



Dr. Chan Chon Kit, Kenneth

Department of Digital and Intelligent Technology

Assistant Professor | Master's Supervisor

Biography

Dr. Kenneth Chan is a senior expert in Bioinformatics and Artificial Intelligence (AI) with over 20 years of experience across academia and industry. He specializes in large-scale genomic data analysis and possesses a 30-year background in software development and systems architecture. Dr. Chan has an established track record in leading multidisciplinary teams to manage complex projects in AI-driven agriculture, environmental microbiology, and translational medicine. He currently focuses on applying deep learning models to multi-omics data to drive innovation in precision medicine and smart breeding.

Working Experience (including Postdoctoral)

- Assistant Professor, Macau Millennium College
- Senior Administrative Officer, University of Macau
- Visiting Lecturer, University of Macau
- Bioinformatics Manager, AGRF, Australia
- Senior Research Fellow, UWA/UQ, Australia
- Bioinformatics Scientist/Data Manager, Monsanto, Beijing
- Business Analyst, Objectiva, Beijing
- Software Development Engineer, Microsoft, Beijing

Education Background

- PhD in Engineering (Specializing in Machine Learning & Bioinformatics), University of Melbourne
- Bachelor of Mechatronics (First Class Honours), University of Melbourne
- Bachelor of Computer Science, University of Melbourne

Research Interests

Bioinformatics, Generative AI, Multimodal Large Models, Smart Agriculture, Metagenomics, Translational Medicine

Teaching Courses

Master's and Doctoral courses in Artificial Intelligence

Honors & Awards

Melbourne Research Scholarship, Universitas 21 Research Mobility Scholarship

Social Service

Managed national bioinformatics platforms at AGRF, facilitating resource sharing between academia and industry

Research Outputs

JOURNAL PUBLICATIONS

1. Nie S, Li F., Li R., Wang J., Ma Y., Chan C-KK*, Zhao J.*, Hu H.*, Challenges in bringing pangenome research into breeding: a case study in rice, Plant Biotechnology Journal, Feb. 2026, doi: 10.1111/pbi.70591 *co-corresponding author (IF:10.5)
2. Huerlimann R, Cowley JA, Wade NM, Wang Y, Kasinadhuni N, Chan C-KK, et al. Genome assembly of the Australian black tiger shrimp (*Penaeus monodon*) reveals a novel fragmented IHHNV EVE sequence. G3 Genes|Genomes|Genetics. 2022;12. doi:10.1093/G3JOURNAL/JKAC034. (IF: 3.154)
3. Liu H, Mullan D, Zhao S, Zhang Y, Ye J, Wang Y, Zhang A, Zhao X, Liu G, Zhang C, Chan K, Lu Z, Yan G (2022). Genomic regions controlling yield-related traits in

spring wheat: a mini review and a case study for rainfed environments in Australia and China. *Genomics*, 114 (2), 110268.

<https://doi.org/10.1016/J.YGENO.2022.110268> (IF = 5.736)

4. Schliebs O, Chan CKK, Bayer PE, Petereit J, Singh A, Hassani-Pak K, Batley J, Edwards D(2021). Daisychain: Search and Interactive Visualisation of Homologs in Genome Assemblies. *Agronomy* 2021, Vol. 11, Page 2587, 11(12), 2587. <https://doi.org/10.3390/AGRONOMY11122587> (IF: 2.24)

5. Yuan Y, Bayer PE, Anderson R, Lee HT, Chan CKK, Zhao R, Batley J, Edwards D. RefKA: A fast and efficient long-read genome assembly approach for large and complex genomes, *bioRxiv* 2020.04.17.035287; doi: <https://doi.org/10.1101/2020.04.17.035287>

6. Scheben A, Verpaalen B, Lawley CT, Chan CKK, Bayer PE, Batley J, et al. CropSNPdb: a database of SNP array data for Brassica crops and hexaploid bread wheat. *Plant J.* 2019;98:142 – 52. doi:10.1111/tpj.14194. (IF: 5.775)

7. Chan CKK, Rosic N, Lorenc MT, Visendi P, Lin M, Kaniewska P, et al. A differential k-mer analysis pipeline for comparing RNA-Seq transcriptome and meta-transcriptome datasets without a reference. *Funct Integr Genomics.* 2019;19:363 – 71. doi:10.1007/s10142-018-0647-3. (IF: 2.745)

8. Bayer PE, Golicz AA, Tirnaz S, Chan CKK, Edwards D, Batley J. Variation in abundance of predicted resistance genes in the Brassica oleracea pangenome. *Plant Biotechnol J.* 2019;17:789 – 800. doi:10.1111/pbi.13015. (IF: 8.154)

9. Scheben A., Chan CKK, Mansueto L., Mauleon R., Larmande P, Alexandrov N., Wing RA, McNally KL, Quesneville H. Edwards D., Progress in single-access information systems for wheat and rice crop improvement, *Briefings in Bioinformatics*, Volume 20, Issue 2, March 2019, Pages 565 – 571, <https://doi.org/10.1093/bib/bby016> (IF: 8.990)

10. Hurgobin B, Golicz AA, Bayer PE, Chan CKK, et al. Homoeologous exchange is a major cause of gene presence/absence variation in the amphidiploid Brassica napus. *Plant Biotechnol J.* 2018;16(7):1265 – 1274. doi:10.1111/pbi.12867. (IF: 6.840)

11. Yuan Y, Bayer PE, Scheben A; Chan CKK and Edwards D: BioNanoAnalyst: A visualisation tool to assess genome assembly quality using BioNano data. *BMC Bioinformatics.* 2017;18 1:323. doi:10.1186/s12859-017-1735-4. (IF: 2.448)

12. Lim DKY, Schuhmann H, Thomas-Hall SR, Chan CKK, Wass TJ, Aguilera F, Adarme-Vega TC, Dal' Molin CGO, Thorpe GJ, Batley J, Edwards D, Schenk PM: RNA-Seq and metabolic flux analysis of *Tetraselmis* sp. M8 1 during nitrogen starvation reveals a 2 two-stage lipid accumulation mechanism. *Bioresource Technology.* 2017; doi:<http://dx.doi.org/10.1016/j.biortech.2017.06.003> (IF: 5.651)

13. Bayer PE, Hurgobin B, Golicz A, Chan CKK, Yuan Y, Lee HT, Renton M, Meng J,

Li R, Long Y, Zou J, Bancroft I, Chalhoub B, King G, Batley J, Edwards D: Assembly and comparison of two closely related *Brassica napus* genomes. *Plant Biotechnology Journal*. 2017; doi:10.1111/pbi.12742. (IF: 6.305)

14. Montenegro JDM, Golicz AA, Bayer PE, Hurgobin B, Lee HT, Chan CKK, Visendi P, Lai K, Doležel J, Batley J, Edwards D: The pan-genome of modern hexaploid bread wheat. *The Plant Journal*. 2017, doi:10.1111/tpj.13515 (IF: 5.901) 1/4

15. Golicz AA, Bayer PE, Barker GC, Edger PP, Kim H, Martinez PA, Chan CKK, Severn-Ellis A, McCombie WR, Parkin IAP et al: The pan-genome of an agronomically important crop plant *Brassica oleracea*. *Nature Communications* 2016, 7:13390. (IF: 12.124)

16. Lee H, Golicz AA, Bayer PE, Jiao Y, Tang H, Paterson AH, Sablok G, Krishnaraj RR, Chan CKK, Batley J, Edwards D: The Genome of a Southern Hemisphere Seagrass Species (*Zostera muelleri*). *Plant Physiol* 2016, 172(1):272-283. (IF: 6.280)

17. Visendi P, Berkman PJ, Hayashi S, Golicz AA, Bayer PE, Ruperao P, Hurgobin B, Montenegro J, Chan CKK, Staňková H et al: An efficient approach to BAC based assembly of complex genomes. *Plant Methods* 2016, 12:2. (IF: 4.140)

18. Kaniewska P, Chan CKK, Kline D, Ling EYS, Rosic N, Edwards D, Hoegh-Guldberg O, Dove S: Transcriptomic Changes in Coral Holobionts Provide Insights into Physiological Challenges of Future Climate and Ocean Change. *PLoS ONE* 2015, 10(10):e0139223. (IF: 2.806)

19. Bayer P, Ruperao P, Mason A, Stiller J, Chan CKK, Hayashi S, Long Y, Meng J, Sutton T, Visendi P et al: High-resolution skim genotyping by sequencing reveals the distribution of crossovers and gene conversions in *Cicer arietinum* and *Brassica napus*. *Theor Appl Genet* 2015:1-9. (IF: 3.264)

20. Golicz AA, Schliep M, Lee HT, Larkum AWD, Dolferus R, Batley J, Chan CKK, Sablok G, Ralph PJ, Edwards D: Genome-wide survey of the seagrass *Zostera muelleri* suggests modification of the ethylene signalling network. *Journal of Experimental Botany* 2015. (IF: 5.830)

21. Rosic N, Kaniewska P, Chan CKK, Ling E, Edwards D, Dove S, Hoegh-Guldberg O: Early transcriptional changes in the reef-building coral *Acropora aspera* in response to thermal and nutrient stress. *BMC Genomics* 2014, 15(1):1052. (IF: 3.729)

22. Rosic N, Ling EYS, Chan CKK, Lee HC, Kaniewska P, Edwards D, Dove S, Hoegh-Guldberg O: Unfolding the secrets of coral-algal symbiosis. *ISME J* 2014. (IF: 9.302)

23. Ruperao P, Chan CKK, Azam S, Karafiátová M, Hayashi S, Čížková J, Saxena RK, Šimková H, Song C, Vrána J et al: A chromosomal genomics approach to assess and validate the desi and kabuli draft chickpea genome assemblies. *Plant Biotechnology Journal* 2014, 12(6):778-786. (IF:5.752)

24. Lai K, Lorenc MT, Lee HC, Berkman PJ, Bayer PE, Visendi P, Ruperao P, Fitzgerald TL, Zander M, Chan CKK et al: Identification and characterization of more than 4 million intervarietal SNPs across the group 7 chromosomes of bread wheat. *Plant Biotechnology Journal* 2014, doi:10.1111/pbi.12240. (IF: 5.752)
25. Chan CKK, Halgamuge SK: A New Generalized Growth Threshold for Dynamic SOM for Comparing Average Mutual Information and Oligonucleotide Frequency as a Species Signature. *International Journal of Bio-Science and Bio-Technology (IJBSBT)*, Vol. 1, No. 1, Dec 2009, Pg1~10
26. Chan CKK, Hsu AL, Halgamuge SK, Tang S-L: Binning sequences using very sparse labels within a metagenome. *BMC Bioinformatics* 2008, 9(215): doi:10.1186/1471-2105-1189-1215. (IF:2.448)
27. Chan CKK, Hsu AL, Tang S-L, Halgamuge SK: Using Growing Self-Organising Maps to Improve the Binning Process in Environmental Whole-Genome Shotgun Sequencing. *Journal of Biomedicine and Biotechnology* 2008, vol. 2008, Article ID 513701:10 pages. doi:10.1155/2008/513701. (IF: 2.476)
28. Guru SM, Fernando S, Halgamuge SK, Chan CKK: Intelligent fastening with A-BOLT Technology and Sensor Network. *Assembly Automation* 2004, 24(4):386-393.

BOOK CHAPTER PUBLICATION

1. Yuan, Y., Scheben, A., Chan, CKK, Edwards, D. (2017). Databases for Wheat Genomics and Crop Improvement. In *Methods in molecular biology* (Clifton, N.J.) (Vol. 1679, pp. 277 – 291). https://doi.org/10.1007/978-1-4939-7337-8_18
2. Ghosh S, Chan CKK: Analysis of RNA-Seq Data Using TopHat and Cufflinks. In: *Plant Bioinformatics: Methods and Protocols*. Edited by Edwards D. New York, NY: Springer New York;2016: 339-361.
3. Tseng C-H, Chan CKK, Hsu AL, Halgamuge SK, Tang S-L: Binning Sequences Using Very Sparse Labels Within a Metagenome. In: *Encyclopedia of Metagenomics*. Edited by Nelson EK. New York, NY: Springer New York; 2013: 1-13.
4. Tseng C-H, Chan CKK, Hsu AL, Halgamuge SK, Tang S-L: Binning Metagenomic Sequences Using Seeded GSOM. In: *Handbook of Molecular Microbial Ecology I*. John Wiley & Sons, Inc.;2011: 369-378. 2/4

CONFERENCE PUBLICATIONS

1. Chan CKK, Halgamuge S.K.: Investigation of Average Mutual Information for Species Separation using GSOM. In: *Future Generation Information Technology (FGIT 2009)*, pp. 42-49. *Lecture Notes in Computer Science*, Springer, Jeju Island, Korea (2009)
2. Chan CKK, Hsu AL, Tang S-L, Halgamuge SK: A method for evaluating quality of clustering DNA fragments encoded in different nucleotide frequencies. In: 2007

Frontiers in the convergence of bioscience and information technologies (FBIT 2007): 11-13 Oct 2007; Jeju Island, Korea; 2007: 60-63.

3. Reinhard J, Chan CKK, Halgamuge SK, Tang S-L, Kruse R: Region Identification on a Trained Growing Self-Organizing Map for Sequence Separation between Different Phylogenetic Genomes. In: BIOINFO 2005: 22-24 Sep 2005; Busan, Korea: KAIST PRESS; 2005: 124-129.

4. Chan CKK, Kansara N, Mirbagheri M, Guru SM, Halgamuge SK, Fernando S: Development of hybrid interface for intelligent sensor management. In: HIS03: Dec 14-17 2003; Melbourne, Australia: IOS Press; 2003: 820-829. 5. Chan CKK, Lam G, Guru SM, Halgamuge MN, Fernando S: Development of a SMARTBOLT prototype with energy model for clustered sensor systems. In: FSKD'02: Nov 18-22 2002; Singapore; 2002: 280-284.

POSTER/ABSTRACT PUBLICATIONS

1. Kasinadhuni K, Noune C, Crockett J, Chan K: Taxonomy characterization of ZymoBIOMICS microbial community controls (D6311) on different Illumina NovaSeq read lengths using various metagenomics tools. In: 41st Lorne Genome Conference, Feb 16, Lorne, Victoria, Australia (2020)

2. Jabbari J, Kasinadhuni N, Stevens M, Siemering K, Chan K: Comparison of microbial community diversity inference by sequencing full-length and variable regions of the 16S rRNA gene using different PCR approaches on PacBio Sequel and Illumina MiSeq. In: AGTA 2019, Oct 7-9, Melbourne, Australia (2019)

3. Kasinadhuni K, Noune C, Crockett J, Chan K: Evaluation of internal controls on V1-V3 & V3-V4 primer sequences across various AGRF nodes on different MiSeq machines. In: AGTA 2018, Nov 4-7, Adelaide, Australia (2018)

4. Bayer PE, Chan CKK, Lee HT, Yuan Y, Edwards D: A fast long-read assembly method for the wheat genome. In: PAG XXVI Conference, Jan 13-17, San Diego, CA, USA (2018)

5. Chan K, Bayer P, Davey R, Alaux M, Pommier C, et al.: Development of WheatIS and collaboration between plant information systems. In: PAG XXV Conference, Jan 14-18, San Diego, CA, USA (2017)

6. Kaur P, Chan CKK, Bayer PE, Edwards D, Erskine W: TrifoliGATE Subterranean Clover Genomic Resources: Building A Comprehensive User-Friendly Platform For Future Forage Legume Breeding. In ICLGG 2017, Sep 18-22, Siófok, Hungary (2017)

7. Ruperao P, Bayer P, Chan CKK, Hayashi S, Roorkiwal M, et al.: Constructing improved chickpea genome assemblies using skimGBS. In: InterDrought-V, Feb 21-25, Hyderabad, India (2017)

8. Golicz A, Bayer PE, Barker G, Edger P, Kim HR, Martinez P, Chan CKK, et al.:

The Pangenome of *Brassica oleracea*. In: PAG XXV Conference, Jan 14-18, San Diego, CA, USA(2017)

9. Lee HT, Golicz A, Bayer PE, Jiao Y, Paterson AH, Tang H, Sablok G, Krishnaraj R, Chan CKK, et al.: The Genome of a Southern Hemisphere Seagrass Species (*Zostera muelleri*). In: PAG XXV Conference, Jan 14-18, San Diego, CA, USA (2017)

10. Montenegro J, Lee HT, Hurgobin B, Visendi P, Chan K, et al.: Improved methods for reassembly and analysis of the 17 Gb bread wheat genome. In PAG XXIV Conference, Jan 9-13, San Diego, CA, USA (2016)

11. Bayer P, Ruperao P, Montenegro J, Chan K, Sutton T, et al.: Improving genome assemblies and capturing genome variation data for applied crop improvement. In: PAG Asia 2015, Jul 13-15, Singapore (2015)

12. Golicz AA, Schliep M, Lee HT, Bayer PE, Larkum AWD, Dolferus R, Batley J, Chan CKK, et al.: Genomic characterisation of seagrass (*Zostera muelleri*), a plant adapted to life in the submerged marine environment. In: PAG Asia 2015, Jul 13-15, Singapore (2015)

13. Montenegro MD, Hurgobin B, Golicz A, Martinez P, Muhindira PV, Lee J, Bayer PE, Ruperao P, Chan K, et al.: Wheat genome assessment and reassembly. In: PAG Asia 2015, Jul 13-15, Singapore (2015)

14. Golicz A, Smits L, Chan K, Schliep M, Dolferus R, et al.: Genomic characterisation of seagrass (*Zostera muelleri*), a plant adapted to life in the submerged marine environment. In: PAG XXII Conference, Jan 10-15, San Diego, CA, USA (2014) 3/4

15. Ruperao P, Bayer P, Chan CKK, Azam S, Karafiátová M, et al.: A chromosomal genomics approach to assess and validate the desi and kabuli draft chickpea genome assemblies. In: PAG XXII Conference, Jan 10-15, San Diego, CA, USA (2014)

16. Bayer PE, Lorenc M, Martinez P, Chan K, Visendi P, et al.: Genome assembly validation and trait association using skim based genotyping by sequencing in canola. In: PAG XXII Conference, Jan 10-15, San Diego, CA, USA (2014)

17. Visendi P, Stankova H, Hayashi S, Berkman P, Chan K, et al.: An optimised approach to sequence and assemble BACs: application to bread wheat chromosome arm 7DS. In: PAG XXII Conference, Jan 10-15, San Diego, CA, USA (2014)

18. Zander MM, Patel DA, Wouw AVd, Lai K, Lorenc MT, Hayward AC, Golicz A, Chan K, et al.: New Insights into the Genome of the Plant Pathogen, *Leptosphaeria maculans*. In: PAG XXII Conference, Jan 10-15, San Diego, CA, USA (2014)

19. Tollenaere R, Alamery S, Saad NSM, Hayward AC, Bayer PE, Dalton-Morgan J, Chan K, et al.: Identification and Characterisation of Candidate Genes for Blackleg Resistance in *Brassica napus* Using Next Generation Sequencing. In: PAG XXII Conference, Jan 10-15, San Diego, CA, USA (2014)

20. Batley J, Tollenaere R, Alamery S, Saad NSM, Hayward AC, Bayer PE, Dalton-Morgan J, Chan K, et al.: Identification and Characterisation of Candidates for Blackleg Resistance QTLs in Brassica napus Using Next Generation Sequencing. In: PAG XXII Conference, Jan 10-15, San Diego, CA, USA (2014)
21. Lim DKY, Schuhmann H, Thomas-Hall SR, Chan K, Edwards D, et al.: Identifying the bottlenecks of microalgal lipid production: a new transcriptional profiling approach. In: IMBC 2013, Nov 11-15, Brisbane Australia (2013)
22. Chan CKK, He K, Lv L, Wu X, Sun J., et al.: In-house rice genome browser. In: TCM 2010 (Monsanto internal conference), Jun 08-11, St. Louis, MO, USA (2010)
23. Sun J, Chan CKK, Tao N, Blanchard M, Cao Y: TE-Viewer: A visualization tool for examine molecular quality of transgenic events in our biotech plant testing pipeline. In: TCM 2010 (Monsanto internal conference), Jun 08-11, St. Louis, MO, USA (2010)
24. He K, Chan CKK, Lv L, Sun J, Wu X, et al.: Visualizing Genomic Data: a survey of publicly available genome browsers and recommendations for Monsanto implementation. In: TCM 2010 (Monsanto internal conference), Jun 08-11, St. Louis, MO, USA (2010)
25. Zhang R, Lv L, Chan CKK, Sun J, He K, et al.: GE-Atlas: A graphical visualization tool for viewing and mining gene expression patterns. In: TCM 2010 (Monsanto internal conference), Jun 08-11, St. Louis, MO, USA (2010)
26. Guru SM, Chan CKK, Halgamuge SK: Advanced Networked Sensor System. In: Knowledge Commercialisation Australasia Forum & Fair of Ideas, Mar 26-28, Sydney, Australia (2003)