Yao-Ting Huang (黃耀廷) *Curriculum Vitae*

PERSONAL INFORMATION

Professor, Department of Computer Science and Information Engineering, National Chung Cheng University.

Head, Division of Information Education, Office of Information Technology, National Chung Cheng University.

RESEARCH INTEREST

We study infectious diseases using NGS/TGS and develop algorithms/software with publications in leading journals including *Genome Research*, *Genome Biology*, and *Bioinformatics*.

PUBLICATION

Journal papers (*: corresponding author, §: equally contributed)

[1] Chiou, C.-S., Chen, B.-H., Wang, Y.-W., Kuo, N.-T., Chang, C.-H., Huang, Y.-T.* Correcting modification-mediated errors in nanopore sequencing by nucleotide demodification and reference-based correction, *Communications Biology*, 2023.

[2] Liao, Y.-C., Huang, Y.-T.§, Tseng, C.-H., Liu, C.-W., Liu, P.-Y.§ Comparative genomics identified PenR E151V substitution associated with carbapenem-resistance Burkholderia cepacia complex and a novel Burkholderia cepacia complex specific OXA-1043 subgroup, *Infection and Drug Resistance,* 2023.

[3] Huang, Y.-T., Mao, Y.-C., Tseng, C.-H., Liu, C.-W., Liu, P.-Y. Identification of combinatorial mutations associated with colistin resistance in Shewanella algae, *Microbes Infection*, 2023.

[4] Huang, Y.-T., Yang, M.-Y., Mao, Y.-C., Lee, D.Y., KUO, Y.-L., Tseng, C.-H., Liu, C.-W., Fu, Y.-C., and Liu, P.-Y. Identification of *Cutibacterium modestum* in spondylitis by metagenomics analysis, *In Vivo*, 2023.

[5] Yeh, T.-K., Lin, K.-P., Chuang, Y.-C., Wang, L.-A., Chen, C.-J., Lee, D.-Y., Huang, Y.-T.*, Liu, Po-Yu, Clinical metagenomics-assisted diagnosis of relapsed HIV-associated cryptococcal meningitis, *International Journal of STD & AIDS*, 2023.

[6] Tseng, C-H., Huang, Y.-T., Mao, Y.-C., Lai, C.-H., Yeh, T.-K., Ho, C.-M. and Liu, P.-Y. Insight into the Mechanisms of Carbapenem Resistance in Klebsiella pneumoniae: A study on IS26 integrons, beta-Lactamases, porin modifications, and plasmidome analysis, *Antibiotics*, 2023.

[7] Huang, P.-H. §, Huang, Y.-T. §, Lee, P.-H., Tseng, C.-H., Liu, P.-Y. and Liu, C.-W. Diagnosis of Legionnaires' Disease assisted by next-generation sequencing in a patient with COVID-19, *Infection and Drug Resistance*, 2023.

[8] Liu, C.-W., Cheng, J.-F., Tung, K.-C., Hong, Y.-K., Lin, J.-H., Lin, Y.-H., Tsai, C.-A., Lin, S.-P., Chen, Y.-C., Shi, Z.-Y., Huang, Y.-T.*, Liu, P.-Y. Evolution of trimethoprim/sulfamethoxazole resistance in *Shewanella algae* from the perspective of comparative genomics and global phylogenic analysis, *Journal of Microbiology, Immunology and Infection*, 2022.

[9] Yang, W.-T., Chiang, I., Tseng, C.-H., Cheng, C., Lin, J.-H., Liu, P.-Y., and Huang, Y.-T.* Metagenomic sequencing and histology on a chronic wound identified Epstein-Barr virus-

associated lymphoma, *Evolutionary Bioinformatics*, 2022.

[10] Yang, W.-T., Chiu, I.-J., Huang, Y.-T.*, Liu, P.-Y. Comparative genomics revealed fluoroquinolone resistance determinants and OmpF deletion in carbapenem-resistant *Escherichia coli*, *Frontiers in Microbiology*, 2022.

[11] Lin, J.-H., Chen, L.-C., Yu, S.-C., Huang, Y.-T.* LongPhase: an ultra-fast chromosome-scale phasing algorithm for small and large variants, *Bioinformatics*, 2022.

[12] Yeh, T.-K. Li, Z.-H., Huang, Y.-T.*, Liu, P.-Y. COVID-19 associated bacteremia with *Chryseobacterium indologenes* co-harboring blaIND-2, blaCIA and blaCcrA, *Infection and Drug Resistance*, 2022.

[13] Li, S.-Y., Huang, Y.-E., Chen, J.-Y., Lai, C.-H., Mao, Y.-C., Huang, Y.-T.*, Liu, P.-Y. Genomics of *Ochrobactrum pseudogrignonense* (newly *Brucella pseudogrignonense*) reveals a new blaoxa subgroup, *Microbial Genomics*, 2021.

[14] Chang, Y.-L., Liao, Y.-W., Chen, M.-H., Chang, S.-Y., Huang, Y.-T.*, Ho, B.-C., Yu, S.-L. IKKε isoform switching governs immune response against EV71 infection, *Communications Biology*, 2021.

[15] Huang, W.-H., Kao, C.-C., Mao, Y.-C., Lai, C.-S., Lai, K.-L., Lai, C.-H., Tseng, C.-H., Huang, Y.-T.*, Liu, P.-Y. *Shewanella algae* and *Morganella morganii* coinfection in cobra-bite wound: a genomic analysis, *Life*, 2021.

[16] Li, S.-Y., Kao, C.-C., Hu, Y.-C., Lai, C.-H., Jiang, Y.-P., Mao, Y.-C., Huang, Y.-T.*, Liu, P.-Y. *Arthrobacter woluwensis* Bacteremia: a clinical-genomic investigation, *Pathogens*, 2021.

[17] Huang, Y.-T.*, Liu, P.-Y., and Shih, P.-W. Homopolish: a method for the removal of systematic errors in Nanopore sequencing by homologous polishing, *Genome Biology,* 2021.

[18] Huang, Y.-T., Yeh, T.-K., Chen, W.-H., Shih, P.-W., Mao, Y.-C., Lu, M.-C., Chen, C.-M., P.-Y. Liu. Genome analysis of *Enterobacter hormaechei* identified ISEcp1 in association with blaCTX-M-236, a new blaCTX-M variant located in both chromosome and plasmid, *Journal of Global Antimicrobial Resistance*, 2021.

[19] Tseng, L.-C., Wang, J.-M., Lu, H.-Y., Mao, Y.-C., Lai, K.-L., Tseng, C.-H., Huang, Y.-T.*, Liu, P.-Y. *Elizabethkingia* intra-abdominal infection and related Trimethoprim Sulfamethoxazole resistance: a clinical-genomic study, *Antibiotics*, 2021.

[20] Chen, Y.-J., He, G.-C., Cheng, J.-F., Lee, Y.-T., Hung, Y.-H., Chen, W.-H., Huang, Y.-T.*, Liu, P.-Y. Comparative genomics reveals insights into characterization and distribution of quorum sensing-related genes in *Shewanella algae* from marine environment and clinical sources, *Comparative Immunology, Microbiology and Infectious Diseases*, 2020.

[21] Tseng, C.-H., Cheng, J.-F., Chen. S.-Y., Chen, W.-H., Shi, Z.-Y., Lin, Y.-H., Tsai, C.-A., Lin, S.-P., Chen, Y.-C., Lin, Y.-C., Huang, Y.-T.*, Liu, P.-Y. Detection of S83V GyrA mutation in quinolone-resistant Shewanella algae using comparative genomics, *Journal of Microbiology, Immunology and Infection*, 2020.

[22] Wang, J.-H., He, G.-C., Huang, Y.-T.*, and P-Y Liu, Comparative Genomics Reveals Pathogenicity-Related Loci in *Shewanella algae*, *Canadian Journal of Infectious Diseases and Medical Microbiology*, 2020.

[23] Chen, Y.-J., Tung, K.-C., Hong, Y.-K., Chen, S.-Y., Huang, Y.-T.*, and Po-Yu Liu. Genome Sequence of colistin-resistant bacteremic *Shewanella algae* carrying the beta-lactamase gene blaOXA-55, *Canadian Journal of Infectious Diseases and Medical Microbiology*, 2019.

[24] Huang, Y.-T., Cheng, J.-F., Wu, Z.-Y., Tung, K.-C., Chen, Y.-J., Hong, Y.-K., Chen, S.-Y., Liu, P.-Y. Genomic and phylogenetic characterization of *Shewanella xiamenensis* isolated from giant grouper (*Epinephelus lanceolatus*) in Taiwan. *Zoonoses and Public Health*, 2019.

[25] Lin, J.-H., Wu, Z.-Y., Gong, L., Wong, C.-H., Chao, W.-C., Yen, C.-M., Wang, C.-P., Wei, C.-L., Huang, Y.-T.*, Liu, P.-Y. Complex microbiome in brain abscess revealed by whole-genome culture-independent and culture-based sequencing, *Journal of Clinical Medicine*, 2019.

[26] Wu, Z.-Y., Huang, Y.-T. Chao, W.-C., Ho, S.-P., Cheng, J.-F., Liu, P.-Y. Reversal of carbapenem-resistance in *Shewanella algae* by CRISPR/Cas9 genome editing, *Journal of Advanced Research*, 2019.

[27] Wu, Z.-Y., Ho, S.-P., Cheng, J.-F., Tung, K.-C., Hong, Y.-K., Chen, S.-Y., Chen, Y.-J., Huang, Y.-T.*, Liu, P.-Y. Whole-genome characterization of *Shewanella algae* strain SYT3 isolated from seawater reveal insight into hemolysis, *Future Microbiology*, 2018.

[28] Lee, Y.-H. Tung, K.-C., Cheng, J.-F., Wu, Z.-Y., Chen, S.-Y., Hong, Y.-K., Huang, Y.-T.*, Liu., P.-Y. Genomic characterization of carbapenem-resistant *Shewanella algae* isolated from Asian hard clam (Meretrix lusoria), *Aquaculture*, 2018.

[29] Tseng, S.-Y., Tung, K.-C., Cheng, J.-F., Lee, Y.-H., Wu, Z.-Y., Hong, Y.-K., Chen, S.-Y., Huang, Y.-T.*, Liu, P.-Y. Genome characterization of bile-isolated *Shewanella algae* ACCC: an insight into bile salt adaption, *Gut Pathogens*, 2018.

[30] Huang, Y.-T., Chuang, W.-Y., Ho, B.-C., Wu, Z.-Y., Kuo, R., Ko M., Liu, P.-Y. Comparative genomics reveals diverse capsular polysaccharide synthesis gene clusters in emerging *Raoultella planticola*, *Memórias do Instituto Oswaldo Cruz*, 2018.

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[32] Huang, Y.-T., Chen, C.-M., Ho, B.-C., Wu, Z-Y., Kuo, C., Liu, P.-Y. Genome sequencing and comparative analysis of *Stenotrophomonas acidaminiphila* reveal evolutionary insights into sulfamethoxazole resistance, *Frontiers in Microbiology*, 2018.

[33] Huang, Y.-T., Tang, Y.-Y., Cheng, J.-F., Wu, Z-Y., Mao, Y.-C., Liu, P.-Y. Genome analysis of multidrug-resistant *Shewanella algae* isolated from human soft tissue sample, *Frontiers in Pharmacology*, 2018.

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W. Shih M.-C. Concomitant loss of NDH complex-related genes within chloroplast and nuclear genomes in some orchids. *The Plant Journal*, 2017.

[38] Ting, C.-K., Lin, C.-S., Chan, M.-T., Chen, J.W., Chuang, S.-T., <u>Huang, Y.-T.</u>* A genetic algorithm for diploid genome reconstruction using paired-end sequencing, *PLOS One*, 2016.

[39] Yeh C.M., Chang L.Y., Lin S.H., Chou J.L., Hsieh H.Y., Zeng L.H., Chuang S.Y., Wang H.W., Dittner C., Lin C.Y., Lin J.M., <u>Huang Y.T.</u>, Ng E.K., Cheng A.S., Wu S.F., Lin J., Yeh K.T., Chan M.W. Epigenetic silencing of the NR4A3 tumor suppressor, by aberrant JAK/STAT signaling, predicts prognosis in gastric cancer, *Scientific Reports*, 2016.

[40] <u>Huang, Y.-T.</u>* and Liao, C.-F. Integration of string and de Bruijn graphs for genome assembly, *Bioinformatics*, 2016.

[41] Lin C.-S., Hsu C.-T., Liao D.-C., Chang W.-J., Chou M.L., <u>Huang, Y.-T.</u>, Chen J.-W., Ko S.-S., Chan M.-T., Shih M.-C. Transcriptome-wide analysis of the MADS-box gene family in the orchid Erycina pusilla. *Plant Biotechnology Journal*, 2016.

[42] Ruhlman, T., Chang, W.-T., Chen, J.-W., <u>Huang, Y.-T.</u>, Chan M.-T., Zhang J., Liao D.-C., Blazier J.-C., Jin X., Shih M.-C., Jansen R.K., Lin C.-S. NDH expression marks major transitions in plant evolution and reveals coordinate intracellular gene loss, *BMC Plant Biology*, 2015.

[43] Lin, C.-S. [§], Chen, J-W. [§], <u>Huang, Y.-T.</u> [§], et al. The location and translocation of NDH genes of chloroplast origin in the Orchidaceae family, *Scientific Reports*, 2015.

[44] Shih, M.-C., Chou, M.-L., Yue J.-J., Hsu C.-T., Chang W.-J., Ko S.-S., Liao D.-C., <u>Huang Y.-T.</u>, Chen J.-J., Yuan J.-L., Gu X.-P., Lin C.-S. BeMADS1 is a key to delivery MADSs into nucleus in reproductive tissues- De novo characterization of Bambusa edulis transcriptome and study of MADS genes in bamboo floral development, *BMC Plant Biology*, 2014.

[45] Lee, M.S., Lin, Y.S., Deng, Y.F., Hsu, W.T., Shen, C.C., Cheng, Y.H., <u>Huang, Y.-T.</u>, Li, C. Modulation of alternative splicing by expression of small nuclear ribonucleoprotein polypeptide N., *FEBS Journal*, 2014.

[46] Chuang, T.-J., Wu, S.-Z., and <u>Huang, Y.-T.</u>* A Novel Framework for the Identification and Analysis of Duplicons between Human and Chimpanzee," *BioMed Research International*, 2013.

[47] Lin, C.-S.[§], Chen, J.-W.[§], <u>Huang, Y.-T.</u>[§], *et al*., Catalog of Erycina pusilla miRNA and categorization of reproductive phase-related miRNAs and their target gene families, *Plant Mole Biol*, 2013.

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[49] Chou, M-L, Shih, M.-C., Chan, M.-T., Liao, S.-Y., Hsu, C-T., <u>Haung, Y.-T.</u>, *et al*., Global Transcriptome Analysis and Identification of a CONSTANS-Like Gene Family in the Orchid Erycina pusill, *Planta*, 2013.

[50] Pačes J., <u>Huang Y.-T.</u>, Pačes V., Rídl, J.and Chang C.-M. New Insight into Transcription of Human Endogenous Retroviral Elements, *New Biotechnology*, 2012.

[51] Wang M.-C., Chen F.-C., Chen Y.-Z., <u>Huang Y.-T.</u>, Chuang T.-J. LDGIdb: a database of gene interactions inferred from long-range strong linkage disequilibrium between pairs of SNPs, *BMC Research Notes*, 2012.

[52] <u>Huang, Y.-T.</u>* and Wu, M.-H. Inference of Chromosome-Specific Copy Numbers Using Population Haplotypes, *BMC Bioinformatics*, 12:194, 2011.

[53] <u>Huang, Y.-T.</u>*, Chang, C-J., and Chao, K.-M. The Extent of Linkage Disequilibrium and Computational Challenges of Single Nucleotide Polymorphisms in Genome-Wide Association Studies, *Current Drug Metabolism*, 12:498-506, 2011.

[54] Ting, C.-K., Chen, F.-C., <u>Huang, Y.-T.</u>* Multi-objective tag SNPs selection using evolutionary algorithms, *Bioinformatics*, 26(11): 1446-1452, 2010.

[55] <u>Huang, Y.-T.</u>*, Chuang, S.-Y., Lin K.-H., Li Y.-D., and Wang S.-W. Computational Approaches for the Discovery and Analysis of Structural Variations, *International Journal of Systems and Synthetic Biology*, 2010.

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[57] <u>Huang, Y.-T.</u> and Chao, K.-M. A new framework for the selection of tag SNPs using multimarker haplotypes. *Journal of Biomedical Informatics*, 41:953-961, 2008.

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[61] <u>Huang, Y.-T.</u>, Zhang, K., Chen, T., and Chao, K.-M. Selecting additional tag SNPs for tolerating missing data in genotyping. *BMC Bioinformatics*, 6:263, 2005.

[62] Lai, Y.-C., Lin, Phone and <u>Huang, Y.-T.</u> Design and implementation of a wireless Internet remote access platform, *Wireless Communications and Mobile Computing*, 6: 413-429, 2004.

Conference papers (*: corresponding author)

[1] <u>Huang, Y.-T.</u>* and Lee, Y.-D. A framework for the discovery of structural variations using next-generation sequencing. National Computing Symposium, Taiwan, 2011.

[2] Kuo-Wei Chen, Chung-Chan Tsai, Chi-Li Tsai and <u>Huang, Y.-T.</u>* On the selection of tag SNPs for capturing human leukocyte antigene, The 26th Workshop on Combinatorics Math and Computation Theory, Taiwan, 241-248, April 2009.

[3] Ren-Fu Wang, Zi-Jien Ho, Wen-Ting Fan, and <u>Huang, Y.-T.</u>* Efficient algorithms for finding a heaviest common increasing subsequence, The 26th Workshop on Combinatorics Math and Computation Theory, Taiwan, 241-248, April 2009.

[4] Shien-Zu Wu and <u>Huang, Y.-T.</u>* A hidden Markov model for identifying duplicons, The 4th Sino-Japanese Optimization Meeting (SJOM), Taiwan, 2008.

[5] Huang, Y.-T. and Chao, K.-M. Approximation algorithms for the optimization problems of SNPs and haplotypes, IEEE Emerging Information Technology Conference (EITC), Taiwan, 2005.

[6] Huang, Y.-T., Chao, K.-M, and Chen, T. An approximation algorithm for haplotype inference by maximum parsimony. The 20th Annual ACM Symposium on Applied Computing (SAC), 146-150, USA, 2005.

[7] Huang, Y.-T., Zhang, K., Chen, T. and Chao, K.-M. Approximation algorithms for the selection of robust tag SNPs. The 4th Workshop on Algorithms in Bioinformatics (WABI), *Lecture Notes in Computer Science / Lecture Notes in Bioinformatics*, 278-289, Norway, 2004.

[8] Huang, Y.-T. and Chao, K.-M. On the selection of robust tag SNPs. The 21th Workshop on Combinatorics Math and Computation Theory, Taiwan, 241-248, 2004.

Book chapters

[1] Huang, Y.-T., Zhang, K., Chen, T., and Chao, K.-M. "Approximation Algorithms for the Selection of Robust Tag SNPs," Chapter 59 of the book "Handbook of Approximation Algorithms and Metaheuristics," edited by Teofilo F. Gonzalez (University of California, Santa Barbara), Chapman & Hall/CRC Press, USA, 2007.

Local Journals

[1] Chang, C.-J., Huang, Y.-T., and Chao, K.-M. Hybrid approaches for the selection of tag SNPs based on block partition and linkage disequilibrium, *Journal of Computers*, 21(4):11-23, 2011.

[2] 「單核苷酸多型性之簡介與研究回顧」, 生物醫學期刊, 2009.

[3] Huang, Y.-T. Inference of Haploid Copy Number, *Information Retrieval and Pattern Recognition*, 2008.

Patent

[1] 中華民國專利(I290692, 2007/12/01)：「以可攜式電子裝置進行遠端監控的方法」。

EDUCATION

- ❖ Ph.D., Computer Science and Information Engineering, National Taiwan University, 2003-2006.
- ❖ M.S., Computer Science and Information Engineering, National Taiwan University, 2001-2003.
- ❖ B.S., Computer Science and Information Engineering, National Chiao Tung University, 1997-2001.

PROFESSIONAL EXPERIENCE

- ❖ 台灣基因體暨遺傳學會理事, 2017-2023
- ❖ 台灣精準健康暨毒理基因體學會理, 2022-2023
- ❖ Associate Editor, Journal of Information Science and Engineering, 2020-2023.
- ❖ Professor, Department of Computer Science and Information Engineering, National Chung Cheng University, 2018/8~

- ❖ Associate professor, Department of Computer Science and Information Engineering, National Chung Cheng University, 2012/8~2018/7
- ❖ Assistant professor, Department of Computer Science and Information Engineering, National Chung Cheng University, 2007/8~2012/7.
- ❖ Postdoctoral research fellow, Computational Genomics Laboratory, Genomics Research Center, Academia Sinica, 2006/8 – 2007/7.

AWARDS AND HONORS

- ❖ 1999, 國立交通大學資訊工程系專題競賽優勝 (First Prize of Project Competition, Department of Computer Science and Information Engineering, National Chiao Tung University)
- ❖ 2000, 國立交通大學十屆思源科技研發競賽第一名 (First Prize of Undergraduate Research and Development Contest, National Chiao Tung University)
- ❖ 2001, 中國大陸第七屆大專生軟體研發競賽台灣代表團(於西安交通大學)
- ❖ 2001, 行政院國科會國家高速電腦中心全國軟體設計競賽第三名 (Third Prize of Software Contest by National Center for High-performance Computing)
- ❖ 2002, MobileHero經濟部工業局無線通訊軟體研發競賽第一名 (First Prize of Mobile Hero Contest by Industrial Development Bureau of Ministry of Economic Affairs)
- ❖ 2002, 中國科技管理學會學生創新育成競賽第二名
- ❖ 2011, 中正大學教學優良教師彈性薪資獎勵

ACADEMIC ACTIVITY
Programming Chair/Committee

- ❖ International Computer Symposium (ICS), (2016, Chair of workshop on algorithms, bioinformatics, and computation theory)
- ❖ Taiwan Epigenomics Symposium and International Conference on Systems Biology, (2016, Session Chair).
- ❖ 次世代定序生物資訊暨轉譯醫學研討會(2015, Chair)
- ❖ IEEE International Conference on Bioinformatics and Biomedical Engineering (BIBE) (2011, Program Committee Member).
- ❖ International Symposium on Application of NGS on Genomics and Epigenomics (2011, Program Committee Member, Session Chair)
- ❖ National Computer Symposium, Algorithms and Bioinformatics Workshop (2011, Program Committee Member, Session Chair)
- ❖ National Computer Symposium, Algorithms and Bioinformatics Workshop (2009, Program Committee Member)
- ❖ International Computer Symposium (PC Chair on Algorithm, Bioinformatics, and Combinatorics), 2016.

Programming Contests

- ❖ 全國大專ITSA程式設計桂冠挑戰賽出題委員與比賽裁判：2015, 2016, 2017, 2018
- ❖ 國際大專院校程式設計競賽(PTC)出題委員：2012, 2013, 2014, 2015, 2016, 2017, 2018
- ❖ 大學程式能力檢定(Collegiate Programming Examination)出題委員：2017

- ❖ ACM-ICPC Asia Chiayi Regional Contest出題委員與比賽裁判：2013
- ❖ 中正大學資訊工程系程式檢定委員與出題：2010、2011
- ❖ 中正大學校內程式競賽委員與出題：2009、2010、2011
- ❖ 南區大專院校程式設計競賽(南程盃)出題：2009、2010
- ❖ 全國大專電腦軟體設計競賽(大專盃)委員與出題：2007