018-19

- A Course in Bayesian Statistics: STATS 270, STATS 370 (Win)

STANFORD ADVISEES

Doctoral Dissertation Reader (AC)

Fang Cai, Jessica Hwang

Postdoctoral Faculty Sponsor

Qiao Liu, Tung-yu Wu, Jingxue Xin, Wanwen Zeng

GRADUATE AND FELLOWSHIP PROGRAM AFFILIATIONS

- Biology (School of Humanities and Sciences) (Phd Program)

Publications

PUBLICATIONS

- **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. 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., 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.
  2014; 2 (1): 1-29

- **Density estimation on multivariate censored data with optional Polya tree** *BIOSTATISTICS*
  Seok, J., Tian, L., Wong, W. H.
  2014; 15 (1): 182-195

- **Characterization of the human ESC transcriptome by hybrid sequencing** *PROCEEDINGS OF THE NATIONAL ACADEMY OF SCIENCES OF THE UNITED STATES OF AMERICA*
  Au, K. F., Sebastiano, V., Afshar, P. T., Durruthy, J. D., Lee, L., Williams, B. A., van Bakel, H., Schadt, E. E., Reijo-Pera, R. A., Underwood, J. G., Wong, W. H.
  2013; 110 (50): E4821-E4830

- **Multivariate Density Estimation by Bayesian Sequential Partitioning** *JOURNAL OF THE AMERICAN STATISTICAL ASSOCIATION*

Lu, L., Jiang, H., Wong, W. H.
2013; 108 (504): 1402-1410

- **Early role for IL-6 signalling during generation of induced pluripotent stem cells revealed by heterokaryon RNA-Seq.** *Nature cell biology*
  Brady, J. J., Li, M., Suthram, S., Jiang, H., Wong, W. H., Blau, H. M.
  2013; 15 (10): 1244-1252

- **Early role for IL-6 signalling during generation of induced pluripotent stem cells revealed by heterokaryon RNA-Seq.** *Nature cell biology*
  Brady, J. J., Li, M., Suthram, S., Jiang, H., Wong, W. H., Blau, H. M.
  2013; 15 (10): 1244-1252

- **LEARNING A NONLINEAR DYNAMICAL SYSTEM MODEL OF GENE REGULATION: A PERTURBED STEADY-STATE APPROACH** *ANNALS OF APPLIED STATISTICS*
  Meister, A., Li, Y. H., Choi, B., Wong, W. H.
  2013; 7 (3): 1311-1333

- **Personalized prediction of first-cycle in vitro fertilization success** *FERTILITY AND STERILITY*
  Choi, B., Bosch, E., Lannon, B. M., Leveille, M., Wong, W. H., Leader, A., Pellicer, A., Penzias, A. S., Yao, M. W.
  2013; 99 (7): 1905-1911

- **Detecting DNA modifications from SMRT sequencing data by modeling sequence context dependence of polymerase kinetic.** *PLoS computational biology*
  Feng, Z., Fang, G., Korlach, J., Clark, T., Luong, K., Zhang, X., Wong, W., Schadt, E.
  2013; 9 (3)

- **RNA sequencing reveals a diverse and dynamic repertoire of the Xenopus tropicalis transcriptome over development** *GENOME RESEARCH*
  Tan, M. H., Au, K. F., Yablonovitch, A. L., Wills, A. E., Chuang, J., Baker, J. C., Wong, W. H., Li, J. B.
  2013; 23 (1): 201-216

- **Modeling kinetic rate variation in third generation DNA sequencing data to detect putative modifications to DNA bases** *GENOME RESEARCH*
  Schadt, E. E., Banerjee, O., Fang, G., Feng, Z., Wong, W. H., Zhang, X., Kislyuk, A., Clark, T. A., Khai Luong, K., Keren-Paz, A., Chess, A., Kumar, V., Chen-Plotkin, et al
  2013; 23 (1): 129-141

- **An Oct4-Sall4-Nanog network controls developmental progression in the pre-implantation mouse embryo** *MOLECULAR SYSTEMS BIOLOGY*
  Tan, M. H., Au, K. F., Leong, D. E., Foygel, K., Wong, W. H., Yao, M. W.
  2013; 9

- **Neural-specific Sox2 input and differential Gli-binding affinity provide context and positional information in Shh-directed neural patterning** *GENES & DEVELOPMENT*
  Peterson, K. A., Nishi, Y., Ma, W., Vedenko, A., Shokri, L., Zhang, X., McFarlane, M., Baizabal, J., Junker, J. P., van Oudenaarden, A., Mikkelsen, T., Bernstein, B. E., Bailey, et al
  2012; 26 (24): 2802-2816

- **Activation of Innate Immunity Is Required for Efficient Nuclear Reprogramming** *CELL*
  Lee, J., Sayed, N., Hunter, A., Au, K. F., Wong, W. H., Mocarski, E. S., Pera, R. R., Yakubov, E., Cooke, J. P.
  2012; 151 (3): 547-558

- **Improving PacBio Long Read Accuracy by Short Read Alignment** *PLOS ONE*
  Au, K. F., Underwood, J. G., Lee, L., Wong, W. H.
  2012; 7 (10)

- **Fast and accurate read alignment for resequencing** *BIOINFORMATICS*
  Mu, J. C., Jiang, H., Kiani, A., Mohiyuddin, M., Asadi, N. B., Wong, W. H.
  2012; 28 (18): 2366-2373

- **Six2 and Wnt Regulate Self-Renewal and Commitment of Nephron Progenitors through Shared Gene Regulatory Networks** *DEVELOPMENTAL CELL*
  Park, J., Ma, W., O'Brien, L. L., Chung, E., Guo, J., Cheng, J., Valerius, M. T., McMahon, J. A., Wong, W. H., McMahon, A. P.
  2012; 23 (3): 637-651

- **Predicting personalized multiple birth risks after in vitro fertilization-double embryo transfer** *FERTILITY AND STERILITY*
  Lannon, B. M., Choi, B., Hacker, M. R., Dodge, L. E., Malizia, B. A., Barrett, C. B., Wong, W. H., Yao, M. W., Penzias, A. S.

2012; 98 (1)

- **A Sparse Transmission Disequilibrium Test for Haplotypes Based on Bradley-Terry Graphs** *HUMAN HEREDITY*
  Ma, L., Wong, W. H., Owen, A. B.
  2012; 73 (1): 52-61

- **Coupling Optional Polya Trees and the Two Sample Problem** *JOURNAL OF THE AMERICAN STATISTICAL ASSOCIATION*
  Ma, L., Wong, W. H.
  2011; 106 (496): 1553-1565

- **A BOOTSTRAP-BASED NON-PARAMETRIC ANOVA METHOD WITH APPLICATIONS TO FACTORIAL MICROARRAY DATA** *STATISTICA SINICA*
  Zhou, B., Wong, W. H.
  2011; 21 (2): 495-514

- **A New FACS Approach Isolates hESC Derived Endoderm Using Transcription Factors** *PLOS ONE*
  Pan, Y., Ouyang, Z., Wong, W. H., Baker, J. C.
  2011; 6 (3)

- **Human transcriptome array for high-throughput clinical studies** *PROCEEDINGS OF THE NATIONAL ACADEMY OF SCIENCES OF THE UNITED STATES OF AMERICA*
  Xu, W., Seok, J., Mindrinos, M. N., Schweitzer, A. C., Jiang, H., Wilhelmy, J., Clark, T. A., Kapur, K., Xing, Y., Faham, M., Storey, J. D., Moldawer, L. L., Maier, et al
  2011; 108 (9): 3707-3712

- **Statistical Modeling of RNA-Seq Data** *STATISTICAL SCIENCE*
  Salzman, J., Jiang, H., Wong, W. H.
  2011; 26 (1): 62-83

- **Completely phased genome sequencing through chromosome sorting** *PROCEEDINGS OF THE NATIONAL ACADEMY OF SCIENCES OF THE UNITED STATES OF AMERICA*
  Yang, H., Chen, X., Wong, W. H.
  2011; 108 (1): 12-17

- **THE ANALYSIS OF CHIP-SEQ DATA** *METHODS IN ENZYMOLOGY, VOL 497: SYNTHETIC BIOLOGY, METHODS FOR PART/DEVICE CHARACTERIZATION AND CHASSIS ENGINEERING, PT A*
  Ma, W., Wong, W. H.
  2011; 497: 51-73

- **Integration of Brassinosteroid Signal Transduction with the Transcription Network for Plant Growth Regulation in Arabidopsis** *DEVELOPMENTAL CELL*
  Sun, Y., Fan, X., Cao, D., Tang, W., He, K., Zhu, J., He, J., Bai, M., Zhu, S., Oh, E., Patil, S., Kim, T., Ji, et al
  2010; 19 (5): 765-777

- **From EM to Data Augmentation: The Emergence of MCMC Bayesian Computation in the 1980s** *STATISTICAL SCIENCE*
  Tanner, M. A., Wong, W. H.
  2010; 25 (4): 506-516

- **Deep phenotyping to predict live birth outcomes in in vitro fertilization** *PROCEEDINGS OF THE NATIONAL ACADEMY OF SCIENCES OF THE UNITED STATES OF AMERICA*
  Banerjee, P., Choi, B., Shahine, L. K., Jun, S. H., O'leary, K., Lathi, R. B., Westphal, L. M., Wong, W. H., Yao, M. W.
  2010; 107 (31): 13570-13575

- **Detection of splice junctions from paired-end RNA-seq data by SpliceMap** *NUCLEIC ACIDS RESEARCH*
  Au, K. F., Jiang, H., Lin, L., Xing, Y., Wong, W. H.
  2010; 38 (14): 4570-4578

- **CisGenome Browser: a flexible tool for genomic data visualization** *BIOINFORMATICS*
  Jiang, H., Wang, F., Dyer, N. P., Wong, W. H.
  2010; 26 (14): 1781-1782

- **An "Almost Exhaustive" Search-Based Sequential Permutation Method for Detecting Epistasis in Disease Association Studies** *GENETIC EPIDEMIOLOGY*

  Ma, L., Assimes, T. L., Asadi, N. B., Iribarren, C., Quertermous, T., Wong, W. H.

  2010; 34 (5): 434-443

- **Analysis of factorial time-course microarrays with application to a clinical study of burn injury.** *Proceedings of the National Academy of Sciences of the United States of America*

  Zhou, B., Xu, W., Herndon, D., Tompkins, R., Davis, R., Xiao, W., Wong, W. H., Toner, M., Warren, H. S., Schoenfeld, D. A., Rahme, L., McDonald-Smith, G. P., Hayden, et al

  2010; 107 (22): 9923-9928

- **Analysis of factorial time-course microarrays with application to a clinical study of burn injury** *PROCEEDINGS OF THE NATIONAL ACADEMY OF SCIENCES OF THE UNITED STATES OF AMERICA*

  Zhou, B., Xu, W., Herndon, D., Tompkins, R., Davis, R., Xiao, W., Wong, W. H.

  2010; 107 (22): 9923-9928

- **OPTIONAL POLYA TREE AND BAYESIAN INFERENCE** *ANNALS OF STATISTICS*

  Wong, W. H., Ma, L.

  2010; 38 (3): 1433-1459

- **Hedgehog pathway-regulated gene networks in cerebellum development and tumorigenesis** *PROCEEDINGS OF THE NATIONAL ACADEMY OF SCIENCES OF THE UNITED STATES OF AMERICA*

  Lee, E. Y., Ji, H., Ouyang, Z., Zhou, B., Ma, W., Vokes, S. A., McMahon, A. P., Wong, W. H., Scott, M. P.

  2010; 107 (21): 9736-9741

- **Modeling Co-Expression across Species for Complex Traits: Insights to the Difference of Human and Mouse Embryonic Stem Cells** *PLOS COMPUTATIONAL BIOLOGY*

  Cai, J., Xie, D., Fan, Z., Chipperfield, H., Marden, J., Wong, W. H., Zhong, S.

  2010; 6 (3)

- **Modeling non-uniformity in short-read rates in RNA-Seq data** *GENOME BIOLOGY*

  Li, J., Jiang, H., Wong, W. H.

  2010; 11 (5)

- **ChIP-Seq of transcription factors predicts absolute and differential gene expression in embryonic stem cells** *PROCEEDINGS OF THE NATIONAL ACADEMY OF SCIENCES OF THE UNITED STATES OF AMERICA*

  Ouyang, Z., Zhou, Q., Wong, W. H.

  2009; 106 (51): 21521-21526

- **Identifiability of isoform deconvolution from junction arrays and RNA-Seq** *BIOINFORMATICS*

  Hiller, D., Jiang, H., Xu, W., Wong, W. H.

  2009; 25 (23): 3056-3059

- **Dissecting Early Differentially Expressed Genes in a Mixture of Differentiating Embryonic Stem Cells** *PLOS COMPUTATIONAL BIOLOGY*

  Hong, F., Fang, F., He, X., Cao, X., Chipperfield, H., Xie, D., Wong, W. H., Ng, H. H., Zhong, S.

  2009; 5 (12)

- **FoxOs Cooperatively Regulate Diverse Pathways Governing Neural Stem Cell Homeostasis** *CELL STEM CELL*

  Paik, J., Ding, Z., Narurkar, R., Ramkissoon, S., Muller, F., Kamoun, W. S., Chae, S., Zheng, H., Ying, H., Mahoney, J., Hiller, D., Jiang, S., Protopopov, et al

  2009; 5 (5): 540-553

- **Energy landscape of a spin-glass model: Exploration and characterization** *PHYSICAL REVIEW E*

  Zhou, Q., Wong, W. H.

  2009; 79 (5)

- **Modeling the spatio-temporal network that drives patterning in the vertebrate central nervous system** *BIOCHIMICA ET BIOPHYSICA ACTA-GENE REGULATORY MECHANISMS*

  Nishi, Y., Ji, H., Wong, W. H., McMahon, A. P., Vokes, S. A.

  2009; 1789 (4): 299-305

- **Cross-hybridization modeling on Affymetrix exon arrays** *BIOINFORMATICS*

  Kapur, K., Jiang, H., Xing, Y., Wong, W. H.

2008; 24 (24): 2887-2893

- **RECONSTRUCTING THE ENERGY LANDSCAPE OF A DISTRIBUTION FROM MONTE CARLO SAMPLES** *ANNALS OF APPLIED STATISTICS*
  Zhou, Q., Wong, W. H.
  2008; 2 (4): 1307-1331

- **An integrated software system for analyzing ChIP-chip and ChIP-seq data** *NATURE BIOTECHNOLOGY*
  Ji, H., Jiang, H., Ma, W., Johnson, D. S., Myers, R. M., Wong, W. H.
  2008; 26 (11): 1293-1300

- **SeqMap: mapping massive amount of oligonucleotides to the genome** *BIOINFORMATICS*
  Jiang, H., Wong, W. H.
  2008; 24 (20): 2395-2396

- **A genome-scale analysis of the cis-regulatory circuitry underlying sonic hedgehog-mediated patterning of the mammalian limb** *GENES & DEVELOPMENT*
  Vokes, S. A., Ji, H., Wong, W. H., McMahon, A. P.
  2008; 22 (19): 2651-2663

- **Isolation and transcriptional profiling of purified hepatic cells derived from human embryonic stem cells** *STEM CELLS*
  Chiao, E., Elazar, M., Xing, Y., Xiong, A., Kmet, M., Millan, M. T., Glenn, J. S., Wong, W. H., Baker, J.
  2008; 26 (8): 2032-2041

- **Defining Human Embryo Phenotypes by Cohort-Specific Prognostic Factors** *PLOS ONE*
  Jun, S. H., Choi, B., Shahine, L., Westphal, L. M., Behr, B., Pera, R. A., Wong, W. H., Yao, M. W.
  2008; 3 (7)

- **Learning causal Bayesian network structures from experimental data** *JOURNAL OF THE AMERICAN STATISTICAL ASSOCIATION*
  Ellis, B., Wong, W. H.
  2008; 103 (482): 778-789

- **Reconfigurable Computing for Learning Bayesian Networks** *16th ACM/SIGDA International Symposium on Field-Programmable Gate Arrays*
  Asadi, N. B., Meng, T. H., Wong, W. H.
  ASSOC COMPUTING MACHINERY.2008: 203–211

- **Optimal discovery of a stochastic genetic network** *American Control Conference 2008*
  Raffard, R. L., Lipan, O., Wong, W. H., Tomlin, C. J.
  IEEE.2008: 2773–2779

- **Evolutionary Monte Carlo methods for clustering** *JOURNAL OF COMPUTATIONAL AND GRAPHICAL STATISTICS*
  Goswami, G., Liu, J. S., Wong, W. H.
  2007; 16 (4): 855-876

- **A gene regulatory network in mouse embryonic stem cells** *PROCEEDINGS OF THE NATIONAL ACADEMY OF SCIENCES OF THE UNITED STATES OF AMERICA*
  Zhou, Q., Chipperfield, H., Melton, D. A., Wong, W. H.
  2007; 104 (42): 16438-16443

- **Assessing the conservation of mammalian gene expression using high-density exon arrays** *MOLECULAR BIOLOGY AND EVOLUTION*
  Xing, Y., Ouyang, Z., Kapur, K., Scott, M. P., Wong, W. H.
  2007; 24 (6): 1283-1285

- **COUPLING HIDDEN MARKOV MODELS FOR THE DISCOVERY OF Cis-REGULATORY MODULES IN MULTIPLE SPECIES** *ANNALS OF APPLIED STATISTICS*
  Zhou, Q., Wong, W. H.
  2007; 1 (1): 36-65

- **Genomic characterization of Gli-activator targets in sonic hedgehog-mediated neural patterning** *DEVELOPMENT*
  Vokes, S. A., Ji, H., McCuine, S., Tenzen, T., Giles, S., Zhong, S., Longabaugh, W. J., Davidson, E. H., Wong, W. H., McMahon, A. P.
  2007; 134 (10): 1977-1989

- **FoxOs are lineage-restricted redundant tumor suppressors and regulate endothelial cell homeostasis** *CELL*

Paik, J., Kollipara, R., Chu, G., Ji, H., Xiao, Y., Ding, Z., Miao, L., Tothova, Z., Horner, J. W., Carrasco, D. R., Jiang, S., Gilliland, D. G., Chin, et al
2007; 128 (2): 309-323

- **Exon arrays provide accurate assessments of gene expression** *GENOME BIOLOGY*
  Kapur, K., Xing, Y., Ouyang, Z., Wong, W. H.
  2007; 8 (5)

- **Probe Selection and Expression Index Computation of Affymetrix Exon Arrays** *PLOS ONE*
  Xing, Y., Kapur, K., Wong, W. H.
  2006; 1 (1)

- **A comparative analysis of genome-wide chromatin immunoprecipitation data for mammalian transcription factors** *NUCLEIC ACIDS RESEARCH*
  Ji, H., Vokes, S. A., Wong, W. H.
  2006; 34 (21)

- **Computational biology: Toward deciphering gene regulatory information in mammalian genomes** *BIOMETRICS*
  Ji, H., Wong, W. H.
  2006; 62 (3): 645-663

- **Is the future biology Shakespearean or Newtonian?** *MOLECULAR BIOSYSTEMS*
  Lipan, O., Wong, W. H.
  2006; 2 (9): 411-416

- **A tale of two morphogen gradients: Identifying Gli targets of Hedgehog Signaling** *65th Annual Meeting of the Society-for-Developmental-Biology*
  Vokes, S. A., Ji, H., Wong, W. H., McMahon, A. P.
  ACADEMIC PRESS INC ELSEVIER SCIENCE.2006: 423–23

- **A study of density of states and ground states in hydrophobic-hydrophilic protein folding models by equi-energy sampling** *JOURNAL OF CHEMICAL PHYSICS*
  Kou, S. C., Oh, J., Wong, W. H.
  2006; 124 (24)

- **Inferring loss-of-heterozygosity from unpaired tumors using high-density oligonucleotide SNP arrays** *PLOS COMPUTATIONAL BIOLOGY*
  Beroukhim, R., Lin, M., Park, Y., Hao, K., Zhao, X., Garraway, L. A., Fox, E. A., Hochberg, E. P., Mellinghoff, I. K., Hofer, M. D., Descazeaud, A., Rubin, M. A., Meyerson, et al
  2006; 2 (5): 323-332

- **Recursive SVM feature selection and sample classification for mass-spectrometry and microarray data** *BMC BIOINFORMATICS*
  Zhang, X. G., Lu, X., Shi, Q., Xu, X. Q., Leung, H. C., Harris, L. N., D Iglehart, J., Miron, A., Liu, J. S., Wong, W. H.
  2006; 7

- **An improved distance measure between the expression profiles linking co-expression and co-regulation in mouse** *BMC BIOINFORMATICS*
  Kim, R. S., Ji, H. K., Wong, W. H.
  2006; 7

- **Reliable prediction of transcription factor binding sites by phylogenetic verification** *PROCEEDINGS OF THE NATIONAL ACADEMY OF SCIENCES OF THE UNITED STATES OF AMERICA*
  Li, X. M., Zhong, S., Wong, W. H.
  2005; 102 (47): 16945-16950

- **De novo discovery of a tissue-specific gene regulatory module in a chordate** *GENOME RESEARCH*
  Johnson, D. S., Zhou, Q., Yagi, K., Satoh, N., Wong, W., Sidow, A.
  2005; 15 (10): 1315-1324

- **HumanUpstream and MouseUpstream: Databases of promoter sequences in the human and mouse genomes** *OMICS-A JOURNAL OF INTEGRATIVE BIOLOGY*
  Leykin, I., Kao, M. C., Wong, W. H.
  2005; 9 (3): 220-224

- **TileMap: create chromosomal map of tiling array hybridizations** *BIOINFORMATICS*
  Ji, H. K., Wong, W. H.

2005; 21 (18): 3629-3636

- **Identification of Gli target genes using chromatin immuno-precipitation with a genetically inducible system on genomic arrays.** *64th Annual Meeting of the Society-for-Development-Biology*
  Vokes, S. A., Ji, H. K., Wong, W. H., MCMAHON, A. P.
  ACADEMIC PRESS INC ELSEVIER SCIENCE.2005: 666–66

- **Sampling motifs on phylogenetic trees** *PROCEEDINGS OF THE NATIONAL ACADEMY OF SCIENCES OF THE UNITED STATES OF AMERICA*
  Li, X. M., Wong, W. H.
  2005; 102 (27): 9481-9486

- **mSin3A corepressor regulates diverse transcriptional networks governing normal and neoplastic growth and survival** *GENES & DEVELOPMENT*
  Dannenberg, J. H., David, G., Zhong, S., van der Torre, J., Wong, W. H., DePinho, R. A.
  2005; 19 (13): 1581-1595

- **A small-molecule inhibitor of mpsl blocks the spindle-checkpoint response to a lack of tension on mitotic chromosomes** *CURRENT BIOLOGY*
  Dorer, R. K., Zhong, S., Tallarico, J. A., Wong, W. H., Mitchison, T. J., Murray, A. W.
  2005; 15 (11): 1070-1076

- **UbIC(2) - Towards ubiquitous bio-information computing: Data protocols, middleware, and web services for heterogeneous biological information integration and retrieval** *INTERNATIONAL JOURNAL OF SOFTWARE ENGINEERING AND KNOWLEDGE ENGINEERING*
  Hong, P. Y., Zhong, S., Wong, W. H.
  2005; 15 (3): 475-485

- **A boosting approach for motif modeling using ChIP-chip data** *BIOINFORMATICS*
  Hong, P. Y., Liu, X. S., Zhou, Q., Lu, X., Liu, J. S., Wong, W. H.
  2005; 21 (11): 2636-2643

- **Tight clustering: A resampling-based approach for identifying stable and tight patterns in data** *BIOMETRICS*
  Tseng, G. C., Wong, W. H.
  2005; 61 (1): 10-16

- **Comparative linkage analysis and visualization of high-density oligonucleotide SNP array data** *BMC GENETICS*
  Leykin, I., Hao, K., Cheng, J. S., Meyer, N., Pollak, M. R., Smith, R. J., Wong, W. H., Rosenow, C., Li, C.
  2005; 6

- **GeneNotes - A novel information management software for biologists** *BMC BIOINFORMATICS*
  Hong, P. Y., Wong, W. H.
  2005; 6

- **Functional annotation and network reconstruction through cross-platform integration of microarray data** *NATURE BIOTECHNOLOGY*
  Zhou, X. H., Kao, M. C., Huang, H. Y., Wong, A., Nunez-Iglesias, J., Primig, M., Aparicio, O. M., Finch, C. E., Morgan, T. E., Wong, W. H.
  2005; 23 (2): 238-243

- **Detect and adjust for population stratification in population-based association study using genomic control markers: an application of Affymetrix Genechip (R) Human Mapping 10K array** *EUROPEAN JOURNAL OF HUMAN GENETICS*
  Hao, K., Li, C., Rosenow, C., Wong, W. H.
  2004; 12 (12): 1001-1006

- **Estimation of genotype error rate using samples with pedigree information - an application on the GeneChip Mapping 10K array** *GENOMICS*
  Hao, K., Li, C., Rosenow, C., Wong, W. H.
  2004; 84 (4): 623-630

- **Genomic analysis of mouse retinal development** *PLOS BIOLOGY*
  Blackshaw, S., Harpavat, S., Trimarchi, J., Cai, L., Huang, H. Y., Kuo, W. P., Weber, G., Lee, K., Fraioli, R. E., Cho, S. H., Yung, R., Asch, E., Ohno-Machado, et al
  2004; 2 (9): 1411-1431

- **CisModule: De novo discovery of' cis-regulatory modules by hierarchical mixture modeling** *PROCEEDINGS OF THE NATIONAL ACADEMY OF SCIENCES OF THE UNITED STATES OF AMERICA*
  Zhou, Q., Wong, W. H.

2004; 101 (33): 12114-12119

- **Integrated analysis of microarray data and gene function information** *OMICS-A JOURNAL OF INTEGRATIVE BIOLOGY*
  Cui, Y., Zhou, M., Wong, W. H.
  2004; 8 (2): 106-117

- **Molecular diversity of astrocytes with implications for neurological disorders** *PROCEEDINGS OF THE NATIONAL ACADEMY OF SCIENCES OF THE UNITED STATES OF AMERICA*
  Bachoo, R. M., Kim, R. S., Ligon, K. L., Maher, E. A., Brennan, C., Billings, N., Chan, S., Li, C., Rowitch, D. H., Wong, W. H., DePinho, R. A.
  2004; 101 (22): 8384-8389

- **dChipSNP: significance curve and clustering of SNP-array-based loss-of-heterozygosity data** *BIOINFORMATICS*
  Lin, M., Wei, L. J., Sellers, W. R., Lieberfarb, M., Wong, W. H., Li, C.
  2004; 20 (8): 1233-1240

- **GoSurfer: a graphical interactive tool for comparative analysis of large gene sets in Gene Ontology space.** *Applied bioinformatics*
  Zhong, S., Storch, K., Lipan, O., Kao, M. J., Weitz, C. J., Wong, W. H.
  2004; 3 (4): 261-264

- **Comparative analysis of gene sets in the gene ontology space under the multiple hypothesis testing framework** *IEEE Computational Systems Bioinformatics Conference (CSB 2004)*
  Zhong, S., Tian, L., Li, C., Storch, K. F., Wong, W. H.
  IEEE COMPUTER SOC.2004: 425–435

- **Clustering analysis of SAGE data using a Poisson approach** *GENOME BIOLOGY*
  Cai, L., Huang, H. Y., Blackshaw, S., Liu, J. S., Cepko, C., Wong, W. H.
  2004; 5 (7)

- **In silico prediction of transcription factors that interact with the E2F family of transcription factors** *8th International Conference on Control, Automation, Robotics and Vision (ICARCV 2004)*
  Zhong, S., Zhou, Q., Giangrande, P., Nevins, J. R., Wong, W. H.
  IEEE.2004: 1325–1330

- **Determination of local statistical significance of patterns in Markov sequences with application to promoter element identification** *JOURNAL OF COMPUTATIONAL BIOLOGY*
  Huang, H. Y., Kao, M. C., Zhou, X. H., Liu, J. S., Wong, W. H.
  2004; 11 (1): 1-14

- **Towards Ubiquitous Bio-Information Computing: Data protocols, middleware, and Web services for heterogeneous biological information integration and retrieval** *4TH IEEE Symposium on Bioinformatics and Bioengineering (BIBE 2004)*
  Hong, P. Y., Zhong, S., Wong, W. H.
  IEEE COMPUTER SOC.2004: 57–64

- **ChipInfo: software for extracting gene annotation and gene ontology information for microarray analysis** *NUCLEIC ACIDS RESEARCH*
  Zhong, S., Li, C., Wong, W. H.
  2003; 31 (13): 3483-3486

- **A method for tight clustering: with application to microarray** *2nd International Computational Systems Bioinformatics Conference*
  Tseng, G. C., Wong, W. H.
  IEEE COMPUTER SOC.2003: 396–397

- **Transitive functional annotation by shortest-path analysis of gene expression data** *PROCEEDINGS OF THE NATIONAL ACADEMY OF SCIENCES OF THE UNITED STATES OF AMERICA*
  Zhou, X. H., Kao, M. C., Wong, W. H.
  2002; 99 (20): 12783-12788

- **Extensive and divergent circadian gene expression in liver and heart** *NATURE*
  Storch, K. F., Lipan, O., Leykin, I., Viswanathan, N., Davis, F. C., Wong, W. H., Weitz, C. J.
  2002; 417 (6884): 78-83

- **Recombinatoric exploration of novel folded structures: A heteropolymer-based model of protein evolutionary landscapes** *PROCEEDINGS OF THE NATIONAL ACADEMY OF SCIENCES OF THE UNITED STATES OF AMERICA*

Cui, Y., Wong, W. H., Bornberg-Bauer, E., Chan, H. S.

2002; 99 (2): 809-814

- **Issues in cDNA microarray analysis: quality filtering, channel normalization, models of variations and assessment of gene effects** *NUCLEIC ACIDS RESEARCH*

  Tseng, G. C., Oh, M. K., Rohlin, L., Liao, J. C., Wong, W. H.

  2001; 29 (12): 2549-2557

- **Real-parameter evolutionary Monte Carlo with applications to Bayesian mixture models** *JOURNAL OF THE AMERICAN STATISTICAL ASSOCIATION*

  Liang, F. M., Wong, W. H.

  2001; 96 (454): 653-666

- **Feature extraction and normalization algorithms for high-density oligonucleotide gene expression array data** *5th Annual Lake Tahoe Symposium*

  Schadt, E. E., Li, C., Ellis, B., Wong, W. H.

  WILEY-LISS.2001: 120–125

- **Evolutionary Monte Carlo: Applications to C-p model sampling and change point problem** *STATISTICA SINICA*

  Liang, F. M., Wong, W. H.

  2000; 10 (2): 317-342

- **Relaxed simulated tempering for VLSI floorplan designs** *4th Asia and South Pacific Design Automation Conference (ASP-DAC 99)*

  Cong, J., Kong, T. M., Xu, D. M., Liang, F. M., Liu, J. S., Wong, W. H.

  IEEE.1999: 13–16

- **Torsional relaxation for biopolymers** *JOURNAL OF COMPUTATIONAL BIOLOGY*

  Wong, W. H., Cui, Y., Chen, R. S.

  1998; 5 (4): 655-665