Jhih-Hua Jhong 鍾智樺

Ph.D
Department of Computer Science and Engineering, Yuan Ze University

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Research Interests

I am interested in combining meta'omics (methods that obtain high-throughput information on microbial communities such as metagenomics and metatranscriptomics) analysis with machine learning approaches to learn about microbial communities in different environments. My work is a mix of method and tool development with applications. A large fraction of my time is spent scaling up algorithms and pipelines to work on very-large problems. I wish to answer basic questions on what determines the structure of a microbial community in a given environment and what are the differences/similarities between different environments.

Education

- **Ph.D. in Bioinformatics** (07/2015 – 02/2021)
  Department of Computer Science and Engineering, Yuan Ze University, Taiwan

- **B.S. in Applied Mathematics** (09/2009 – 06/2012)
  Department of Applied Mathematics, Chung Yuan Christian University, Taiwan.

Positions and Work Experience

- 05/2021 – 08-2022 Engineer
  ACT Genomics Co. Ltd
  1. Development, validation and testing the production of cancer genetic detection:
     - Verification and validation analyses for new products (NGS assays for clinical diagnostics)
     - Data analysis and visualization for supporting product development
  2. Software development, automation and validation (IQ/OQ):
     - Software automation, function testing, version control and container deployment
     - Project management with Jira Scrum

3. Bioinformatics pipeline development
    - SaaS development through Nextflow platform

- 12/2018 – 02/2021 Research Assistant
  The Chinese University of Hong Kong, Shenzhen

- 07/2016 – 12/2020 Research Assistant (part-time job)
  Tao Yuan General Hospital

- 07/2015 – 06/2016 Research Assistant (part-time job)
  Graduate Institute of Biomedical Informatics, Taipei Medical University

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Fields of Specialty

Bioinformatics, Big data analytics, Computational system biology, Microarray/RNA-seq (NGS) data analysis, Metagenomics/Metatranscriptomics, Biological databases and tools development, Data mining and machine learning, Transcriptome assembly.

Skills

Programming		
Linux bash	Advanced	●●●●○
Python	Advanced	●●●●○
Development		
PHP	Excellent	●●●●●
HTML	Advanced	●●●●○
CSS	Intermediate	●●●○○
Database		
MySQL	Excellent	●●●●●
Version control		
GitHub	Excellent	●●●●●
Bitbucket	Excellent	●●●●●
Docker	Advanced	●●●●○
Frameworks		
WDL	Intermediate	●●●○○
Nextflow	Advanced	●●●●○
Scrum		
Jira	Excellent	●●●●●

Personal Strengths

- Good organizational and communication skill.
- Enjoy teamwork, but can also work independently.
- Strongly committed to laboratory safety and hygiene.
- Positive attitude towards learning.
- Adaptable.

Career Objectives

I’ve learnt the skills necessary to become a bioinformatics engineer, but find my passion lies towards microbiology, antimicrobial resistance and disease control overall leading up to clinical research and drug development. I look forward to working with a global organization which offers challenging opportunities that would allow me to contribute to the organization and to humankind. I hope to apply my research knowledge to clinical treatment, including the development of possible new antibiotic drugs to fight bacterial and fungal infections.

Publication Google Scholar Profile: https://scholar.google.com.tw/citations?user=fFkd2QMAAAAJ

- Journal Papers († Co-first authorship)

1. **Jhih-Hua Jhong**, Wan-Hua Tsai, Li-Chan Yang, Chia-Hsuan Chou, Tzong-Yi Lee, Yao-Tsung Yeh, Cheng-Hsieh Huang, Yueh-Hsia Luo (2022). Heat-Killed Lacticaseibacillus paracasei GMNL-653 Exerts Antiosteoporotic Effects by Restoring the Gut Microbiota Dysbiosis in Ovariectomized Mice. Front Nutr. 2022 Feb 4;9:804210. (SCI, 2022 IF: 6.01)

2. Yigang Chen†, Lantian Yao†, Yun Tang, **Jhih-Hua Jhong**, Jingting Wan, Jingyue Chang, Shidong Cui, Yijun Luo, Xiaoxuan Cai, Wenshuo Li, Qi Chen, Hsi-Yuan Huang, Zhuo Wang, Weiming Chen, Tzu-Hao Chang, Fengxiang Wei, Tzong-Yi Lee, Hsien-Da Huang (2022). CircNet 2.0: an updated database for exploring circular RNA regulatory networks in cancers. Nucleic Acids Res, 50(D1), D93-D101. (SCI, 2022 IF:**16.971**)

3. **Jhih-Hua Jhong†**, Lantian Yao†, Yuxuan Pang†, Zhongyan Li, Chia-Ru Chung, Rulan Wang, Shangfu Li 1, Wenshuo Li, Mengqi Luo, Renfei Ma, Yuqi Huang, Xiaoning Zhu, Jiahong Zhang, Hexiang Feng, Qifan Cheng, Chunxuan Wang, Kun Xi, Li-Ching Wu, Tzu-Hao Chang, Jorng-Tzong Horng, Lizhe Zhu, Ying-Chih Chiang, Zhuo Wang, Tzong-Yi Lee (2022). dbAMP 2.0: updated resource for antimicrobial peptides with an enhanced scanning method for genomic and proteomic data. Nucleic Acids Res, 50(D1), D460-D470. (SCI, 2022 IF:**16.971**)

4. Zhongyan Li†, Shangfu Li†, Mengqi Luo, **Jhih-Hua Jhong**, Wenshuo Li, Lantian Yao, Yuxuan Pang, Zhuo Wang, Rulan Wang, Renfei Ma, Jinhan Yu, Yuqi Huang, Xiaoning Zhu, Qifan Cheng, Hexiang Feng, Jiahong Zhang, Chunxuan Wang, Justin Bo-Kai Hsu, Wen-Chi Chang, Feng-Xiang Wei, Hsien-Da Huang, Tzong-Yi Lee "Dbptm in 2022: An Updated Database for Exploring Regulatory Networks and Functional Associations of Protein Post-Translational Modifications." Nucleic Acids Res 50, no. D1 (Jan 7 2022): D471-D79. (SCI, 2022 IF:**16.971**)

5. Lizhi He, **Jhih-Hua Jhong**, Qi Chen, Kai-Yao Huang, Karin Strittmatter, Johannes Kreuzer, Michael DeRan, Xu Wu, Tzong-Yi Lee, Nikolai Slavov, Wilhelm Haas and Alexander G Marneros (2021). Global characterization of macrophage polarization mechanisms and identification of M2-type polarization inhibitors. Cell Rep, 37(5), 109955. (SCI, 2021 IF: **9.423**)

6. Yuxuan Pang†, Lantian Yao†, **Jhih-Hua Jhong†**, Zhuo Wang, Tzong-Yi Lee (2021). AVPIden: a new scheme for identification and functional prediction of antiviral peptides based on machine learning approaches. Brief Bioinform, 22(6). (SCI, 2021 IF: **11.622**)

7. Yuxuan Pang, Zhuo Wang, **Jhih-Hua Jhong**, Tzong-Yi Lee (2021). Identifying anti-coronavirus peptides by incorporating different negative datasets and imbalanced learning strategies. Brief Bioinform, 22(2), 1085-1095. (SCI, 2021 IF: **11.622**)

8. Wei-Te Lei†, Kai-Yao Huang†, **Jhih-Hua Jhong**, Chia-Hung Chen and Shun-Long Weng (2021). Metagenomic analysis of the gut microbiome composition associated with vitamin D supplementation

in Taiwanese infants. Sci Rep, 11(1), 2856. (SCI, 2021 IF: 4.38)

9. Zhongyan Li, Siyu Chen, **Jhih-Hua Jhong**, Yuxuan Pang, Kai-Yao Huang, Shangfu Li and Tzong-Yi Lee, (2021). UbiNet 2.0: a verified, classified, annotated and updated database of E3 ubiquitin ligase-substrate interactions. Database (Oxford), 2021. (SCI, 2021 IF: 3.451)

10. Chia-Ru Chung, **Jhih-Hua Jhong**, Zhuo Wang, Siyu Chen, Yu Wan, Jorng-Tzong Horng and Tzong-Yi Lee*, 2017, "Characterization and Identification of Natural Antimicrobial Peptides on Different Organisms", International Journal of Molecular Sciences, 21(3), 986. (SCI, 2020 IF: 5.924)

11. **Jhih-Hua Jhong**, Yu-Hsiang Chi, Wen-Chi Li, Tsai-Hsuan Lin, Kai-Yao Huang, and Tzong-Yi Lee, 2019, "dbAMP: an integrated resource for exploring antimicrobial peptides with functional activities and physicochemical properties on transcriptome and proteome data", Nucleic Acids Research 2018 Oct. 31, Vol. 47(D1):D285-D297. (SCI, 2018 IF:**16.971**; 8/295 in BIOCHEMISTRY & MOLECULAR BIOLOGY)

12. Kai-Yao Huang†, Tzu-Hao Chang†, **Jhih-Hua Jhong**, Yu-Hsiang Chi, Wen-Chi Li, Chien-Lung Chan, K. Robert Lai and Tzong-Yi Lee*, 2017, "Identification of natural antimicrobial peptides from bacteria through metagenomic and metatranscriptomic analysis of high-throughput transcriptome data of Taiwanese oolong teas", BMC Systems Biology, Vol. 11 (Suppl 7):131. (SCI, 2016 IF:2.048; 11/57 in MATHEMATICAL & COMPUTATIONAL BIOLOGY)

13. Kai-Yao Huang, Min-Gang Su, Hui-Ju Kao, Yun-Chung Hsieh, **Jhih-Hua Jhong**, Kuang-Hao Cheng, Hsien-Da Huang, Tzong-Yi Lee*, 2016, "dbPTM 2016: ten-year anniversary of a resource of post-translational modification of proteins", Nucleic Acids Research 2016 Jan. 4, Vol. 44(D1):D435-D446. (SCI, 2017 IF: **16.971**; 8/295 in BIOCHEMISTRY & MOLECULAR BIOLOGY)

14. Chien-Hsun Huang, Min-Gang Su, Hui-Ju Kao, **Jhih-Hua Jhong**, Shun-Long Weng and Tzong-Yi Lee*, 2016, "UbiSite: Incorporating two-layered machine learning method with substrate motifs to predict ubiquitin-conjugation site on lysines", BMC Systems Biology, Vol. 10 (Suppl 1):6. (SCI, 2016 IF: 2.048; 11/57 in MATHEMATICAL & COMPUTATIONAL BIOLOGY)

- Conference Paperrs (*: presenter)

1. Kai-Yao Huang†, Tzu-Hao Chang†, **Jhih-Hua Jhong***, Yu-Hsiang Chi, Wen-Chi Li, Chien-Lung Chan, K. Robert Lai and Tzong-Yi Lee, 2017, "Identification of natural antimicrobial peptides from bacteria through metagenomic and metatranscriptomic analysis of high-throughput transcriptome data of Taiwanese oolong teas", The 16th International Conference on Bioinformatics (InCoB 2017). **Best Paper Awards (Gold Awards)**

2. Chien-Hsun Huang, Min-Gang Su, Hui-Ju Kao, **Jhih-Hua Jhong**, Shun-Long Weng and Tzong-Yi Lee*, 2016, "UbiSite: Incorporating two-layered machine learning method with substrate motifs to predict ubiquitin-conjugation site on lysines", The Fourteenth Asia Pacific Bioinformatics Conference (APBC 2016).

Experiences of Project

參與研究計畫

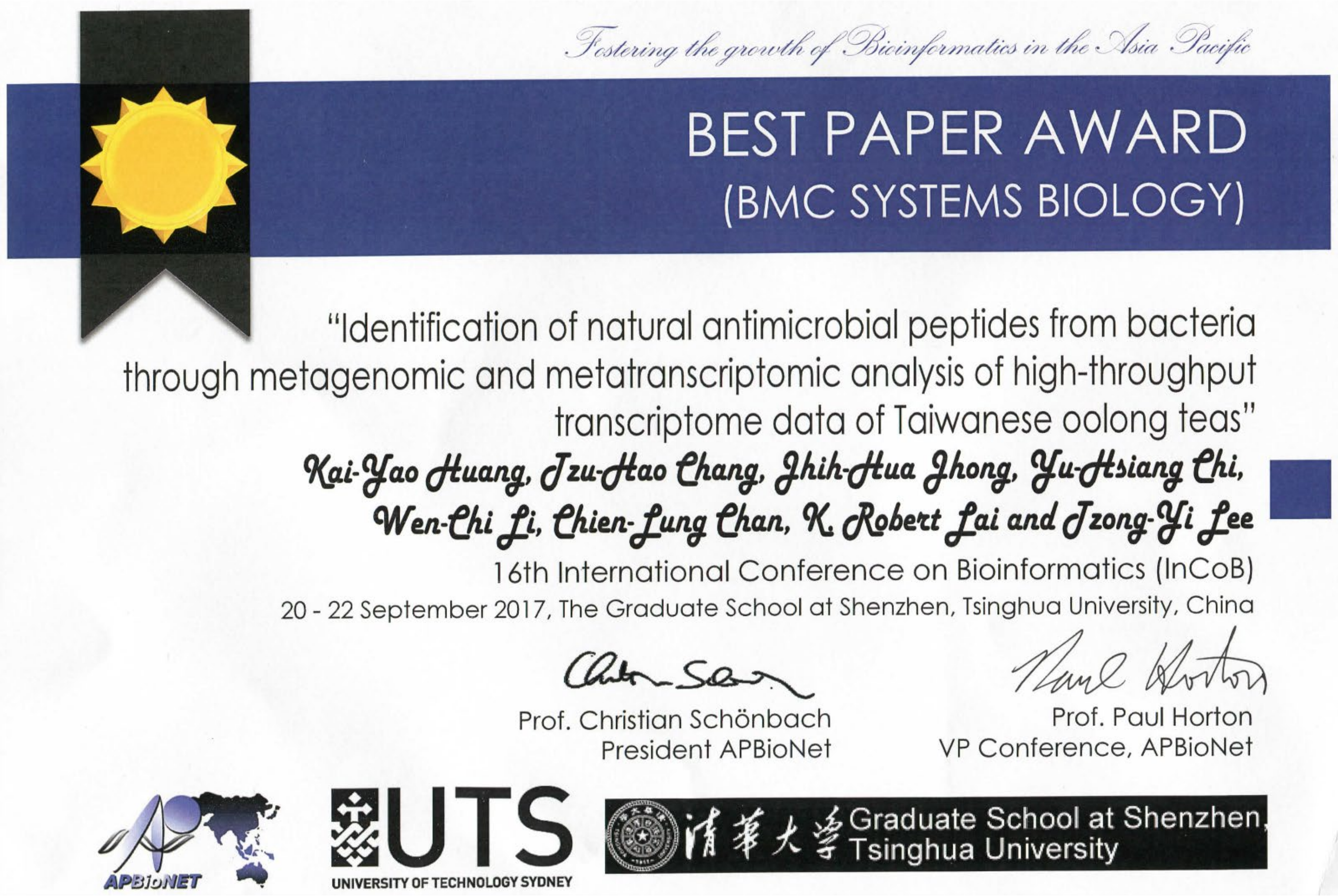
科技部 研究計畫	● RD1060118, 透過病毒基因體之大數據分析發現人類乳突病毒不同型別之微小核醣核酸 ● RD1060318, 利用次世代定序技術進行功能性益生菌之全基因體定序與基因註解 ● RD1040115, 蛋白質醣基化之結構分析、調控網路與藥物設計 ● RD1030085, 結合生物資訊方法與蛋白質譜實驗研究大腸癌亞硝基化與一氧化氮訊息傳遞網路
科技部 產學合作計畫	● 景岳生物科技公司 利用次世代定序技術進行功能性益生菌之全基因體定序與基因註解

分析實作經驗

次世代定序分析 RNA Sequencing Analysis (NGS)	● 利用 NGS 資料建置環境微生物物種檢測平台 ● 建立人體微生物群落分析之整合系統 ● 總體基因體學及總體轉錄體學(微生物群集分析) ● 台灣茶葉環境微生物物種檢測及轉錄體分析 ● 台灣健康新生兒腸道菌群宏基因組分析 ● HPV 病毒影響女性生殖系統宏基因組分析 ● 鑑定 IL-4 誘導巨噬細胞極化的藥理抑製劑和活化劑
蛋白質序列分析 Protein Sequence Analysis	● 開發蛋白質泛素化(Ubiquitination)位置預測工具 ● 開發 UbiNet 人類泛素化蛋白質調控網路分析工具
生醫資料庫建置 Biological Database	● 建置 dbPTM 蛋白質後轉譯修飾作用資料庫 ● 建置 dbAMP 抗菌肽功能活性和理化性質整合資料庫
第三代定序分析 Oxford Nanopore Sequence	● 開發結合次世代及第三代定序全基因定序與基因註解平台 ● LP-33 益生菌全基因定序與基因註解

Awards

1. 最佳論文獎(金獎) – 台灣烏龍茶微生物相與抗菌蛋白檢測分析



Fostering the growth of Bioinformatics in the Asia Pacific

BEST PAPER AWARD
(BMC SYSTEMS BIOLOGY)

"Identification of natural antimicrobial peptides from bacteria through metagenomic and metatranscriptomic analysis of high-throughput transcriptome data of Taiwanese oolong teas"

Kai-Yao Huang, Tzu-Hao Chang, Jhih-Hua Jhong, Yu-Hsiang Chi, Wen-Chi Li, Chien-Lung Chan, K. Robert Lai and Tzong-Yi Lee

16th International Conference on Bioinformatics (InCoB)
20 - 22 September 2017, The Graduate School at Shenzhen, Tsinghua University, China

Prof. Christian Schönbach
President APBioNet

Prof. Paul Horton
VP Conference, APBioNet

APBioNET

UTS
UNIVERSITY OF TECHNOLOGY SYDNEY

清華大學 Graduate School at Shenzhen, Tsinghua University

Training

1. 精準醫療教育訓練課程

「110 年精準醫療教育訓練系列課程」

訓練證明書

學員 鍾智樺 君

參加本院於中華民國 110 年 06 月 19 日舉辦之「110 年精準醫療教育訓練課程-婦癌精準醫療最新趨勢研習會」，共計 3 小時，特頒此證，以資證明。

財團法人國家衛生研究院

院長 梁賡義

中華民國 110 年 06 月 19 日

2. LDT 資深實驗室開發檢測人員訓練課程

施行實驗室開發檢測之實驗室人員訓練課程學分證明

茲證明 鍾智樺 君

參加 110 年 11 月 14 日

實驗室開發檢測之資深實驗室人員訓練課程

專任檢測開發、分析、校正、生物資訊處理及其他相關人員

教育訓練總時數 8 小時

特頒此証，以資證明。

主辦單位：台灣精準醫療及分子檢測產業協會

合辦單位：社團法人台灣精準醫學會

協辦單位：台灣病理學會

台灣精準醫療及分子檢測產業協會

西元 2021 年 11 月 26 日

證書編號：精準醫療產協證第 20211126130