Chen-Hsiang Yeang

Associate Research Fellow
Address: Institute of Statistical Science
Academia Sinica
No. 128 Academia Road Sec. 2,
Nankang, Taipei 115, Taiwan
Telephone: +886-2-27835611
E-mail: chyeang@stat.sinica.edu.tw
URL: https://staff.stat.sinica.edu.tw/chyeang/

EDUCATION

Massachusetts Institute of Technology, Cambridge, MA, U.S.A.
Doctor of Science in Electrical Engineering and Computer Science, September 2004.
Dissertation: Inferring Gene Regulatory Networks from multiple Sources of Genomic Data. Established a modeling framework of integrating multiple sources of data to reconstruct the gene regulatory networks.
Supervisor: Tommi Jaakkola.

Massachusetts Institute of Technology, Cambridge, MA, U.S.A.
Master for City Planning, June 1998.
Concentrating on building computerized planning support systems for environmental planning, and studying the roles of information systems in developing countries.

Massachusetts Institute of Technology, Cambridge, MA, U.S.A.
Master of Science, June 1996.
Concentrating on implementing an integrated virtual environment system for aiding landscape design.

National Taiwan University, Taipei, Taiwan
Bachelor of Science, June 1992.

ACADEMIC EXPERIENCE

Institute of Statistical Science, Academia Sinica, Taipei, Taiwan
Associate Research Fellow. August 2023-present.
Developing an integrative model of cancer genomics datasets, building quantitative models of the evolution of biomolecular systems and human populations, analyzing topological characteristics of networks, and developing self-supervised learning algorithms on image data.

Institute of Statistical Science, Academia Sinica, Taipei, Taiwan
Associate Research Fellow. July 2013-July 2023.
Developing an integrative model of cancer genomics datasets, building quantitative models of the evolution of biomolecular systems and human populations, analyzing topological characteristics of networks, and developing self-supervised learning algorithms on image data.

Institute of Statistical Science, Academia Sinica, Taipei, Taiwan
Assistant Research Fellow. October 2008-June 2013.
Developing an integrative model of cancer genomics datasets and building quantitative models of the evolution of biomolecular systems.

Broad Institute of MIT and Harvard University, Cambridge, M.A., U.S.A.
Visiting scientist. October 2014-September 2015.
Analyzing the data of oncogenic states.

College of Life Science, National Taiwan University, Taipei, Taiwan
Adjunct Assistant Professor, September 2010-present.
Serving as a core faculty member in the Academia Sinica-National Taiwan University Joint Graduate
Program on Genomics & Systems Biology.

Simons Center for Systems Biology, Institute for Advanced Study, Princeton, NJ, U.S.A.
Member, Arnold Levine's group. January 2007-September 2008.
Studying the combinatorial patterns of somatic gene mutations in cancer and an integrated approach to
characterize genetic alterations in cancer.

University of California Santa Cruz Center for Biomolecular Science & Engineering, Santa Cruz, CA,
U.S.A.
Postdoctoral Researcher, David Haussler's group. February 2005-December 2006.
Modeling the coevolution of nucleotides and amino acid residues in functional RNAs and protein domains.
Inferring the gene regulatory circuitry of colon cancer invasiveness and cholera surface phenotypes.

Max-Planck Institute for Molecular Genetics, Berlin, Germany
Postdoctoral Scholar, Martin Vingron's group. September 2004-December 2004.
Modeling the coupled processes of gene regulation and metabolic reactions.

MIT Computer Science and Artificial Intelligence Laboratory, Cambridge, MA, U.S.A.
Research Assistant, Tommi Jaakkola's group. September 1999-September 2004.
Developing computational methods of integrating multiple data sources to uncover gene regulatory
networks. Devising an experimental design scheme to prioritize gene knock-out experiments in order to
disambiguate models (in collaboration with Trey Ideker's group at UCSD). Investigating the combinatorial
control mechanisms and functions of transcription factors. Studying the geometric properties of statistical
models and their applications in active learning. Applying classical and quantum field theories in
continuous Markov random walks (in collaboration with Martin Szummer at Microsoft Research, UK).

Whitehead Institute of Biomedical Research, Cambridge, MA, U.S.A.
Research Assistant, Whitehead Genome Center (Now Broad Institute) Cancer Genomics Group, June-
September 2000.
Participating in the pioneering project of classifying tumor types using mRNA expression data. Applying
the error-correcting output coding algorithm of multi-class classification and developed a hierarchical
partitioning algorithm to the problem.

PROFESSIONAL EXPERIENCE

AQUA Communications, Inc., Cambridge, MA, U.S.A.
Hardware Engineer, September 1998-June 1999.
Designing and testing embedded systems for industrial control and home appliances. Works including
schematic design at system level, writing and modifying device drivers, and circuit testing.

Asian Institute of Technology, Bangkok, Thailand
Visiting Student and Research Associate, June 1997-August 1997.
Investigating the role of information systems and information collection in the rural development of
Thailand. Project under the United Nations Development Program-MIT Department of Urban Studies and
Planning decentralization program.

GRANTS AND FELLOWSHIPS

Decomposition of gene expression data into spatial-temporal patterns. National Science and Technology Council, Taiwan. 114-2118-M-001 -007 -MY2. August 1st 2025 – July 31st 2027.

Identifying holes of arbitrary dimensions and quantifying their distributions in large-scale networks. Academia Sinica Seed Grant. AS-GCS-113-M05. January 1st 2024 – December 31st 2025.

Inferring cellular compositions of biological specimens from bulk and single-cell RNASeq data and associating cellular compositions with phenotypes. National Science and Technology Council, Taiwan. 112-2118-M-001 -007 -MY2. August 1st 2023 – July 31st 2025.

Building association models between molecular and clinical signatures in cancer patients. Fisher/Tukey Project. Institute of Statistical Science, Academia Sinica, Taiwan. May 1st 2022 – December 31st 2023.

Using deep supervised learning algorithms to cluster data. Seed grant. Institute of Statistical Science, Academia Sinica, Taiwan. August 1st 2021 – December 31st 2023.

Characterization of transcriptomic heterogeneity of cancer cells and associations with clinical phenotypes. Ministry of Science and Technology, Taiwan. 110-2118-M-001 -003 -MY2. August 2021-July 2023.

Modeling the reversible and irreversible mechanisms of drug resistance in cancer cells. Ministry of Science and Technology, Taiwan. 108-2118-M-001 -001 -MY2. August 2019-July 2021.

Explaining Cancer Type Specific Mutations with Transcriptomic and Genomic Features in Normal Tissues. Ministry of Science and Technology, Taiwan. 107-2118-M-001 -007 -. August 2018-July 2019.

Integrated Analysis of Pancancer Data from the Cancer Genome Atlas. Ministry of Science and Technology, Taiwan. 106-2118-M-001-012 -. August 2017-July 2018.

Interdisciplinary Research Group Program, National Center of Theoretical Science, Ministry of Science and Technology, January 2015-December 2016.

Career Development Award. Academia Sinica. 104-CDA-M04. January 1st 2015-December 31st 2019.

Designing combinatorial therapeutics for fast-evolving, heterogeneous tumors. Ministry of Science and Technology, Taiwan. 103-21180M-001 -011 –MY2. August 2015-July 2017.

Comparative and evolutionary analysis of molecular process perturbations in cancer cells. Ministry of Science and Technology, Taiwan. 103-2918-I-001 -008 -. September 2014-September 2015.

In-silico design and in-vitro validation of combinatorial treatment strategies of cancer. National Science Council of Taiwan. 102-2221-E-001-030-. August 1st, 2013-July 31st, 2014.

Deciphering the temporal orders and causal relations of molecular alterations in cancer. National Science Council of Taiwan. 100-2118-M-001-008-MY2. August 1st 2011-July 31st, 2013.

Analysis of the dependent evolution of biomolecular networks. National Science Council of Taiwan. 99-2221-E-001-021-, August 1st, 2010-July 31st, 2011.

A data-integration model to detect the statistical and causal dependencies of aberrations in cancer and other diseases. National Science Council of Taiwan. 98-2118-M-001-025-MY2. August 1st, 2009-July 31st, 2011.

United States Fulbright Scholarship to Taiwan. Conducting research in computational biology at Academia

Sinica, Taipei, Taiwan. October 1st, 2008-July 31st, 2009.

PRESENTATIONS, INVITED TALKS, AND POSTERS

"Algorithms of finding independent holes in a network". Invited talk. Virtual presentation. Sunbelt Conference, Edinburgh, 2024.

"An integrated analysis of the cancer genome atlas data discovers a hierarchical association structure across thirty three cancer types". Invited talk. Virtual presentation. INFORMS/ALIO/ASOCIO International Conference, Medellin, Colombia, 2024.

"Exploring the relation between the geometry of a fixed embedding space and the underlying cluster structure of image data". Invited talk. ISM-ISI-ISSAS meeting, Kolkata, India, 2023.

"An integrated analysis of the cancer genome atlas data discovers a hierarchical association structure across thirty three cancer types". Invited talk. Cancer Institute of New Jersey at Rutgers University, NJ, USA, 2023.

"An integrated analysis of the cancer genome atlas data discovers a hierarchical association structure across thirty three cancer types". Oral presentation. The International Conference of Systems Biology (ICSB), Hartford, CT, USA, 2023.

"An integrated analysis of the cancer genome atlas data discovers a hierarchical association structure across thirty three cancer types". Invited talk. Georgetown University, Washington DC, USA, 2023.

"An integrated analysis of the cancer genome atlas data discovers a hierarchical association structure across thirty three cancer types". Invited talk. University of Illinois Urbana Champaign, Champaign, IL, USA, 2023.

"Inferring associations along the causal chains in a network". Invited talk. The 6st International Conference on Econometrics and Statistics (EcoSta), Tokyo, Japan, 2023.

"An integrated analysis of the cancer genome atlas data discovers a hierarchical association structure across thirty three cancer types". Poster presentation. The International Conference of the Intelligent Systems for Molecular Biology (ISMB), Lyon, France, 2023.

"An integrated analysis of the cancer genome atlas data discovers a hierarchical association structure across thirty three cancer types". Group meeting talk. Cancer Research Institute, University of Cambridge, 2023.

"An integrated analysis of the cancer genome atlas data discovers a hierarchical association structure across thirty three cancer types". Seminar talk. The seminar series of AI and medicine, Warwick University School of Medicine, Coventry, United Kingdom, 2023.

"An integrated analysis of the cancer genome atlas data discovers a hierarchical association structure across thirty three cancer types". Group meeting talk. Biomedical Research Facility, University of California, San Diego, USA, 2023.

"An integrated analysis of the cancer genome atlas data discovers a hierarchical association structure across thirty three cancer types". Group meeting talk. Center for Novel Therapeutics, University of California, San Diego, USA, 2023.

"An integrated analysis of the cancer genome atlas data discovers a hierarchical association

structure across thirty three cancer types". Group meeting talk. Department of Biomedical Engineering, University of California, Santa Cruz, USA, 2023.

"An integrated analysis of the cancer genome atlas data discovers a hierarchical association structure across thirty three cancer types". Group meeting talk. Department of Statistics, Stanford University, USA, 2023.

"Cooperative stability renders protein complex formation more robust and controllable". Invited talk. ISI-ISM-ISSAS Joint Conference. Taipei, Taiwan, 2023.

"Clustering image data with a fixed embedding". Poster presentation. 21st IEEE International Conference on Machine Learning and Applications (ICMLA). Nassau, Bahamas, 2022.

"Clustering image data with a fixed embedding". Invited talk. Workshop of Robust Statistical Inference for High Dimensional Data and Deep Models. Institute of Statistical Science, Academia Sinica, Taipei, Taiwan, 2022.

"Genotypes of informative loci from 1000 Genomes data allude evolution and mixing of human populations". Invited talk. ISM-ISI-ASISS joint meeting, Taipei, Taiwan, 2022.

"An integrative analysis of the cancer genome atlas data". Seminar talk. University of California, San Diego, 2019.

"Modeling bistable tumour population dynamics to design effective treatment strategies". Poster presentation. The International Conference of the Intelligent Systems for Molecular Biology (ISMB), Basel, Switzerland, 2019.

"Three levels of computational approaches toward cancer omics". Seminar talk. Cancer Institute of New Jersey, Rutgers University, New Brunswick, USA, 2019.

"C-terminal end-directed protein elimination shapes the eukaryotic proteome". Poster presentation. EMBO Conference of Genomics and Systems Biology, Heidelberg, Germany, 2018.

"Analysis and modeling of the evolution and dynamics of cancer". Seminar talk. Max-Planck Institute for Molecular Genetics, Berlin, Germany, 2018.

"Modeling bistable tumour population dynamics to design effective treatment strategies". Oral presentation. The International Conference of Systems Biology (ICSB), Lyon, France, 2018.

"Combinatorial and recurrent patterns of associations between molecular alterations across cancer types in TCGA data". Poster presentation. TCGA Symposium, Washington DC, USA, 2018.

"Analysis and modeling of the evolution and dynamics of cancer". Invited talk. Department of Biology, Southern University of Science and Technology, Shenzhen, China, 2018.

"Explaining cancer type specific mutations with transcriptomic and epigenomic features in normal tissues". Invited talk. The International Conference of Chinese Statisticians, Qingdao, China, 2018.

"Ten (personal) commandments for applying artificial intelligence in data science". Oral presentation. Invited speaker. Workshop of Applications for Artificial Intelligence in Data Science", National Sun Yet-San University, Kaoshiung, Taiwan, 2017.

"Genomic mixing across the United States". Oral presentation. The Annual Joint Conference of the three statistical institutes, Institute of Statistical Mathematics, Tokyo, Japan, 2017.

"Explaining cancer type specific mutations with transcriptomic and epigenomic features in normal tissues". Oral presentation. Invited speaker. The 2nd Pacific Rim Cancer Biostatistics Workshop, Kanazawa, Japan, 2017.

"A quantitative model for the rate-limiting process of UGA alternative assignments to stop and selenocysteine codons". Invited talk. Department of Bioinformatics, National Yang-Ming University, Taipei, Taiwan, 2017.

"A quantitative framework of integrating multi-modal cancer genomic data". Oral presentation. The 8th Moscow Conference on Computational Molecular Biology, Moscow, Russia, 2017.

"A quantitative model for the rate-limiting process of UGA alternative assignments to stop and selenocysteine codons". Poster presentation. The International Conference of the Intelligent Systems for Molecular Biology (ISMB), Prague, Czech Republic, 2017.

"A quantitative framework of integrating multi-modal cancer genomic data". Oral presentation. VI International Symposium on OMICS and Bioinformatics, Varadero, Cuba, 2016.

"Computational methods of characterizing molecular aberrations on cancer genomes and optimizing treatment outcomes". Invited talk. Systems Biology and Bioinformatics Laboratory, King Mongkut's University of Technology, Thonburi, Thailand, 2015.

"Putative effectors for prognosis in lung adenocarcinoma are ethnic and gender specific". Poster presentation. The International Conference of Systems Biology (ISCB), Singapore, 2015.

"Integrative analysis of molecular aberrations in cancers". Invited talk. Lombardi Comprehensive Cancer and Innovation Center for Biomedical Informatics, Georgetown University Medical Center, Washington DC, USA, 2015.

"Alternative definitions of UGA codon regulated by translational regulatory factors and selenium". Poster presentation. The International Conference of Research in Computational Biology (RECOMB), Warsaw, Poland, 2015.

"Alternative definitions of UGA codon regulated by translational regulatory factors and selenium". Poster presentation. The International Conference of Systems Biology (ISCB), Melbourne, Australia, 2014.

"Computational methods of characterizing molecular aberrations on cancer genomes and optimizing treatment outcomes". Invited talk. The young scholar forum of math, computer and life sciences, Beijing, China, 2014.

"Impact of genetic dynamics and single-cell heterogeneity on development of nonstandard personalized medicine strategies for cancer". Oral presentation. ISM-ISI-ISSAS Joint Conference, Delhi, India, 2014.

"An integrative characterization of recurrent molecular aberrations in glioblastoma genomes". Invited talk. The International Society of Computational Biology (ISCB) Asia meeting, Seoul, Korea, 2013.

"Impact of genetic dynamics and single cell heterogeneity on development of nonstandard personalized medicine strategies for cancer". Highlight track presentation. The International Conference of the Intelligent Systems for Molecular Biology (ISMB), Berlin, Germany, 2013.

"Recurrent structural motifs reflect characteristics of distinct networks". Oral presentation. International Network for Social Network Analysis Conference (INSNA), Xian, China, 2013.

"Recurrent structural motifs reflect characteristics of distinct networks". Poster presentation and general participation. Sixth French-Taiwanese Frontiers of Science Symposium, Bordeaux, France, 2013.

"Functional characterization of motif sequences under purifying selection". Oral presentation. International Conference of Computational Biology (ISCB) Africa Meeting, Casablanca, Morocco, 2013.

"Computational methods of characterizing molecular aberrations on cancer genomes and optimizing treatment outcomes". Seminar talk. Institute of Mathematical Sciences, Tel Aviv University, Israel, 2012.

"Recurrent structural motifs reflect characteristics of distinct networks". Oral presentation. With Liang-Cheng Huang. The 2012 IEEE/ACM International Conference on Advances in Social Networks Analysis and Mining (ASONAM), Istanbul, Turkey, 2012.

"Next generation personalized medicine strategies incorporating genetic dynamics and single cell heterogeneity may lead to improved outcomes". Poster presentation. The International Conference of the Intelligent Systems for Molecular Biology (ISMB), Long Beach, USA, 2012.

"An integrative characterization of recurrent molecular aberrations in glioblastoma". Oral presentation. The Second Joint Biostatistics Symposium, Beijing, China, 2012.

"Evolution of domain architectures and catalytic functions of enzymes in metabolic systems". Oral presentation. International Conference of Computational Biology (ISCB) Latin America Meeting, Santiago, Chile, 2012.

"A probabilistic graphical model of quantum systems". Oral presentation. ISM-ISI-ISSAS Joint Conference, Tokyo, Japan, 2012.

"Deciphering causal and statistical associations of molecular aberrations and gene expressions from integrated cancer genomic data". Oral presentation. Cold Spring Harbor Asia Meeting on Bioinformatics of Human and Animal Genomics, Suzhou, China, 2011.

"An integrated analysis of molecular aberrations in cancer". Oral presentation. Cancer Bioinformatics Workshop, Cambridge Research Institute, Cambridge, UK, 2010.

"An integrated analysis of molecular aberrations in cancer". BIT Life Science's 3rd World Cancer Congress, Singapore, 2010.

"An integrated analysis of molecular aberrations in cancer". Oral presentation. ISM-ISI-ISSAS Joint Conference, Kolkata, India, 2010.

"An integrated analysis of molecular aberrations in cancer". Invited seminar talk. Ontario Institute of Cancer Research, Toronto, Canada, 2009.

"An integrated analysis of molecular aberrations in cancer". Invited seminar talk. National Health Research Institute, Taiwan, 2009.

"Combinatorial patterns of somatic gene mutations in cancer", with A. Levine and F. McCormick. Invited talk. The 5th Statistical and Machine Learning Workshop, National Cheng Kung University, Tainan, Taiwan, 2009.

"An integrated analysis of molecular aberrations in cancer". Invited seminar talk. Taiwan International Graduate Program Bioinformatics Program, Academia Sinica, Taipei, Taiwan, 2009.

"An integrated analysis of molecular aberrations in cancer". Invited seminar talk. Institute of Life Science, National Tsing-Hua University, Hsin-Chu, Taiwan, 2009.

"An integrated analysis of molecular aberrations in cancer". Invited seminar talk. Department of Statistics, National Chiao-Tung University, Hsin-Chu, Taiwan, 2009.

"An integrated analysis of molecular aberrations in cancer". Invited seminar talk. Changhua Christian Hospital, Changhua, Taiwan, 2009.

"An integrated analysis of molecular aberrations in cancer". Invited seminar talk. Department of Chemical and Biomolecular Engineering, University of Science and Technology, Hong Kong, China, 2009.

Invited participation. Fulbright China Research Forum. Hong Kong and Macau, China, 2009.

"An integrated analysis of molecular aberrations in cancer". Invited seminar talk. Institute of Statistical Science, Academia Sinica, Taipei, Taiwan, 2009.

"Combinatorial patterns of somatic gene mutations in cancer", with A. Levine and F. McCormick. Invited talk. The Ontario Institute of Cancer Research seminar. Toronto, Canada, 2008.

"Detecting coevolution in and among protein domains and RNA sequences", with D. Haussler. Highlights Tracks Presentation. The 16th Annual International Conference Intelligent Systems for Molecular Biology (ISMB), Toronto, Canada, 2008.

"Combinatorial patterns of somatic gene mutations in cancer", with A. Levine and F. McCormick. Poster. The Cold Spring Harbor Laboratory Meeting "Genome Biology", Cold Spring Harbor, New York, U.S.A., 2008.

"Combinatorial patterns of somatic gene mutations in cancer", with A. Levine and F. McCormick. Invited talk. The Department of Biomedical Engineering seminar. University of California, Santa Cruz, California, U.S.A., 2008.

"Combinatorial patterns of somatic gene mutations in cancer", with A. Levine and F. McCormick. Invited talk. Program in Integrative Information, Computer and Application Sciences (PICASso). Princeton University, New Jersey, U.S.A., 2007.

"A general model for coevolution of biosequences", with J. Darot and D. Haussler. Poster. The Cold Spring Harbor Laboratory Meeting "Genome Biology", Cold Spring Harbor, New York, U.S.A., 2006.

"Experimental design for validating and refining pathway models of gene regulation", with C. Mak, S. McCuine, C. Workman, T. Jaakkloa, and T. Ideker. Poster. The Cold Spring Harbor Laboratory Meeting "Genome Biology", Cold Spring Harbor, New York, U.S.A., 2005.

"Inferring regulatory networks from multiple sources of genomic data", Invited talk. Berlin Center for Genome Based Bioinformatics Seminar, Berlin, Germany, 2004.

"Inferring regulatory networks from multiple sources of genomic data". Invited talk. The Reverse Engineering Group Seminar, Swiss Federal Institute of Technology, Zurich (ETH), Zurich, Switzerland, 2004.

"Inferring molecular interaction networks", with Tommi Jaakkola. Presentation. The 3rd Annual Northwest Gene Expression Conference, Seattle, Washington, U.S.A., 2003.

"Feature selection and clustering for tumor classification". Poster. The 6th Annual International Conference of the Research in Computational Molecular Biology (RECOMB), Washington DC, U.S.A., 2002.

PUBLICATIONS

Journal Articles

W. He, M.D. McCoy, R.B. Riggins, R.A. Beckman, C.H. Yeang. "Personalized cancer treatment strategies incorporating irreversible and reversible drug resistance mechanisms". npj Systems Biology and Applications, 11:70, 2025.

M.D. McCoy, C.H. Yeang, S. Tam, S. Bahnassy, R.B. Reggins, D. Parashar, R.A. Beckman. "A generalized evolutionary classifier (EC) for evolutionary guided precision medicine (EGPM)", JCO Precision Oncology, 9, 2025.

Y.B. Chen, K.L. Tiong, C.H. Yeang. "Exploring the relationship between the geometry of a fixed embedding of image data and its underlying cluster structure", Journal of Computational & Graphical Statistics, 2025.

C.W. Yeh, K.L. Hsu, S.T. Lin, W.C. Huang, K.H. Yeh, C.J. Liu. L.C. Wang, T.T. Li, S.C. Chen, C.H. Yu, J.Y. Leu, C.H. Yeang, H.S. Yen. "Altered assembly paths mitigate interference among paralogous complexes", Nature Communications 15(1):7169, 2024.

K.L. Tiong, D. Luzhbin, C.H. Yeang. "Assessing transcriptomic heterogeneity of single-cell RNASeq data by bulk-level gene expression data", BMC Bioinformatics 25(1):209, 2024.

K.L. Tiong, N. Sintupisut, M.C. Lin, C.H. Cheng, A. Woolston, C.H. Lin, M. Ho, Y.W. Lin, S. Padakanti, C.H. Yeang. "An integrated analysis of the cancer genome atlas data discovers a hierarchical association structure across thirty three cancer types", PLOS Digital Health 1(12):e0000151, 2022.

K.L. Hsu, H.C. Yen, C.H. Yeang. "Cooperative stability renders protein complex formation more robust and controllable", Scientific Reports 12(1):10490, 2022.

K.L. Tiong, Y.W. Lin, C.H. Yeang. "Characterization of gene cluster heterogeneity in single-cell transcriptomic data within and across cancer types", Biology Open 11(6):bio59256, 2022.

S. Padakanti, K.L. Tiong, Y.B. Chen, C.H. Yeang. "Genotypes of informative loci from 1000 Genomes data allude evolution and mixing of human populations". Scientific Reports 11(1):17741, 2021.

C.W. Yeh, W.C. Huang, P.H. Hsu, K.H. Yeh, L.C. Wang, P.W. Hsu, H.C. Lin, Y.N. Chen, S.C. Chen, C.H. Yeang, H.S. Yen. "The C-degron pathway eliminates mislocalizedproteins and products of deubiquitinating enzymes". EMBO Journal 40(7):e105846, 2021.

C.L. Dai, M.M. Vazifeh, C.H. Yeang, R. Tachet, R.S. Wells, M.G. Vilar, M.J. Daly, C. Ratti, A.R. Martin. "Population histories of the United States revealed through fine-scale migration and haplotype analysis". American Journal of Human Genetics 106(3):371-388, 2020.

A.R. Akhmetzhanov, J.W. Kim, R. Sullivan, R.A. Beckman, P. Tamayo, C.H. Yeang. "Modelling bistable tumour population dynamics to design effective treatment strategies", Journal of Theoretical Biology 474:88-102, 2019.

K.L. Tiong and C.H. Yeang. "MGSEA – a multivariate gene set enrichment analysis", BMC Bioinformatics 20(1):145, 2019.

K.L. Tiong and C.H. Yeang. "Explaining cancer type specific mutations with transcriptomic and epigenomic features in normal tissues", Scientific Reports 8(1):11456, 2018.

M. Simak, C.H. Yeang, and H.H. Lu. "Exploring candidate biological functioms by Boolean function networks for Saccharomyces cerevisiae". PLoS One 12(10):e0185475, 2017.

J.W. Kim, O.O. Abudayyeh, H. Yeerna, C.H. Yeang, M. Stewart, R.W. jenkins, S. Kitajima, D.J. Konieczkowski,, E. Damato, A.J. Aguirre, J. Liang, A. Liberzon, G. Alexe, J. Doench, M. Ghandi, F. Vazquez, B.A. Weir, A. Tsherniak, A. Subramanian, K. Meneses-Cime, J. Park, P. Clemons, L.A. Garraw, D. Thomas, J.S. Boehm, D.A. Barbie, W.C. Hahn, J.P. Mesirov, P. Tamayo. "Decomposing oncogenic transcriptional signatures to generate maps of divergent cellular states". Cell Systems 5(2):105-118, 2017.

Y.F. Chen, H.C. Lin, K.N. Chuang, C.H. Lin, H.S. Yen, and C.H. Yeang. "A quantitative model for the rate-limiting process of UGA alternative assignments to stop and selenocysteine codons". PLoS Computational Biology 13(2):e1005367, 2017.

C.H. Yeang and R.A. Beckman. "Long range personalized cancer treatment strategies incorporating evolutionary dynamics". Biology Direct 11(1):56, 2016.

S.J. Chou, C. Wang, N. Sintupisut, Z.X. Niu, C.H. Lin, K.C. Li, and C.H. Yeang. "Analysis of spatial-temporal gene expression patterns reveals dynamics and regionalization in developing mouse brain". Scientific Reports 6:19274, 2016.

A. Woolston, N. Sintupisut, T.P. Lu, L.C. Lai, M.H. Tsai, E.Y. Chuang, and C.H. Yeang. "Putative effectors for prognosis in lung adenocarcinoma are ethnic and gender specific". Oncotarget 6(23):19483-19499, 2015.

C.H. Yeang, G.C. Ma, H.W. Hsu, Y.S. Lin, S.M. Chang, P.J. Cheng, Y.H. Ni, and M. Chen. "Genome-wide normalized score: a novel counting algorithm to detect fetal trisomy 21 in non-invasive prenatal testing". Ultrasound in Obstetrics and Gynecology, 44(1):25-30, 2014.

I.Y. Lin, F.L. Chiu, C.H. Yeang, H.F. Chen, C.Y. Chuang, S.Y. Yang, P.S. Hou, N. Sintupisut, H.N. Ho, H.C. Kuo, and K.I. Lin. "Suppression of the SOX2 neural effector gene by PRDM1 promotes human germ cell fate in embryonic stem cells". Stem Cell Reports 2(2):189-204, 2014.

N. Sintupisut, P.L. Liu, and C.H. Yeang. "An integrated characterization of recurrent molecular aberrations in glioblastoma". Nucleic Acids Research, 41(19):8803-8821, 2013.

N. Sintupisut and C.H. Yeang. "Sequence mutations pertaining to malignancy in cancer". Journal of Data Science, 11(4):673-714, 2013.

D.H. Chen, Y.F. Chang, B.Y. Liao, and C.H. Yeang. "Functional characterization of motif sequences under purifying selection", Nucleic Acids Research, 41(4):2105-2120, 2013.

S. Suen, H.S. Lu, and C.H. Yeang. "Evolution of domain architectures and catalytic functions of enzymes in metabolic systems". Genome Biology and Evolution, 4(9):852-869, 2012.

R. A. Beckman, G.S. Schemmann, and C.H. Yeang. "Impact of genetic dynamics and single cell heterogeneity on development of nonstandard personalized medicine strategies for cancer". Proceedings of National Academic Science, U.S.A. (PNAS), 109(36):14586-14591, 2012.

C.H. Yeang, G.C. Ma, J.C. Shih, Y.S. Yang, C.P. Chen, S.P. Chang, S.H. Wu, C.S. Liu, S.J. Kuo, H.C. Chou, W.L. Hwu, A. Cameron, N. Ginsberg, M. Chen. "Genome-wide gene expression analysis implicates the immune response and lymphangiogenesis in the pathogenesis of fetal chylothorax". PLoS One, 7(4):e34901, 2012.

S.D. Li, T. Tagami, Y.F. Ho, and C.H. Yeang. "Deciphering causal and statistical relations of molecular aberrations and gene expressions in NCI-60 cell lines". BMC Systems Biology, 5(1):186, 2011.

C.H. Yeang. "Integration of metabolic reactions and gene regulation". Molecular Biotechnology, 47(1):70-82, 2011.

C.H. Yeang. "An integrated analysis of molecular aberrations in NCI-60 cell lines". BMC Bioinformatics, 11:495, 2010.

C.J. Vaske, C. House, T. Luu, B. Frank, C.H. Yeang, N. Lee, and J.M. Stuart. "A factor graph nested effects model to identify networks from genetic perturbations." PLoS Computational Biology, 9(5):e1000274, 2009.

C.H. Yeang, F. McCormick, A. Levine. "Combinatorial patterns of somatic gene mutations in cancer". The FASEB Journal 22:2605-2622, 2008.

C.H. Yeang. "Identify coevolving patterns from paralogous gene families". Evolutionary Bioinformatics 4:97-107, 2008.

C.H. Yeang, D. Haussler. "Detecting coevolution in and among protein domains". PLoS Computational Biology 3(11):e211, 2007.

C.H Yeang, J.F.J. Darot, H.F. Noller, D. Haussler. "Detecting the coevolution of biosequences – an example of RNA interaction prediction". Molecular Biology and Evolution 24(9):2119-2131, 2007.

C.H. Yeang, M. Vingron. "A joint model of regulatory and metabolic networks". BMC Bioinformatics, 7:332-354, 2006.

C.H. Yeang, T. Jaakkola. "Modeling the combinatorial functions of multiple transcription factors". Journal of Computational Biology (JCB), 13(2): 463-480, 2006.

C.H. Yeang, C. Mak, C. Workman, S. McCuine, T.Jaakkola, T. Ideker. "Validation and refinement of gene-regulatory pathways on a network of physical interactions". Genome Biology, 6:R62.1-R62.10, 2005.

C.H. Yeang, T. Ideker, T. Jaakkola. "Physical network models". Journal of Computational Biology (JCB), 11(2-3): 243-262, 2004.

S. Ramaswamy, P. Tamayo, R. Rifkin, S. Mukherjee, C.H. Yeang, M. Angelo, C. Ladd, M. Reich, E. Latulippe, J.P. Mesirov, T. Poggio, W/ Gerald, M. Loda, E.S. Lander, T.R. Golub.. "Multiclass cancer diagnosis using tumor gene expression signatures". Proceedings of National Academy of Science U.S.A. (PNAS) 98:15149-15154, 2001.

Peer-reviewed Conference Papers

Y.B. Chen, K.L. Tiong, C.H. Yeang. Clustering image data with a fixed embedding. Proceedings, 21st IEEE International Conference on Machine Learning and Applications (ICMLA), Nassau, Bahamas, 2022.

C.H. Yeang, L.C. Huang, W.C. Liu. Recurrent structural motifs reflect characteristics of distinct networks. Proceedings, The 2012 IEEE/ACM International Conference on Advances in Social Networks Analysis and Mining (ASONAM), Istanbul, Turkey, 2012.

C.H. Yeang. A probabilistic model of quantum systems. Proceedings, the 9th International Conference on Machine Learning and Applications (ICMLA), Washington DC, USA, 2010.

C.H. Yeang. Quantifying the strength of natural selection of a motif sequence. Proceedings, the 10th Workshop on Algorithms in Bioinformatics (WABI), Liverpool, U.K., 2010.

C.H. Yeang. Exact loopy belief propagation on Euler graphs. Proceedings, the 2010 World Congress in Computer Science, Computer Engineering and Applied Computing (WORLDCOMP), Las Vegas, U.S.A., 2010.

C.H. Yeang. Analysis of the bipartite networks of domain compositions and metabolic reactions. Proceedings, the Second International Conference on Biomedical Engineering and Informatics (BMEI), Tianjin, China, 2009.

C.H. Yeang and N.A. Baas. Evolution of domain compositions in the metabolic networks of human and Escherichia coli. Proceedings, the 2009 World Congress in Computer Science, Computer Engineering and Applied Computing (WORLDCOMP), Las Vegas, U.S.A., 2009.

P.N. Kanabar, C.J. Vaske, C.H. Yeang, F.H. Yildiz, and J.M. Stuart. Inferring disease-related pathways using a probabilistic epistasis model. Proceedings, the 15th Pacific Symposium of Biocomputing (PSB), Hawaii, U.S.A., 2009.

L. Perez-Breva, L.E. Ortiz, C.H. Yeang, T. Jaakkola. "Game theoretic algorithms for protein-DNA binding". Proceedings, the 12th Annual Conference on Information Processing (NIPS), Vancouver, Canada, 2006.

J. Darot, C.H. Yeang (co-first author) and D. Haussler. "Detecting the dependent evolution of biosequences". Proceedings, the 10th Annual International Conference of the Research in Computational Molecular Biology (RECOMB), Venice, Italy, 2006.

C.H. Yeang and T. Jaakkola. "Modeling the combinatorial functions of multiple transcription factors". Proceedings, the 9th Annual International Conference of the Research in Computational Molecular Biology (RECOMB), Boston, Massachusetts, U.S.A., 2005.

C.H. Yeang and M. Szummer. "Continuous Markov random walks". Proceedings, the 18th conference of uncertainty in artificial intelligence (UAI), Acapulco, Mexico, 2003.

C.H. Yeang and T. Jaakkola, "Physical network models and multi-source data integration". Proceedings, the 7th conference on research in computational biology (RECOMB), Berlin, Germany, 2003.

C.H. Yeang and T. Jaakkola. "Time-series analysis of gene expression and location data". Proceedings, the 3rd IEEE conference on bioinformatics and bioengineering (BIBE), Bethesda, Maryland, U.S.A., 2003.

C.H. Yeang. "An information geometric perspective on active learning". Proceedings, the 13th European conference on machine learning (ECML), Helsinki, Finland, 2002.

C.H. Yeang, S. Ramaswamy, P. Tamayo, S. Mukherjee, R.M. Rifkin, M. Angelo, M. Reich, E. Lander, J. Mesirov, T. Golub. "Molecular classification of multiple tumor types". Proceedings, the 9th conference on intelligent systems for molecular biology (ISMB), Copenhagen, Denmark, 2001.

C.H. Yeang, A,A, Ismail, and J. Ferreira. "Distributed GIS for monitoring and modeling urban air quality". Proceedings, the 7th conference on computers in urban planning and urban management (CUPUM), Venice, Italy, 1999.

C.H. Yeang, "GISVE: a virtual environment for aiding landscape design processes". Proceedings, the 5th conference on computers in urban planning and urban management (CUPUM), Mumbai, India, 1997.

Book Chapters

C.H. Yeang. "Integration of metabolic reactions and gene regulation". In Plants Systems Biology. Series of Methods in Molecular Biology, Vol 553. Belostotsky D.A. (Ed.), 2009.

Thesis

"Inferring regulatory networks from multiple sources of genomic data". Sc. D. thesis. Massachusetts

Institute of Technology. September 2004.

TEACHING

Biological computing II. Academia Sinica The International Graduate Program. Spring 2009-present.

Biomedical Statistics. Academia Sinica/National Taiwan University Joint Graduate Program of Translational Medicine. Spring 2011-2014.

Seminar on Systems Biology and Genomics. Academia Sinica/National Taiwan University Joint Graduate Program of Systems Biology and Genomics. Spring 2011.

Inferring gene networks with probabilistic graphical models. Tutorial lecture. The Eighth Asia Pacific Bioinformatics Conference, Bangalore, India, 2010.

MEMBERSHIPS AND SERVICES

Editorial Board Member, The Scientific World Journal
Editorial Board Member, Frontiers in Statistical Genetics and Methodology.
Organizer of the workshop on cancer genomics, The International Society for Computational Biology Asia Meeting, Shenzhen, China, 2012 (ISCB-Asia 2012).
Member of the International Society for Computational Biology (ISCB).

REVIEW EXPERIENCE

Science.
Nature Methods.
Nature Biotechnology.
PLoS Computational Biology.
PLoS One.
PLoS Digital Health
Oncogene.
Oncotarget.
Bioinformatics.
Molecular Biology and Evolution.
Nucleic Acids Research.
BMC Bioinformatics.
BMC Evolutionary Biology.
BMC Systems Biology.
BMC Genomics.
BMC Medical Genomics.
Scientific Reports.
IEEE Transactions on Signal Processing.
Neuroinformatics.
Transactions on Social Computing.
Evolutionary Bioinformatics.
ACM Conference on Bioinformatics, Computational Biology and Biomedicine (ACM-BCB), 2011.
Pacific Symposium of Biocomputing (PSB), 2004.
The 8th Conference on Research in Computational Biology (RECOMB), 2004.

The 7th Conference on Research in Computational Biology (RECOMB), 2003.

PERSONAL DATA

Languages: English, Chinese, German, French.